

Identifier: AAH51470 DNA Sequence 1001 BP
 Release Info: Derwent Geneseq Database Release No. 200124; Date released 26-NOV-01
 Database XReference: WPI; 2000-638353/61.
 Accession Number: AAH51470
 Patent Title: Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping -
 Patented by: (GEST) GENSET.
 Inventor: Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A
 Description: Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 361.
 Patent Number: WO200058508-A2
 Patent Publication Date: 05-OCT-2000
 Modification Date: 29-AUG-2001 (first entry)
 Local Filing: 24-MAR-2000; 2000WO-IB00403
 Priority: 25-MAR-1999
 Abstract: Sequences AAH51110-AAH51593 represent human DNA fragments which contain biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSTII), malate decarboxylase enzyme (DME1/ME1), cytochrome P450, glutathione reductase/synthase (GSHR/GSHS), flavin-containing monooxygenases (FMO), gamma-glutamyltransferase 5 (GGT5), dipeptidase (DP), glucose 6-phosphate dehydrogenase (G6PDH), phosphogluconate dehydrogenase (PGDH), and uridine diphosphate glucuronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drug metabolism. Sequences AAH51594 - AAH51598 represent the genomic sequence of the MGSTII gene and four alternative MGSTII cDNA sequences. AAB62905-AAB62906 are MGSTII gene products. PCR primers AAH51599 and AAH51600 are used in an example for the amplification of human genomic DNA fragments. The invention includes a method of genotyping comprising determining the identity of a nucleotide at a DME- or MGSTII-related biallelic marker in a biological sample. The method is used to determine the frequency in population of an allele of a DME- or MGST-II related biallelic marker and to select an individual for inclusion in a clinical trial of a drug treatment. The method is also used to detect association between allele and phenotype, and to detect association between haplotype and phenotype. The polynucleotides are used, in hybridization assays, sequencing assays or allele specific amplification assays. The method can be used to determine whether an individual suffers or is at risk of developing asthma or is at risk of developing hepatotoxicity on treatment with zileuton.

KeyWords: Human;biallelic marker;single nucleotide polymorphism;SNP;MGSTII;microsomal glutathione S-transferase II;malate decarboxylase enzyme;DME1;ME1;cytochrome P450;glutathione reductase;GSHR;GSHS;GGT5;flavin-containing monooxygenase;FMO;gamma-glutamyltransferase 5;dipeptidase;DP;glucose 6-phosphate dehydrogenase;G6PDH;haplotype;phosphogluconate dehydrogenase;PGDH;drug metabolism;phenotype;uridine diphosphate glucuronosyl transferase;UGT2;asthma;hepatotoxicity;zileuton;ds.

Organism Homo sapiens.

Sequence Composition: Sequence 1001 BP; 331 A; 177 C; 153 G; 300 T; 40 other;

Sequence: >AAH51470 WO200058508-A2 PA (GEST) PR 25-MAR-1999 PF 24-MAR-2000 Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 361. [Homo sapiens.]
 NNNNTNNNGTGNNNNNNNNNNNCTNNNNANANNNNNNANANNNNCCNNNNGAAGAAAGGC
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 AGAGTTCCTCACATGCAGTTAGAAATAGCACATCAATTTAACAGTGTGATTTTCAGGGCAA
 TAGGTGTTCCACCTAAACAATNAACCTGAAAGGTACAATTATTCAACAACCTAACTATAAA

CTCTACAATTCCATGTGATAAATGAGACTCCCAAGACTGATTCATAAAAAATTCCAAATCA
CAATACTAGACTCAGGAATGTCAGTGATTCTTAACCACCAGCTTTTATTTTCATTTTTTG
AAAACTACTGGAAAACTCTGACAACTTTAAGTGAAGCATAAAGCATTGTAGAGGAACA
TAAATGTAGATATAAAATTATCCCAACTGTGAATAGCTTTTCCTCAGTGCTCATATTTAG
GGAAGTAGACCACTAATGKCTTCAAACCTAAAAGAATTCTACAGAAAACCTGCCTGAAATA
AACACAAGTGATTTAGTAGAACAAAAATATAGGATTAAAGCCTAGTGGTGCCACTTTTCC
AAGAAGTTATATTAGTAATTATAGTATTATAAGTGAAGAGTCTGGGTATATTTTTTCACA
TTATCTCCCTGACTACAATGTAATAGCTCCATTTCTTTTCTCCATTACACACATGCAGAC
ACATACATACATATACACACATATTTACACAAATATCCTTAACAGAGGCCAACTATCTCA
AATATCTTCTTGCAAAGAACTGAGTGATTGAGTCAGTTAAAAAATATTATTTACTCCAA
TAATTCCTCAAAATACTTGATTTTCTCTCTTTAATATTTGGTACCAGTTCTTTAGTAGTG
CCTGCTGTGGTGATACTCTTTTGTGATTAAACAATTTTTTTTTTTCACAGGAAATGGAGGAG
TTTGTACAGAGCTCTGGAGAAAATGGTGTTGTGGTGTTTTC

Identifier: AAH51513 DNA Sequence 1001 BP
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 Patented by: (GEST) GENSET.
 Inventor: Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A
 Description: Human UGT2B10 related DNA containing a biallelic polymorphism SEQ ID 404.
 Patent Number: WO200058508-A2
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 Organism Homo sapiens.
 Sequence Composition: Sequence 1001 BP; 346 A; 157 C; 147 G; 343 T; 8 other;
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 CATTAGTCCAACTGGAAANTCTTGTTATTAANGTTTTGCAGTCTGAAGTCACACCACCATA
 TAGCCTTCAGTTACATCTCCAACACAAGTACCTGTTTTTNCCTCTGAAATCTGAAAAGT
 AATAGCAAATTAGTTCAGTGTGTTATCTAGAAAACACTGTCACTTTCAGAGCCTTTTCATT
 GTGCATCTCATTTTATTCCTATGAATAATTTNTGCTAAAATTCATCCAATCCTAGGTCAT

CCAAAAACCAGAGCTTTTATAACTCATGGTGGAGCCAATGGCATCTATGAGGCAATCTAC
CATGGGATCCCTATGGTGGGCATTCCATTGTTTTTTNGATCAACCTGATAATATTGCTCA
CATGAAGGCCAAGGGAGCAGCTGTTAGAGTGGACTTCAACACAATGTCGAGTACAGACCT
GCTGAATGCACTGAAGACAGTAATTAATGATCCTTCGTGAGTAGAACAATATTTTCACT
AGATGGTATTAATAGATAGCTTYTCTTGTCAGTAGTGAGNCATGAGTTTCATCCTTTTAA
TAAGAGAGTGATTTTGAAAGAATTTAAATGATTTAACCAATCCGAAATCTGCTTTTACTT
TTTATCTGTTATTTAAAAATTGTATTTGAACCCCATACATCTAATGAGTAACCAGTTAGT
NGAAACAGTTTTCTAAATAAAAAATAATTTTAAATGATATAGATAATATAAAAAAATACA
TTTCTTAAAAATTTGACATAATGAATCCATAGTAGAAAGGAAGAATAATCTTGAAATAAT
ATAATAAAATGTTTTAATTAAATATCTAAATGTCTCAGAATATAACTATTTTCTTGCAG
AAAAATTAATTTTTATTATTATCTTTATTGTAACAGACTTGAAAATGAGATTTAATTTTG
ATAGCATAAAACCCACCTATTTATGGCAAAAATTCCAAATATTTTACTATGTTTACAGA
GTCATGAAGTCATCACCAGTGTATAAGTTTGGAACATTTTT



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(21) International Application Number: PCT/IB00/00403 (22) International Filing Date: 24 March 2000 (24.03.00) (30) Priority Data: 60/126,269 25 March 1999 (25.03.99) US 60/131,961 30 April 1999 (30.04.99) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; Intellectual Property Department, 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): BLUMENFELD, Marta [FR/FR]; 5, rue Tagore, F-75013 Paris (FR). BOUGUEL- ERET, Lydie [FR/FR]; 108, avenue Victor Hugo, F-92170 Vanves (FR). CHUMAKOV, Ilya [FR/FR]; 196, rue des Chevreuilles, F-77000 Vaux-le-Penil (FR). CO- HEN-AKENINE, Annick [FR/FR]; 76, boulevard Diderot, F-75012 Paris (FR). (74) Common Representative: GENSET; Intellectual Property De- partment, 24, rue Royale, F-75008 Paris (FR).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM (57) Abstract The invention provides polynucleotides including biallelic markers derived from genes involved in the biotransformation of xenobiotics such as drugs and from genomic regions flanking those genes. Primers hybridizing to regions flanking these biallelic markers are also provided. This invention also provides polynucleotides and methods suitable for genotyping a nucleic acid containing sample for one or more biallelic markers of the invention. Further, the invention provides methods to detect a statistical correlation between a biallelic marker allele and a phenotype and/or between a biallelic marker haplotype and a phenotype.		

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BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

FIELD OF THE INVENTION

5 The present invention is in the field of pharmacogenomics, and is primarily directed to biallelic markers that are located in or in the vicinity of genes, which have an impact on the metabolism of xenobiotics such as drugs and the uses of these markers. The present invention encompasses methods of establishing associations between these markers and a phenotype such as drug response, toxicity and susceptibility to disease. The present
10 invention also provides means to determine the genetic predisposition of individuals to such drug responses, toxicity and diseases.

BACKGROUND OF THE INVENTION

To assess the origins of individual variations in drug response, pharmacogenomics uses the genomics technologies to identify polymorphisms within genes associated with drug
15 response. In this respect, there are three main categories of genes that may theoretically be expected to be associated with drug response, namely genes linked with the targeted disease, genes related to the drug's mode of action and genes involved in the drug's metabolism. Among these genes of pharmacogenomic importance, genes coding for drug-metabolizing enzymes have a central role.

20 Drug Metabolism

Drug-metabolizing enzymes are important determinants of drug disposition, safety and efficacy. The enzyme systems involved in the metabolism and the subsequent elimination from the body of environmental chemicals, food toxins and drugs are mainly localized in the liver, although every tissue examined has some metabolic activity.

25 In order to produce its characteristic effects, a given drug must be present in appropriate concentrations at its sites of action. The absorption, distribution, biotransformation and excretion of a drug all involve its passage across cell membranes. The lipophilic characteristics of drugs that promote their passage through biological membranes and subsequent access to their site of action reduce their elimination from the
30 body. Renal excretion of unchanged drug plays only a modest role in the overall elimination of most therapeutic agents, since lipophilic compounds filtered through the glomerulus are largely reabsorbed through the tubular membranes. Biotransformation of drugs into more hydrophilic metabolites plays a major role in the termination of their biological activity and their elimination from the body. In general, biotransformation

reactions generate more polar, inactive metabolites that are readily excreted from the body. However in some cases, metabolites with potent biological activity or toxic properties are generated and may result in adverse side effects. Metabolic biotransformation of drugs can be classified as either Phase I functionalization reactions or Phase II biosynthetic reactions.

- 5 Phase I reactions introduce or expose a functional group on the parent compound, and generally result in the loss of pharmacological activity although there are some examples of retention or enhancement of activity. Phase II conjugation reactions lead to the formation of a covalent linkage between a functional group on the parent compound with glucuronic acid, sulfate, glutathione, amino acids or acetate. These highly polar conjugates are
- 10 generally inactive and are excreted rapidly in the urine and feces. Within a given cell, most drug metabolizing Phase I enzymes are located primarily in the endoplasmic reticulum, while the Phase II conjugation enzyme systems are mainly cytosolic. In some cases, drugs biotransformed through a Phase I reaction in the endoplasmic reticulum are further metabolized by conjugation in the cytosolic fraction of the same cell (Hardman J.G.,
- 15 Goodman, Gilman A., Limbird L.E.; *Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th edition, McGraw-Hill, N.Y., 1996).

Enzymes Involved in the Biotransformation of Xenobiotics

- Besides being involved in the biotransformation of drugs, drug-metabolizing enzymes are also involved in the metabolism of xenobiotics (foreign compounds) as well as
- 20 in the metabolism of endogenous compounds including steroids, vitamins and fatty acids. Foreign compounds include therapeutic agents, carcinogens, plant metabolites, environmental pollutants, foodstuffs and other dietary components as well as industrial chemicals. The biotransformation of foreign compounds (xenobiotics) is often regarded as detoxification because it usually converts compounds into more water-soluble, readily
- 25 excreted substances. This tends to decrease the exposure of the organism to the compound and therefore tends to decrease toxicity. However, in some cases the reverse occurs and a metabolite is produced which is more toxic than the parent compound. For example, drug-metabolizing enzymes may activate some carcinogens, and interindividual differences in cancer susceptibilities, have been linked to polymorphisms in drug-metabolizing enzymes.
- 30 There are many factors, which affect biotransformation and toxicity, such as the dose, availability of cofactors and the relative activity of the various drug-metabolizing enzymes. There may also be several competing pathways of metabolism – some leading to detoxification others to toxicity. Factors, such as genetic factors or environmental factors,

which influence the balance between these competing pathways, will also determine the eventual toxicity.

As mentioned above, the metabolic conversion of drugs and other xenobiotics is enzymatic in nature. The enzyme systems involved in the biotransformation of drugs are localized in the liver, although every tissue examined has some metabolic activity. Other organs with significant metabolic capacity include the kidneys, gastrointestinal tract, skin and lungs. Following non-parenteral administration of a drug, a significant portion of the dose may be metabolically inactivated in either the liver or intestines before it reaches the systemic circulation. This first-pass metabolism significantly limits the oral availability of highly metabolized drugs.

Cytochrome P450

The cytochrome P450 enzyme family is the major catalyst of biotransformation reactions. Since its origin, the cytochrome P450 gene family has diversified to accommodate the metabolism of a growing number of environmental chemicals, food toxins and drugs. The resulting superfamily of enzymes catalyzes a wide variety of oxidative and reductive reactions and has activity towards a chemically diverse group of substrates. Cytochrome P450 enzymes are heme-containing membrane proteins localized in the smooth endoplasmic reticulum of numerous tissues. Oxidative reactions catalyzed by the microsomal monooxygenase system require the cytochrome P450 hemoprotein, NADPH-cytochrome P450 reductase, NADPH, and molecular oxygen. Oxidative biotransformations catalyzed by cytochrome P450 monooxygenases include aromatic and side chain hydroxylation, N-, O-, S- dealkylation, N-oxidation, sulfoxidation, N-hydroxylation, deamination, dehalogenation, and desulfuration. Cytochrome P450 enzymes also catalyze a number of reductive reactions, generally under conditions of low oxygen tension. The only common structural feature of the diverse group of xenobiotics oxidized by cytochrome P450 enzymes is their high lipid solubility.

Twelve cytochrome P450 gene families have been identified in human beings, and a number of distinct cytochrome P450 enzymes often exist within a single cell. The cytochrome P450 1, 2 and 3 families (CYP1, CYP2, CYP3) encode the enzymes involved in the majority of all drug biotransformations, while the gene products of the remaining cytochrome P450 families are important in the metabolism of endogenous compounds such as steroids and fatty acids. CYP1A2 gene expression may play an important role in individual risk of environmental toxicity or cancer. CYP1A2 substrates include clinically important drugs such as imipramine, propranolol, paracetamol, clozapine, theophylline,

caffeine and acetaminophen. CYP1A2 is also involved in the conversion of heterocyclic amines and arylamines to their proximal carcinogenic and mutagenic forms, as well as in the metabolism of endogenous substances including estradiol and uroporphyrinogen III.

Interindividual differences in susceptibility to arylamine- and heterocyclicamine-induced
5 cancers have been linked to CYP1A2 polymorphism. CYP2C8 appears to be responsible for retinol and retinoic acid metabolism and actively catalyzes benzphetamine N-demethylation. CYP2C9 catalyzes the hydroxylation of tolbutamide, a hypoglycemic agent used in the treatment of type II diabetes mellitus, and one allelic variant of CYP2C9 accounts for the occurrence of poor metabolizers of tolbutamide. CYP2C9 may also have an important role
10 in terminating the anti-coagulant activity of warfarin. Wide spread interindividual differences in the response to warfarin have been recognized. Such variability is particularly important for drugs such as warfarin which have narrow therapeutic indices (Steward D.J. et al., *Pharmacogenetics*, 7:361-367, 1997). CYP2C9 is further involved in the oxidation of tielinic acid and several non-steroidal anti-inflammatory agents. The
15 oxidative metabolism through CYP2C9 of tilenic acid can result in the emergence of a drug induced autoimmune hepatitis. CYP3A4 is involved in the biotransformation of a majority of drugs and is expressed at significant levels extrahepatically. It is now recognized that extensive metabolism by CYP3A4 in the gastrointestinal tract is a significant factor contributing to the poor oral availability of many drugs (first-pass metabolism).
20 Barbiturates, certain steroids and macrolide antibiotics can induce this enzyme. It appears to play a central role in the metabolism of the immunosuppressive cyclic peptide cyclosporin A as well as macrolide antibiotics, such as erythromycin.

Flavin-containing monooxygenases (FMOs)

The mammalian flavin-containing monooxygenases (FMOs) are microsomal
25 enzymes that catalyze the NADPH-dependent oxygenation of a wide variety of drugs and other xenobiotics that possess a soft nucleophilic heteroatom, typically a nitrogen, sulfur, phosphorus or selenium atom. Of special clinical interest is the oxidation of trimethylamine in the liver by the FMO, because its deficiency causes the "Fish Odor Syndrome." Drugs oxidized by FMOs include, among others, antidepressant, antipsychotic-neuroleptic,
30 antihypertensive drugs. FMOs have been implicated in the detoxification but also in the metabolic activation of several different environmental toxins and carcinogens.

Unlike all other known oxidases and monooxygenases, among which the well-studied cytochrome P450 monooxygenases, FMOs have the unique property of forming a stable enzyme intermediate in the absence of an oxygenatable substrate. Because the energy

for catalysis is already present in the FMO enzyme before contact with the potential substrate, the fit of the substrate does not need to be as stringent as with the other enzymes. This feature, unique to FMOs among monooxygenases, is responsible for the wide range of substrates accepted by FMOs (including tertiary and secondary alkyl- and arylamines, many hydrazines, thiocarbamides, thioamides, sulfides, disulfides, thiols, among others), and determines that any soft nucleophilic xenobiotic accessible to the active enzyme will probably be oxidized by FMO *in vivo*. Although some FMO substrates are oxidized to less active derivatives, several soft nucleophiles are metabolized to highly reactive and potentially toxic intermediates.

10 The FMOs represent a multigene family. Five distinct mammalian FMO isoenzymes have been identified and cloned from various animal and human tissues: FMO1, FMO2, FMO3, FMO4 and FMO5. Human FMO2 and human FMOX were cloned and sequenced by the inventors as described in PCT Publication WO 9824914. FMOX represents a new member of the FMO gene family not previously identified in mammals.

15 Tissue specificity and activities of the different FMOs have been thoroughly characterized. FMO1 is known to be expressed in the human kidney but is absent from the liver. In man the enzyme is subject to developmental regulation. FMO2 is predominantly expressed in lung of all mammalian species tested. FMO3 was isolated from human liver, and accounts for the majority of FMO expressed in adult human liver.

20 Many of the FMO substrates may also be oxidized by the cytochrome P450 monooxygenases. However, the final oxidation products are usually different, and the nitrogen of a specific compound is rarely N-oxygenated by both types of monooxygenases. Today, a large number of drugs in human clinical trials contain a nitrogen, sulfur, phosphorous or some other nucleophilic functionality. Of the two major monooxygenase systems considered to be responsible for heteroatom-containing chemical and drug oxidative metabolism (CYP 450 and FMO), relatively little is known concerning the role of the FMO in human drug metabolism. Yet, given the wide range of substrates potentially oxidized by FMOs, this class of monooxygenases seems to represent a major determinant of drug safety and efficacy.

30 **Uridine diphosphate glucuronosyl transferase (UGTs)**

Glucuronidation is a major detoxification pathway of Phase II metabolism that is catalyzed by the UDP-glucuronosyl transferase family of enzymes. Glucuronidation is quantitatively the most important conjugation reaction. Members of this enzyme family catalyze the conjugation of numerous endogenous substances of widely differing structures

such as bilirubin, steroid hormones and fat-soluble vitamins. In general, xenobiotics become substrates for glucoronidation by first passing through Phase I metabolism, but many compounds do not require this step because they already possess reactive functionalities (e.g. hydroxyl, carboxyl, amino, sulfhydryl etc.) that are direct targets for glucuronosyl transferase. The human UGT genes appear to have evolved by a series of gene-duplication and gene-conversion events resulting in the emergence of a diversity of isoforms. They are divided into two families, UGT1 which is known to have bilirubin and phenol as substrates, and UGT2 which is known to have steroid, bile, and odorant as substrates, with these two families located on different chromosomes. The UGT2 family is divided into subfamilies UGT2A and UGT2B. The UGTs have different but sometimes overlapping substrate specificities. They catalyze the transfer of an activated glucuronic acid molecule to aromatic and aliphatic alcohols, carboxylic acids, amines and free sulfhydryl groups of both exogenous and endogenous compounds, to form O- N- and S-glucuronide conjugates. The increased water solubility of the glucuronide conjugates promotes their elimination in the urine or bile. In addition to high levels of expression in the liver, UGTs are also found in the kidney, intestine, brain and skin. Glucoronidation constitutes, from a general point of view, a reaction of detoxification and elimination. It generally leads to the formation of inactive metabolites and therefore, glucoronidation can dramatically modify the pharmacological activity of a drug. Moreover, UGTs play a major role in the elimination of nucleophilic metabolites of carcinogens, such as phenols and quinols of polycyclic aromatic hydrocarbons. In this way they prevent their further oxidation to electrophiles, which may react with DNA, RNA or protein. On the other hand, glucoronidation of certain compounds facilitates metabolic activation. Aromatic amines are some of the most studied examples of the role glucoronidation plays in metabolic activation of carcinogens. Glucoronidation has also been implicated in adverse drug reactions of certain carboxylic drugs, which resulted in a toxic immunological response. Glucoronidation although generally a detoxification reaction, may occasionally be involved in increasing toxicity.

Glutathione conjugation and further metabolism

Glutathione is a tripeptide (γ -glutamylcysteinylglycine, GSH) found in high concentrations in most mammalian tissues, but especially in the liver. Glutathione has several functions including roles in metabolism, transport and catalysis. Glutathione is also important for the maintenance of the thiol moieties of proteins and for the maintenance of the reduced form of other molecules such as cysteine, coenzyme A, and antioxidants such as

ascorbic acid; it is also used in the formation of deoxyribonucleic acids (Anderson M.E., *Advances in Pharmacology*, 38: 65-74, 1997). Glutathione has a major protective role in the body, as it is the major cellular antioxidant. GSH can react non-enzymatically with reactive oxygen species (ROS) and thereby protect the cell from oxidative damage. ROS have been
5 widely implicated in the pathology of numerous diseases such as arteriosclerosis, rheumatoid arthritis, cancer, AIDS, adult respiratory distress syndrome and Parkinson's disease.

Moreover, conjugation with the tripeptide glutathione represents a major detoxification pathway for xenobiotics including drugs and carcinogens. Glutathione may
10 react either chemically or in enzyme catalyzed reactions with a variety of compounds, which are reactive electrophilic metabolites produced in Phase I reactions. The glutathione S-transferase enzymes (GSTs) that catalyze these reactions are members of a multigene family and are expressed in virtually all tissues. Glutathione conjugates are cleaved to cysteine derivatives and subsequently are acetylated by a series of enzymes located
15 primarily in the kidney to give N-acetylcysteine conjugates collectively referred to as mercapturic acids. Mercapturic acid derivatives are the ultimate metabolites excreted in the urine. This is a particularly important route of Phase II metabolism from the toxicological point of view, as it is often involved in the removal of reactive intermediates. Xenobiotics that act as substrates for the glutathione S-transferases (GSTs) fall into four broad
20 categories: electrophilic carbon, nitrogen, sulfur and oxygen. Examples of substrates for glutathione S-transferases include aromatic, heterocyclic, alicyclic and aliphatic epoxides; aromatic halogen and nitro compounds; alkyl halides; and unsaturated aliphatic compounds (Ballantyne, B., Marrs T. and Turner P., *General & Applied Toxicology*, Stockton Press, New York, 1993). The GSTs are also involved in the metabolism of endogenous molecules
25 such as the leukotrienes. As mentioned above, many of the enzymes involved in xenobiotic metabolism are also involved in specific aspects of the metabolism of normal cellular biochemical constituents. Leukotrienes are important mediators and modulators of the inflammatory reaction and contribute to a number of physiological and pathological processes. Moreover, the GSTs are also capable of directly binding hydrophobic
30 compounds such as heme, bilirubin, and steroids, which may enable them to serve as intracellular storage and transport proteins for biological substances with limited water solubility. By their catalytic activity and their capacity for binding, the GSTs provide the cell with mechanism to protect itself from the noxious effects of various xenobiotics and endogenous substances. Further, GSTs may undergo amplification in tumors and may

thereby be implicated in drug resistance in cancer chemotherapy. GSTs are mostly cytosolic although, more recently, microsomal GSTs have been identified. Human microsomal GST II (MGST II) is a member of the microsomal glutathione S-transferase family. This enzyme catalyzes the production of LTC₄ (leukotriene C₄) from LTA₄ (leukotriene A₄) and reduced glutathione. Leukotrienes are derived from arachidonic acid and related fatty acids. Metabolites of arachidonic acid have been collectively termed eicosanoids, the principal eicosanoids are prostaglandins, thromboxanes and leukotrienes (LT). Eicosanoids are among the most important chemical mediators and modulators of the inflammatory reaction and contribute to a number of physiological and pathological processes (see Hardman J.G., Goodman, Gilman A., Limbird L.E.; *Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th edition, McGraw-Hill, N.Y., 1996). The ability to mount an inflammatory response is essential for survival in the face of environmental pathogens and injury, although in some situations and diseases the inflammatory response may be exaggerated and sustained for no apparent beneficial reason. This is the case in numerous chronic inflammatory diseases and allergic inflammation. Acute allergic inflammation is characterized by increased blood flow, extravasation of plasma and recruitment of leukocytes. These events are triggered by locally released inflammatory mediators including eicosanoids and more particularly leukotrienes. The participation of arachidonic acid metabolism in inflammatory diseases such as rheumatoid arthritis, asthma and acute allergy is well established. Pathological actions of leukotrienes are best understood in terms of their roles in immediate hypersensitivity and asthma. LTC₄ and LTD₄ are potent bronchoconstrictors, they act principally on smooth muscle in peripheral airways and are a 1000 times more potent than histamine both *in vitro* and *in vivo*. They also stimulate bronchial mucus secretion and cause mucosal edema. A complex mixture of chemical messengers is released when sensitized lung tissue is challenged by the appropriate antigen. Various prostaglandins and leukotrienes are prominent components of this mixture. Response to the leukotrienes probably dominates during allergic constriction of the airway. A particularly important role for the cysteinyl-leukotrienes (LTC₄, LTD₄, and LTE₄) has been suggested in pathogenesis of asthma, which is now recognized as a chronic inflammatory condition. They are potent spasmogens causing a contraction of bronchiolar muscle and an increase in mucus secretion. An increased LTC₄ formation has also been reported in leukocytes from patients with chronic myelogenous leukemia (Stenke et al., *Acta Oncologica*, 27:803-805, 1987) and in experimental glomerulonephritis (Petric et al., *Biochim. Biophys. Acta*, 1254:207-215, 1995).

Moreover, MGST II has the capacity to conjugate other compounds such as 1-chloro-2, 4 dinitrobenzene with glutathione and may be involved in a general metabolic system for detoxifying fatty acid epoxides (Jakobsson et al., *Journal of Biological Chemistry*, 271:22203-22210, 1996).

5 The resulting glutathione conjugate usually undergoes further metabolism, which involves first a removal of the glutamyl residue, catalyzed by γ -glutamyltransferase (GGT). In addition to catalyzing the initial step in the conversion of glutathione-conjugated compounds to mercapturic acids, GGT also converts LTC₄ to LTD₄. Interestingly, expression of GGT is often increased in cancerous tissues.

10 Renal dipeptidase is also implicated in the renal metabolism of glutathione and its conjugates including conjugated xenobiotics and endogenous molecules such as Leukotriene D₄. Pharmacologically it is an important enzyme, for it is responsible for hydrolysis of some β -lactam antibiotics such as penem and carbapenem.

The effectiveness of the GSTs and therefore of detoxification by glutathione
15 conjugation in general as well as the ability of the cell to resist to oxidative stress, are strongly influenced by the availability of reduced glutathione. Reduction of oxidized glutathione and *de novo* synthesis of glutathione, are both completely dependent on NADPH. Glutathione reductase (GSHR) maintains high levels of reduced glutathione in the cytosol in an NADPH dependent reaction. Reduced glutathione is synthesized *de novo* in
20 the cytosol of most cells via the γ -glutamyl cycle; a series of tightly controlled, enzyme catalyzed reactions. The first and second step in the *de novo* glutathione biosynthesis are catalyzed by γ -glutamylcysteine synthetase (GLCL) and glutathione synthase (GSHS) respectively. Deficiencies in γ -glutamylcysteine synthetase and GSH synthetase are associated with hemolytic anemia and impaired central nervous system function.

25 **Glucose 6-phosphate dehydrogenase (G6PDH), phosphogluconate dehydrogenase (PGDH) and malate dehydrogenase: generation of NADPH**

NADPH (nicotinamide adenine dinucleotide phosphate) serves as an electron donor in reductive biosyntheses. In the pentose phosphate pathway, NADPH is generated when glucose 6-phosphate is oxidized to ribose 5-phosphate. G6PDH and PGDH are key
30 enzymes of the pentose phosphate pathway and directly lead to the generation of NADPH. Another major source of NADPH is the oxidative decarboxylation of malate by malic enzyme.

NADPH may be used in anabolic processes such as fatty acid biosynthesis. One of the major functions of malic enzyme may be supplying NADPH to the cytosol for the

synthesis of fatty acids from acetyl CoA (coenzyme A). Further, the cytochrome P450 system is dependent on NADPH. As mentioned above, availability of NADPH is also critical for the reduction of glutathione. The connection between generation of NADPH and reduction of glutathione is clearer in tissues that have limited glycolytic metabolism, e.g. the lens and the erythrocyte. Thus the viability of the erythrocyte depends on glutathione, kept reduced by this pathway. Moreover, factors that influence the availability of reduced glutathione drastically alter the effectiveness of glutathione S-transferases therefore also affecting drug metabolism. Under most conditions saturating levels of NADPH are provided to the cell. However, certain conditions can stress the ability of the cell to provide NADPH and it may become rate limiting.

G6PDH and PGDH are present in most cells and tissues. They serve as the key enzymes of the pentose phosphate pathway that control the flow of carbon through the pathway and produce reducing equivalents as NADPH to meet cellular needs for reductive biosynthesis and to maintain the redox state of the cell at physiological levels. Deficiency of G6PDH and PGDH leads to decreased levels of NADPH and is associated with hemolytic anemia in response to oxidative stress. The red cells of G6PDH deficient persons are susceptible to hemolysis by dietary substances, and by drugs such as primaquine, sulfones, sulfonamides, nitrofurans, vitamin K analogs, acetophenetidin, chloramphenicol, and many others.

Genetic Polymorphisms in Drug Metabolizing Enzymes and Pharmacogenomics

Genetic, environmental, and physiological factors are involved in the regulation of drug biotransformation reactions. Results obtained from epidemiological studies and experimental animal model systems have shown a wide range of phenotypic variation in the ability of individuals to metabolize drugs and environmental chemicals. While some of this variation can be attributed to different environmental exposures, it has become clear that genetic factors also play an important role in determining the response of the individual to exogenous agents. Certain allelic forms of drug-metabolizing enzymes can render the individual either more sensitive or resistant to the toxic or therapeutic effects of exogenous drugs and chemicals. Genetic factors seem to be the major determinants of the variability of drug effects and are responsible for a number of striking quantitative and qualitative differences in pharmacological activity. Genetic differences in the ability of individuals to metabolize a drug through a given pathway are an important contributor to the large interindividual differences of drug efficacy and adverse effects within a population. There are many diverse examples of xenobiotics whose toxicity is directly dependent on the

activity of drug-metabolizing enzymes. Often impaired metabolism of a drug through a genetically polymorphic pathway has been associated with an increased incidence of adverse effects in the slow metabolizer population (Weber W.W., *Pharmacogenetics*, Oxford University Press, N.Y., 1997). Moreover, genetic differences in the regulation, expression and activity of genes coding for Phase I and Phase II drug-metabolizing enzymes can be crucial factors in defining cancer susceptibility and the toxic or carcinogenic power of environmental chemicals and xenobiotics. In addition, the majority of serious cases of drug-drug interactions are a result of the interference of the metabolic clearance of one drug by a coadministered drug. The interference usually occurs via inhibition or induction of drug-metabolizing enzymes. Interindividual differences in susceptibility to severe drug-drug interactions also involve drug-metabolizing enzyme polymorphism. In some cases the design of the drug takes into account the activity of drug-metabolizing enzymes. For example, prodrugs require activation by drug-metabolizing enzymes to exhibit their therapeutic activity. The activation and efficiency of such prodrugs depends on interindividual polymorphism in drug-metabolizing enzymes.

Individual differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure. Therapeutic management and drug development can be markedly improved by the identification of specific genetic polymorphisms that determine and predict patient susceptibility to diseases or patient responses to drugs. Assessing individual risk rather than population risk will lead to better targeted therapeutic strategies defining individual drug usage based on a benefit/risk prognosis. To assess the origins of individual variations in disease susceptibility or drug response, pharmacogenomics uses the genomic technologies to identify polymorphisms within genes, which are part of biological pathways involved in disease susceptibility, etiology, and development, or more specifically in drug response pathways responsible for a drug's efficacy, tolerance or toxicity. It can provide tools to refine the design of drug development by decreasing the incidence of adverse events in drug tolerance studies, by better defining patient subpopulations of responders and non-responders in efficacy studies and, by combining the results obtained therefrom, to further allow better enlightened individualized drug usage based on efficacy/tolerance prognosis. Pharmacogenomics can also provide tools to identify new targets for designing drugs and to optimize the use of already existing drugs, in order to either increase their response rate and/or exclude non-responders from corresponding treatment, or decrease their undesirable side effects and/or exclude from corresponding treatment patients with marked susceptibility to undesirable side effects.

Drug-metabolizing enzymes are highly relevant to pharmacogenomics because they are at the core of drug response, drug efficacy and toxicity. Drug-metabolizing enzymes also determine an individual's susceptibility to exogenous chemicals and to a number of diseases associated with exposure to toxic or carcinogenic chemicals.

5 The complexity of the pathways and enzymes that are involved in detoxification and metabolism of drugs has limited the precise identification of the drug-metabolizing enzymes, which play the causal role in pathologies or in drug response. Therapeutic management and drug development can be markedly improved by the identification of genetic markers derived from drug-metabolizing enzymes that predict patient susceptibility
10 to diseases or patient responses to drugs.

Genetic Analysis of Complex Traits

Until recently, the identification of genes linked with detectable traits has relied mainly on a statistical approach called linkage analysis. Linkage analysis is based upon establishing a correlation between the transmission of genetic markers and that of a specific
15 trait throughout generations within a family. Linkage analysis involves the study of families with multiple affected individuals and is useful in the detection of inherited traits, which are caused by a single gene, or possibly a very small number of genes. Linkage analysis has been successfully applied to map simple genetic traits that show clear Mendelian inheritance patterns and which have a high penetrance (the probability that a person with a given
20 genotype will exhibit a trait). About 100 pathological trait-causing genes have been discovered using linkage analysis over the last 10 years.

But, most traits of medical relevance do not follow simple Mendelian monogenic inheritance and linkage studies have proven difficult when applied to complex genetic traits. Many complex traits such as height, blood pressure or cancer susceptibility have been
25 known to run in families and are at least partially determined by genetic factors. However, the genes or combination of genes that underlie these observable characteristics or traits remain unknown in most cases. Such complex traits are often due to the combined action of multiple genes as well as environmental factors. Because of their low penetrance, such complex traits do not segregate in a clear-cut Mendelian manner as they are passed from one
30 generation to the next. Drug efficacy, response and tolerance/toxicity can also be considered as multifactoral traits involving a genetic component in the same way as complex diseases. Linkage analysis is impractical when the trait under study is drug response due to the lack of availability of familial cases. In fact, the likelihood of having more than one individual in a family being exposed to the same drug at the same time is very low. Linkage analysis

cannot be applied to the study of such traits for which no large informative families are available. Attempts to map complex traits have been plagued by inconclusive results, demonstrating the need for more sophisticated genetic tools.

Knowledge of genetic variation in drug-metabolizing enzymes is important for understanding why some people are more susceptible to toxicity, pathology or respond differently to drugs. Ways to identify genetic polymorphism and to analyze how they impact and predict disease susceptibility and response to treatment are needed.

Whereas a number of polymorphisms and rare mutations have been identified in drug-metabolizing enzymes (see Weber W.W., *Pharmacogenetics*, Oxford University Press, New York, 1997), genetic markers for use in determining which genes contribute to multigenic or quantitative traits and suitable methods for exploiting those markers have not been found and brought to bare on the genes coding for drug-metabolizing enzymes.

SUMMARY OF THE INVENTION

The present invention is based on the discovery of a set of novel DME-related biallelic markers. See Figure 1. These markers are located in the coding regions as well as non-coding regions adjacent to genes which are involved in the metabolic conversion of drugs and other xenobiotics. The position of these markers and knowledge of the surrounding sequence has been used to design polynucleotide compositions which are useful in determining the identity of nucleotides at the marker position, as well as more complex association and haplotyping studies which are useful in determining the genetic basis for variability in drug response and adverse reactions to drugs as well as the genetic basis for disease states involving the metabolic conversion of xenobiotics such as drugs. In addition, the compositions and methods of the invention find use in the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterization of the differential efficacious responses to and side effects from pharmaceutical agents.

The present invention further stems from the isolation and characterization of the genomic sequence of the MGST-II gene including its regulatory regions and of the complete cDNA sequence encoding the MGST-II enzyme. Oligonucleotide probes and primers hybridizing specifically with a genomic sequence of MGST-II are also part of the invention. A further object of the invention consists of recombinant vectors comprising any of the nucleic acid sequences described in the present invention, and in particular of recombinant vectors comprising the promoter region of MGST-II or a sequence encoding the MGST-II enzyme, as well as cell hosts comprising said nucleic acid sequences or recombinant

vectors. The invention also encompasses methods of screening of molecules which, modulate or inhibit the expression of the MGST-II gene. The invention is also directed to biallelic markers that are located within the MGST-II genomic sequence. these biallelic markers representing useful tools in order to identify a statistically significant association
5 between specific alleles of MGST-II gene and one or several disorders related to asthma and/or hepatotoxicity.

A first embodiment of the invention encompasses polynucleotides consisting of, consisting essentially of, or comprising a contiguous span of nucleotides of a sequence selected as an individual or in any combination from the group consisting of SEQ ID No. 1-
10 38, 40-54, 56-463, 465-487, 490-493, the complements thereof, the sequences described in any one or more of Figures 2, 3, 4, 5, 6, 7, and 8, and the complements thereof, wherein said contiguous span is at least 6, 8, 10, 12, 15, 20, 25, 30, 35, 40, 50, 75, 100, 200, 500, or 1000 nucleotides in length, to the extent that such a length is consistent with the lengths of the particular Sequence ID. The present invention also relates to polynucleotides hybridizing
15 under stringent or intermediate conditions to a sequence selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof. In addition, the polynucleotides of the invention encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination: Said contiguous span may optionally include the DME-related biallelic marker
20 in said sequence; Optionally either the original or the alternative allele of Figure 3 may be specified as being present at said DME-related biallelic marker; Optionally either the first or the second allele of Figure 2 or 4 may be specified as being present at said DME-related biallelic marker; Optionally, said polynucleotide may comprise, consists of, or consist essentially of a contiguous span which ranges in length from 8, 10, 12, 15, 18 or 20 to 25,
25 35, 40, 50, 60, 70, or 80 nucleotides, or be specified as being 12, 15, 18, 20, 25, 35, 40, or 50 nucleotides in length and including a DME-related biallelic marker of said sequence, and optionally the original allele of Figure 3 is present at said biallelic marker; Optionally, said biallelic marker may be within 6, 5, 4, 3, 2, or 1 nucleotides of the center of said polynucleotide or at the center of said polynucleotide; Optionally, the 3' end of said
30 contiguous span may be present at the 3' end of said polynucleotide; Optionally, biallelic marker may be present at the 3' end of said polynucleotide; Optionally, the 3' end of said polynucleotide may be located within or at least 2, 4, 6, 8, 10, 12, 15, 18, 20, 25, 50, 100, 250, 500, or 1000 nucleotides upstream of a DME-related biallelic marker in said sequence, to the extent that such a distance is consistent with the lengths of the particular Sequence

ID; Optionally, the 3' end of said polynucleotide may be located 1 nucleotide upstream of a DME-related biallelic marker in said sequence; and Optionally, said polynucleotide may further comprise a label.

A second embodiment of the invention encompasses any polynucleotide of the invention attached to a solid support. In addition, the polynucleotides of the invention which are attached to a solid support encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said polynucleotides may be specified as attached individually or in groups of at least 2, 5, 8, 10, 12, 15, 20, or 25 distinct polynucleotides of the inventions to a single solid support; Optionally, polynucleotides other than those of the invention may be attached to the same solid support as polynucleotides of the invention; Optionally, when multiple polynucleotides are attached to a solid support they may be attached at random locations, or in an ordered array; Optionally, said ordered array may be addressable.

A third embodiment of the invention encompasses the use of any polynucleotide for, or any polynucleotide for use in, determining the identity of one or more nucleotides at a DME-related biallelic marker. In addition, the polynucleotides of the invention for use in determining the identity of one or more nucleotides at a DME-related biallelic marker encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination. Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof; Optionally, said polynucleotide may comprise a sequence disclosed in the present specification; Optionally, said polynucleotide may consist of, or consist essentially of any polynucleotide described in the present specification; Optionally, said determining may be performed in a hybridization assay, sequencing assay, microsequencing assay, or an enzyme-based mismatch detection assay; Optionally, said polynucleotide may be attached to a solid support, array, or addressable array; Optionally, said polynucleotide may be labeled.

A fourth embodiment of the invention encompasses the use of any polynucleotide for, or any polynucleotide for use in, amplifying a segment of nucleotides comprising a DME-related biallelic marker. In addition, the polynucleotides of the invention for use in amplifying a segment of nucleotides comprising a DME-related biallelic marker encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may

be in a sequence selected individually or in any combination from the group consisting of SEQ ID 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker
5 may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, said
10 polynucleotide may comprise a sequence disclosed in the present specification; Optionally, said polynucleotide may consist of, or consist essentially of any polynucleotide described in the present specification; Optionally, said amplifying may be performed by a PCR or LCR. Optionally, said polynucleotide may be attached to a solid support, array, or addressable array. Optionally, said polynucleotide may be labeled.

15 A fifth embodiment of the invention encompasses methods of genotyping a biological sample comprising determining the identity of a nucleotide at a DME-related biallelic marker. In addition, the genotyping methods of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence
20 selected individually or in any combination from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in
25 Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-
30 219, 12-721-440, and 10-420-284; Optionally, said method further comprises determining the identity of a second nucleotide at said biallelic marker, wherein said first nucleotide and second nucleotide are not base paired (by Watson & Crick base pairing) to one another; Optionally, said biological sample is derived from a single individual or subject; Optionally, said method is performed in vitro; Optionally, said biallelic marker is

determined for both copies of said biallelic marker present in said individual's genome; Optionally, said biological sample is derived from multiple subjects or individuals; Optionally, said method further comprises amplifying a portion of said sequence comprising the biallelic marker prior to said determining step; Optionally, wherein said amplifying is performed by PCR, LCR, or replication of a recombinant vector comprising an origin of replication and said portion in a host cell; Optionally, wherein said determining is performed by a hybridization assay, sequencing assay, microsequencing assay, or an enzyme-based mismatch detection assay.

A sixth embodiment of the invention comprises methods of estimating the frequency of an allele in a population comprising genotyping individuals from said population for a DME-related biallelic marker and determining the proportional representation of said biallelic marker in said population. In addition, the methods of estimating the frequency of an allele in a population of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination:

Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ No. 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof; Optionally, said DME-related biallelic marker may be selected from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, determining the frequency of a biallelic marker allele in a population may be accomplished by determining the identity of the nucleotides for both copies of said biallelic marker present in the genome of each individual in said population and calculating the proportional representation of said nucleotide at said DME-related biallelic marker for the population; Optionally, determining the frequency of a biallelic marker allele in a population may be accomplished by performing a genotyping method on a pooled biological sample derived from a representative number of individuals, or each individual, in said population, and calculating the proportional amount of said nucleotide compared with the total.

A seventh embodiment of the invention comprises methods of detecting an association between an allele and a phenotype, comprising the steps of a) determining the frequency of at least one DME-related biallelic marker allele in a case (trait positive) population, b) determining the frequency of said DME-related biallelic marker allele in a control population and; c) determining whether a statistically significant association exists between said genotype and said phenotype. In addition, the methods of detecting an association between an allele and a phenotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID No.1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic marker may be selected from the biallelic markers described in Figure 1; Optionally, said control population may be a trait negative population, or a random population; Optionally, said phenotype is a response to a drug, or a side effects to a drug, or a disease involving the metabolic conversion of xenobiotics; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the following sequences: SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 is determined in steps a) and b).

An eighth embodiment of the present invention encompasses methods of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising the steps of: a) genotyping each individual in said population for at least one DME-related biallelic marker, b) genotyping each individual in said population for a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome; and c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency. In addition, the methods of estimating the frequency of a haplotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark method, or an expectation maximization algorithm; Optionally, said second biallelic marker is a DME-related biallelic marker in a sequence selected from the group consisting of the biallelic markers of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic markers may be selected individually or in any combination from the biallelic markers described in Figure 1;

Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following

5 biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the sequences of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 is determined in steps a)

10 and b).

A ninth embodiment of the present invention encompasses methods of detecting an association between a haplotype and a phenotype, comprising the steps of: a) estimating the frequency of at least one haplotype in a trait positive population according to a method of estimating the frequency of a haplotype of the invention; b) estimating the frequency of said

15 haplotype in a control population according to the method of estimating the frequency of a haplotype of the invention; and c) determining whether a statistically significant association exists between said haplotype and said phenotype. In addition, the methods of detecting an association between a haplotype and a phenotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in

20 any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic markers may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may

25 be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-

30 156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, said control population may be a trait negative population, or a random population; Optionally, said phenotype is a response to a drug, or a side effects to a drug, or a disease involving the metabolic conversion of xenobiotics; Optionally, said drug is zileuton and said side effect to said drug is

hepatotoxicity; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the following sequences: SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 is included in the estimating steps a) and b).

A tenth embodiment of the present invention is a method of administering a drug or
5 a treatment comprising the steps of: a) obtaining a nucleic acid sample from an individual;
b) determining the identity of the polymorphic base of at least one DME-related biallelic
marker which is associated with a positive response to the treatment or the drug; or at least
one biallelic DME-related biallelic marker which is associated with a negative response to
the treatment or the drug; and c) administering the treatment or the drug to the individual if
10 the nucleic acid sample contains said biallelic marker associated with a positive response to
the treatment or the drug or if the nucleic acid sample lacks said biallelic marker associated
with a negative response to the treatment or the drug. In addition, the methods of the
present invention for administering a drug or a treatment encompass methods with any
further limitation described in this disclosure, or those following, specified alone or in any
15 combination: optionally, said DME-related biallelic marker may be in a sequence selected
individually or in any combination from the group consisting of SEQ ID Nos. 1-38, 40-54,
56-463, 465-487, 490-493; the complements thereof; or preferably SEQ ID Nos. 3, 5, 9, 13-
15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, 380; and the complements thereof or
optionally, the administering step comprises administering the drug or the treatment to the
20 individual if the nucleic acid sample contains said biallelic marker associated with a positive
response to the treatment or the drug and the nucleic acid sample lacks said biallelic marker
associated with a negative response to the treatment or the drug.

An eleventh embodiment of the present invention is a method of selecting an
individual for inclusion in a clinical trial of a treatment or drug comprising the steps of: a)
25 obtaining a nucleic acid sample from an individual; b) determining the identity of the
polymorphic base of at least one DME-related biallelic marker which is associated with a
positive response to the treatment or the drug, or at least one DME-related biallelic marker
which is associated with a negative response to the treatment or the drug in the nucleic acid
sample, and c) including the individual in the clinical trial if the nucleic acid sample
30 contains said DME-related biallelic marker associated with a positive response to the
treatment or the drug or if the nucleic acid sample lacks said biallelic marker associated with
a negative response to the treatment or the drug. In addition, the methods of the present
invention for selecting an individual for inclusion in a clinical trial of a treatment or drug
encompass methods with any further limitation described in this disclosure, or those

following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID Nos. 1-38, 40-54, 56-463, 465-487, 490-493; the complements thereof; or preferably SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, 380; and the complements thereof, optionally, the including step comprises administering the drug or the treatment to the individual if the nucleic acid sample contains said biallelic marker associated with a positive response to the treatment or the drug and the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug.

Additional embodiments are set forth in the Detailed Description of the Invention and in the Examples.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a chart containing a list of all of the DME-related biallelic markers for each gene with an indication of the gene for which the marker is in closest physical proximity, an indication of whether the markers have been validated by microsequencing (with a Y indicating that the markers have been validated by microsequencing and an N indicating that it has not), and an indication of the identity and frequency of the least common allele determined by genotyping (with a blank left to indicate that the frequency has not yet been reported for some markers).

Figure 2, 3, and 4 are charts containing lists of the DME-related biallelic markers. Each marker is described by indicating its SEQ ID, the biallelic marker ID, and the two most common alleles. Figure 2 is a chart containing a list of biallelic markers surrounded by preferred sequences. In the column labeled, "POSITION RANGE OF PREFERRED SEQUENCE" of Figure 2, regions of particularly preferred sequences are listed for each SEQ ID, which contain a DME-related biallelic marker, as well as particularly preferred regions of sequences that may not contain a DME-related biallelic marker but, which are in sufficiently close proximity to a DME-related biallelic marker to be useful as amplification or sequencing primers.

Figure 5 is a chart listing particular preferred sequences that are useful for designing some of the primers and probes of the invention. Each sequence is described by indicating its Sequence ID and the positions of the first and last nucleotides (position range) of the particular sequence in the Sequence ID.

Figure 6 is a chart listing microsequencing primers which have been used to genotype DME-related biallelic markers (indicated by an *) and other preferred

microsequencing primers for use in genotyping DME-related biallelic markers. Each of the primers which falls within the strand of nucleotides included in the Sequence Listing are described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the primers in the Sequence ID. Since the sequences in the Sequence Listing are single stranded and half the possible microsequencing primers are composed of nucleotide sequences from the complementary strand, the primers that are composed of nucleotides in the complementary strand are described by indicating their SEQ ID numbers and the positions of the first and last nucleotides to which they are complementary (complementary position range) in the Sequence ID.

Figure 7 is a chart listing amplification primers which have been used to amplify polynucleotides containing one or more DME-related biallelic markers. Each of the primers which falls within the strand of nucleotides included in the Sequence Listing are described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the primers in the Sequence ID. Since the sequences in the Sequence Listing are single stranded and half the possible amplification primers are composed of nucleotide sequences from the complementary strand, the primers that are composed of nucleotides in the complementary strand are defined by the SEQ ID numbers and the positions of the first and last nucleotides to which they are complementary (complementary position range) in the Sequence ID.

Figure 8 is a chart listing preferred probes useful in genotyping DME-related biallelic markers by hybridization assays. The probes are generally 25-mers with a DME-related biallelic marker in the center position, and described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the probes in the Sequence ID. The probes complementary to the sequences in each position range in each Sequence ID are also understood to be a part of this preferred list even though they are not specified separately.

Figure 9 is a chart containing a list of preferred MGST-II-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies were determined in a random US Caucasian population.

Figure 10 is a chart containing a list of preferred ME1-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies were determined in a random US Caucasian population.

Figure 11 is a chart containing a list of preferred UGT1A7-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies

were determined in a random US Caucasian population and a random French Caucasian population.

Figure 12 is a chart containing a list of preferred UGT2B4-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies
5 were determined in a random US Caucasian population and a random French Caucasian population..

Figure 13 is a chart showing the results of a haplotype analysis study demonstrating an association between asthma and MGST-II-related biallelic marker haplotypes.

Figure 14 is a chart showing the results of a permutation test which evaluates the
10 statistical significance of the results obtained for the haplotype analysis.

Figure 15 is a chart showing the results of a haplotype analysis study demonstrating an association between side effects upon treatment with the anti-asthmatic drug Zyflo™ (zileuton) and MGST-II related biallelic marker haplotypes.

Figure 16 is a table showing the results of a phenotypic permutation test which
15 evaluates the statistical significance of the results obtained for the haplotype analysis in Figure 15.

Figure 17 is a block diagram of an exemplary computer system.

Figure 18 is a flow diagram illustrating one embodiment of a process 200 for
20 comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

Figure 19 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous.

Figure 20 is a flow diagram illustrating one embodiment of an identifier process 300
25 for detecting the presence of a feature in a sequence.

BRIEF DESCRIPTION OF THE SEQUENCES PROVIDED IN THE SEQUENCE LISTING

SEQ ID Nos. 1-484 contain the nucleotide sequence of genomic DNA fragments located in the vicinity of the candidate genes.

30 SEQ ID No. 485 contains the genomic sequence of the MGST-II gene comprising the 5' regulatory region (upstream untranscribed region), the exons and introns, and the 3' regulatory region (downstream untranscribed region).

SEQ ID No. 486 contains a cDNA sequence of MGST-II.

SEQ ID No. 487 contains a cDNA sequence of MGST-II corresponding to an alternative messenger RNA which is due to alternative splicing joining exon 1 to exon 3 and resulting in the absence of exon 2.

SEQ ID No. 488 contains the amino acid sequence encoded by the cDNA of SEQ ID No. 486.

SEQ ID No. 489 contains the amino acid sequence encoded by the cDNA of SEQ ID No. 487.

SEQ ID No. 490 contains a partial cDNA sequence of MGST-II sequence corresponding to a cloned partial messenger RNA.

10 SEQ ID No. 491 contains a partial cDNA sequence of MGST-II sequence corresponding to a cloned partial messenger RNA.

SEQ ID No. 492 contains a primer containing the additional PU 5' sequence described further in Example 1.

SEQ ID No. 493 contains a primer containing the additional RP 5' sequence
15 described further in Example 1.

DETAILED DESCRIPTION OF THE INVENTION

Advantages of the biallelic markers of the present invention

The DME-related biallelic markers of the present invention offer a number of important advantages over other genetic markers such as RFLP (Restriction fragment length
20 polymorphism) and VNTR (Variable Number of Tandem Repeats) markers.

The first generation of markers, were RFLPs, which are variations that modify the length of a restriction fragment. But methods used to identify and to type RFLPs are relatively wasteful of materials, effort, and time. The second generation of genetic markers were VNTRs, which can be categorized as either minisatellites or microsatellites.

25 Minisatellites are tandemly repeated DNA sequences present in units of 5-50 repeats which are distributed along regions of the human chromosomes ranging from 0.1 to 20 kilobases in length. Since they present many possible alleles, their informative content is very high. Minisatellites are scored by performing Southern blots to identify the number of tandem repeats present in a nucleic acid sample from the individual being tested. However, there
30 are only 10^4 potential VNTRs that can be typed by Southern blotting. Moreover, both RFLP and VNTR markers are costly and time-consuming to develop and assay in large numbers.

Single nucleotide polymorphism or biallelic markers can be used in the same manner as RFLPs and VNTRs but offer several advantages. Single nucleotide polymorphisms are densely spaced in the human genome and represent the most frequent type of variation. An

estimated number of more than 10^7 sites are scattered along the 3×10^9 base pairs of the human genome. Therefore, single nucleotide polymorphism occur at a greater frequency and with greater uniformity than RFLP or VNTR markers which means that there is a greater probability that such a marker will be found in close proximity to a genetic locus of interest. Single nucleotide polymorphisms are less variable than VNTR markers but are mutationally more stable.

Also, the different forms of a characterized single nucleotide polymorphism, such as the biallelic markers of the present invention, are often easier to distinguish and can therefore be typed easily on a routine basis. Biallelic markers have single nucleotide based alleles and they have only two common alleles, which allows highly parallel detection and automated scoring. The biallelic markers of the present invention offer the possibility of rapid, high-throughput genotyping of a large number of individuals.

Biallelic markers are densely spaced in the genome, sufficiently informative and can be assayed in large numbers. The combined effects of these advantages make biallelic markers extremely valuable in genetic studies. Biallelic markers can be used in linkage studies in families, in allele sharing methods, in linkage disequilibrium studies in populations, in association studies of case-control populations. An important aspect of the present invention is that biallelic markers allow association studies to be performed to identify genes involved in complex traits. Association studies examine the frequency of marker alleles in unrelated case- and control-populations and are generally employed in the detection of polygenic or sporadic traits. Association studies may be conducted within the general population and are not limited to studies performed on related individuals in affected families (linkage studies). Biallelic markers in different genes can be screened in parallel for direct association with disease or response to a treatment. This multiple gene approach is a powerful tool for a variety of human genetic studies as it provides the necessary statistical power to examine the synergistic effect of multiple genetic factors on a particular phenotype, drug response, sporadic trait, or disease state with a complex genetic etiology.

Candidate genes of the present invention

Different approaches can be employed to perform association studies: genome-wide association studies, candidate region association studies and candidate gene association studies. Genome-wide association studies rely on the screening of genetic markers evenly spaced and covering the entire genome. Candidate region association studies rely on the screening of genetic markers evenly spaced covering a region identified as linked to the trait

of interest. The candidate gene approach is based on the study of genetic markers specifically derived from genes potentially involved in a biological pathway related to the trait of interest. In the present invention, genes involved in drug metabolism have been chosen as candidate genes. As mentioned above, these genes are highly relevant to

5 pharmacogenetics because they are at the core of drug response, drug efficacy and toxicity, moreover, drug-metabolizing enzymes also determine an individuals susceptibility to exogenous chemicals and to a number of diseases associated with exposure to toxic or carcinogenic chemicals. The candidate gene analysis clearly provides a short-cut approach to the identification of genes and gene polymorphisms related to a particular trait when

10 some information concerning the biology of the trait is available. However, it should be noted that all of the biallelic markers disclosed in the instant application can be employed as part of genome-wide association studies or as part of candidate region association studies and such uses are specifically contemplated in the present invention and claims. All of the markers are known to be in close proximity to the genes with which they are listed in Figure

15 1. For a portion of the markers, the precise position of the marker with respect to the various coding and non-coding elements of the genes has also been determined.

The following is a table of abbreviations for the candidate genes as they appear throughout the specification and figures:

20 **Table 1**

Candidate Gene	Abbreviation
Microsomal glutathione S-transferase II	MGST2 or MGST II
Malate decarboxylase enzyme	DME or ME1
Cytochrome P450 1A2	CYP1A2
Cytochrome P450 2C8	CYP2C8
Cytochrome P450 2C9	CYP2C9
Cytochrome P450 2C18	CYP2C18
Cytochrome P450 3A4-3A7	CYP3A4-CYP3A7
Cytochrome P450 3A7	CYP3A7
Flavin-containing monooxygenases	FMO
Glutathione reductase	GSHR
Glutathione synthase	GSHS
γ -glutamylcysteine synthetase	GLCL

γ -glutamyltransferase 5	GGT5
Dipeptidase	DP
Glucose 6-phosphate dehydrogenase	G6PDH
Phosphogluconate dehydrogenase	PGDH
Uridine diphosphate glucuronosyl transferase 1A7	UGT1A7
Uridine diphosphate glucuronosyl transferase B4	UGT2B4
Uridine diphosphate glucuronosyl transferase B7	UGT2B7
Uridine diphosphate glucuronosyl transferase B10	UGT2B10
Uridine diphosphate glucuronosyl transferase B15	UGT2B15

Definitions

As used interchangeably herein, the terms "nucleic acids," "oligonucleotides" and "polynucleotides" include RNA, DNA, or RNA/DNA hybrid sequences of more than one nucleotide in either single chain or duplex form. The term "nucleotide" as used herein as an adjective to describe molecules comprising RNA, DNA, or RNA/DNA hybrid sequences of any length in single-stranded or duplex form. The term "nucleotide" is also used herein as a noun to refer to individual nucleotides or varieties of nucleotides, meaning a molecule, or individual unit in a larger nucleic acid molecule, comprising a purine or pyrimidine, a ribose or deoxyribose sugar moiety, and a phosphate group, or phosphodiester linkage in the case of nucleotides within an oligonucleotide or polynucleotide. Although the term "nucleotide" is also used herein to encompass "modified nucleotides" which comprise at least one modifications (a) an alternative linking group, (b) an analogous form of purine, (c) an analogous form of pyrimidine, or (d) an analogous sugar, for examples of analogous linking groups, purine, pyrimidines, and sugars see for example PCT publication No. WO 95/04064. However, the polynucleotides of the invention are preferably comprised of greater than 50% conventional deoxyribose nucleotides, and most preferably greater than 90% conventional deoxyribose nucleotides. The polynucleotide sequences of the invention may be prepared by any known method, including synthetic, recombinant, *ex vivo* generation, or a combination thereof, as well as utilizing any purification methods known in the art.

Throughout the present specification, the expression "nucleotide sequence" may be employed to designate indifferently a polynucleotide or a nucleic acid. More precisely, the expression "nucleotide sequence" encompasses the nucleic material itself and is thus not

restricted to the sequence information (i.e. the succession of letters chosen among the four base letters) that biochemically characterizes a specific DNA or RNA molecule.

The term "polypeptide" refers to a polymer of amino without regard to the length of the polymer; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not specify or exclude post-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian systems etc.), polypeptides with substituted linkages, as well as other modifications known in the art, both naturally occurring and non-naturally occurring.

The term "recombinant polypeptide" is used herein to refer to polypeptides that have been artificially designed and which comprise at least two polypeptide sequences that are not found as contiguous polypeptide sequences in their initial natural environment, or to refer to polypeptides which have been expressed from a recombinant polynucleotide.

The term "isolated" requires that the material be removed from its original environment (e. g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or DNA or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotide could be part of a vector and/or such polynucleotide or polypeptide could be part of a composition, and still be isolated in that the vector or composition is not part of its natural environment.

The term "purified" is used herein to describe a polynucleotide or polynucleotide vector of the invention which has been separated from other compounds including, but not limited to other nucleic acids, carbohydrates, lipids and proteins (such as the enzymes used in the synthesis of the polynucleotide), or the separation of covalently closed polynucleotides from linear polynucleotides. A polynucleotide is substantially pure when at least about 50 %, preferably 60 to 75% of a sample exhibits a single polynucleotide sequence and conformation (linear versus covalently close). A substantially pure polynucleotide typically comprises about 50 %, preferably 60 to 90% weight/weight of a nucleic acid sample, more usually about 95%, and preferably is over about 99% pure. Polynucleotide purity or homogeneity may be indicated by a number of means well known

in the art, such as agarose or polyacrylamide gel electrophoresis of a sample, followed by visualizing a single polynucleotide band upon staining the gel. For certain purposes higher resolution can be provided by using HPLC or other means well known in the art.

The term "purified" is further used herein to describe a polypeptide of the invention
5 which, has been separated from other compounds including, but not limited to nucleic acids, lipids, carbohydrates and other proteins. A polypeptide is substantially pure when at least about 50%, preferably 60 to 75% of a sample exhibits a single polypeptide sequence. A substantially pure polypeptide typically comprises about 50%, preferably 60 to 90% weight/weight of a protein sample, more usually about 95%, and preferably is over about
10 99% pure. Polypeptide purity or homogeneity is indicated by a number of means well known in the art, such as agarose or polyacrylamide gel electrophoresis of a sample, followed by visualizing a single polypeptide band upon staining the gel. For certain purposes higher resolution can be provided by using HPLC or other means well known in the art.

15 As used herein, the term "non-human animal" refers to any non-human vertebrate, birds and more usually mammals, preferably primates, farm animals such as swine, goats, sheep, donkeys, and horses, rabbits or rodents, more preferably rats or mice. As used herein, the term "animal" is used to refer to any vertebrate, preferable a mammal. Both the terms "animal" and "mammal" expressly embrace human subjects unless preceded with the
20 term "non-human".

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides which are comprised of at least one binding domain, where an antibody binding domain is formed from the folding of variable domains of an antibody molecule to form three-dimensional binding spaces with an internal surface shape and charge distribution
25 complementary to the features of an antigenic determinant of an antigen., which allows an immunological reaction with the antigen. Antibodies include recombinant proteins comprising the binding domains, as wells as fragments, including Fab, Fab', F(ab)₂, and F(ab')₂ fragments.

As used herein, an "antigenic determinant" is the portion of an antigen molecule, in
30 this case a MGST-II polypeptide, that determines the specificity of the antigen-antibody reaction. An "epitope" refers to an antigenic determinant of a polypeptide. An epitope can comprise as few as 3 amino acids in a spatial conformation which, is unique to the epitope. Generally an epitope consists of at least 6 such amino acids, and more usually at least 8-10 such amino acids. Methods for determining the amino acids which make up an epitope

include x-ray crystallography, 2-dimensional nuclear magnetic resonance, and epitope mapping e.g. the Pepscan method described by H. Mario Geysen et al. 1984. *Proc. Natl. Acad. Sci. U.S.A.* 81:3998-4002; PCT Publication No. WO 84/03564; and PCT Publication No. WO 84/03506.

5 The term "primer" denotes a specific oligonucleotide sequence which is complementary to a target nucleotide sequence and used to hybridize to the target nucleotide sequence. A primer serves as an initiation point for nucleotide polymerization catalyzed by either DNA polymerase, RNA polymerase or reverse transcriptase.

10 The term "probe" denotes a defined nucleic acid segment (or nucleotide analog segment, e.g., polynucleotide as defined herein) which can be used to identify a specific polynucleotide sequence present in samples, said nucleic acid segment comprising a nucleotide sequence complementary of the specific polynucleotide sequence to be identified.

15 The terms "trait" and "phenotype" are used interchangeably herein and refer to any visible, detectable or otherwise measurable property of an organism such as symptoms of, or susceptibility to a disease for example. Typically the terms "trait" or "phenotype" are used herein to refer to symptoms of, or susceptibility to a disease; or to refer to an individual's response to a drug; or to refer to symptoms of, or susceptibility to side effects to a drug. In addition, the terms "trait" or "phenotype" may be used herein to refer to symptoms of, or
20 susceptibility to a disease involving arachidonic acid metabolism; or to refer to an individual's response to an agent acting on arachidonic acid metabolism; or to refer to symptoms of, or susceptibility to side effects to an agent acting on arachidonic acid metabolism.

25 The term "allele" is used herein to refer to variants of a nucleotide sequence. A biallelic polymorphism has two forms. Typically the first identified allele is designated as the original allele whereas other alleles are designated as alternative alleles. Diploid organisms may be homozygous or heterozygous for an allelic form.

30 The term "heterozygosity rate" is used herein to refer to the incidence of individuals in a population, which are heterozygous at a particular allele. In a biallelic system the heterozygosity rate is on average equal to $2P_a(1-P_a)$, where P_a is the frequency of the least common allele. In order to be useful in genetic studies a genetic marker should have an adequate level of heterozygosity to allow a reasonable probability that a randomly selected person will be heterozygous.

The term "genotype" as used herein refers the identity of the alleles present in an individual or a sample. In the context of the present invention a genotype preferably refers to the description of the biallelic marker alleles present in an individual or a sample. The term "genotyping" a sample or an individual for a biallelic marker consists of determining
5 the specific allele or the specific nucleotide carried by an individual at a biallelic marker.

The term "mutation" as used herein refers to a difference in DNA sequence between or among different genomes or individuals which has a frequency below 1%.

The term "haplotype" refers to a combination of alleles present in an individual or a sample. In the context of the present invention a haplotype preferably refers to a
10 combination of biallelic marker alleles found in a given individual and which may be associated with a phenotype.

The term "polymorphism" as used herein refers to the occurrence of two or more alternative genomic sequences or alleles between or among different genomes or individuals. "Polymorphic" refers to the condition in which two or more variants of a
15 specific genomic sequence can be found in a population. A "polymorphic site" is the locus at which the variation occurs. A single nucleotide polymorphism is a single base pair change. Typically a single nucleotide polymorphism is the replacement of one nucleotide by another nucleotide at the polymorphic site. Deletion of a single nucleotide or insertion of a single nucleotide, also give rise to single nucleotide polymorphisms. In the context of the
20 present invention "single nucleotide polymorphism" preferably refers to a single nucleotide substitution. Typically, between different genomes or between different individuals, the polymorphic site may be occupied by two different nucleotides.

The terms "biallelic polymorphism" and "biallelic marker" are used interchangeably herein to refer to a polymorphism having two alleles at a fairly high frequency in the
25 population, preferably a single nucleotide polymorphism. A "biallelic marker allele" refers to the nucleotide variants present at a biallelic marker site. Typically the frequency of the less common allele of the biallelic markers of the present invention has been validated to be greater than 1%, preferably the frequency is greater than 10%, more preferably the frequency is at least 20% (i.e. heterozygosity rate of at least 0.32), even more preferably the
30 frequency is at least 30% (i.e. heterozygosity rate of at least 0.42). A biallelic marker wherein the frequency of the less common allele is 30% or more is termed a "high quality biallelic marker."

The location of nucleotides in a polynucleotide with respect to the center of the polynucleotide are described herein in the following manner. When a polynucleotide has an

odd number of nucleotides, the nucleotide at an equal distance from the 3' and 5' ends of the polynucleotide is considered to be "at the center" of the polynucleotide, and any nucleotide immediately adjacent to the nucleotide at the center, or the nucleotide at the center itself is considered to be "within 1 nucleotide of the center." With an odd number of nucleotides in a polynucleotide any of the five nucleotides positions in the middle of the polynucleotide would be considered to be within 2 nucleotides of the center, and so on. When a polynucleotide has an even number of nucleotides, there would be a bond and not a nucleotide at the center of the polynucleotide. Thus, either of the two central nucleotides would be considered to be "within 1 nucleotide of the center" and any of the four nucleotides in the middle of the polynucleotide would be considered to be "within 2 nucleotides of the center", and so on. For polymorphisms which involve the substitution, insertion or deletion of 1 or more nucleotides, the polymorphism, allele or biallelic marker is "at the center" of a polynucleotide if the difference between the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 3' end of the polynucleotide, and the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 5' end of the polynucleotide is zero or one nucleotide. If this difference is 0 to 3, then the polymorphism is considered to be "within 1 nucleotide of the center." If the difference is 0 to 5, the polymorphism is considered to be "within 2 nucleotides of the center." If the difference is 0 to 7, the polymorphism is considered to be "within 3 nucleotides of the center," and so on. For polymorphisms which involve the substitution, insertion or deletion of 1 or more nucleotides, the polymorphism, allele or biallelic marker is "at the center" of a polynucleotide if the difference between the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 3' end of the polynucleotide, and the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 5' end of the polynucleotide is zero or one nucleotide. If this difference is 0 to 3, then the polymorphism is considered to be "within 1 nucleotide of the center." If the difference is 0 to 5, the polymorphism is considered to be "within 2 nucleotides of the center." If the difference is 0 to 7, the polymorphism is considered to be "within 3 nucleotides of the center," and so on.

30 The term "upstream" is used herein to refer to a location which, is toward the 5' end of the polynucleotide from a specific reference point.

The terms "base paired" and "Watson & Crick base paired" are used interchangeably herein to refer to nucleotides which can be hydrogen bonded to one another by virtue of their sequence identities in a manner like that found in double-helical DNA with thymine or

uracil residues linked to adenine residues by two hydrogen bonds and cytosine and guanine residues linked by three hydrogen bonds (See Stryer, L., *Biochemistry*, 4th edition, 1995).

The terms "complementary" or "complement thereof" are used herein to refer to the sequences of polynucleotides which is capable of forming Watson & Crick base pairing
5 with another specified polynucleotide throughout the entirety of the complementary region. This term is applied to pairs of polynucleotides based solely upon their sequences and not any particular set of conditions under which the two polynucleotides would actually bind.

A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell required to initiate the specific transcription of a gene.

10 A sequence which is "operably linked" to a regulatory sequence such as a promoter means that said regulatory element is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the nucleic acid of interest.

As used herein, the term "operably linked" refers to a linkage of polynucleotide
15 elements in a functional relationship. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the coding sequence. More precisely, two DNA molecules (such as a polynucleotide containing a promoter region and a polynucleotide encoding a desired polypeptide or polynucleotide) are said to be "operably linked" if the nature of the linkage between the two polynucleotides does not (1) result in
20 the introduction of a frame-shift mutation or (2) interfere with the ability of the polynucleotide containing the promoter to direct the transcription of the coding polynucleotide.

The terms "disease involving the metabolic conversion of xenobiotics" refers to susceptibility to a condition or to a condition linked to any of the genes listed in Figure 1.
25 "Disease involving the metabolic conversion of xenobiotics" further refers to a condition involving the biotransformation of drugs and other xenobiotics such as environmental chemicals, food toxins, plant metabolites, carcinogens and industrial chemicals. Such conditions include susceptibility to the toxic or carcinogenic effect of exogenous compounds. "Disease involving the metabolic conversion of xenobiotics" also refers to
30 disorders in the metabolism of some endogenous compounds such as the metabolism of steroids, vitamins, fatty acids and eicosanoids such as leukotrienes involving any of the drug-metabolizing enzymes shown in Figure 1. "Disease involving the metabolic conversion of xenobiotics" includes, but is not limited to, disorders involving the

cytochrome P450 enzyme family, the flavin containing monooxygenases, glucoronidation, the metabolism of glutathione, the pentose pathway and the generation of NADPH.

The term "disease involving arachidonic acid metabolism" refers to a condition linked to disturbances in expression, production or cellular response to eicosanoids such as
5 prostaglandins, thromboxanes, prostacyclins, leukotrienes or hydroperoxyeicosatrenoic acids. A disease involving arachidonic acid metabolism further refers to a condition involving one or several enzymes of the distinct enzyme systems contributing to arachidonate metabolism including particularly the 5-lipoxygenase pathway. "Diseases involving arachidonic acid metabolism" also include chronic inflammatory diseases, acute
10 allergic inflammation and inflammatory conditions such as pain, fever, hypersensitivity, asthma, psoriasis and arthritis. "Diseases involving arachidonic acid metabolism" also include disorders in platelet function, blood pressure, thrombosis, renal function, host defense mechanism, hemostasis, smooth muscle tone, male infertility, primary dysmenorrhea, disorders in parturition, and disorders in tissue injury repair, as well as
15 disorders in cellular function and development. "Diseases involving arachidonic acid metabolism" also include diseases such as gastrointestinal ulceration, coronary and cerebrovascular syndromes, glomerular immune injury and cancer. Preferably the terms "disease involving arachidonic acid metabolism" refer to a disease including diseases such as cancer, prostate cancer, breast cancer, psoriasis and inflammatory diseases. Preferably
20 the terms "disease involving arachidonic acid metabolism" refer to a disease involving the 5-lipoxygenase pathway and the biosynthesis of the leukotrienes. More preferably the terms "disease involving arachidonic acid metabolism" refer to a disease involving the synthesis of leukotriene C4 (LTC₄) and refers to disturbances in expression, activity or function of the human MGST-II enzyme.

25 As used herein the term "DME-related biallelic marker" relates to a set of biallelic markers located in or in the vicinity of the genes disclosed in Figure 1 and further relates to biallelic markers in linkage disequilibrium with the biallelic markers disclosed in Figure 1. The term DME-related biallelic marker encompasses all of the biallelic markers disclosed in Figure 1.

30 The invention also concerns MGST-II-related biallelic markers. The term "MGST-II-related biallelic marker" is used interchangeably herein to relate to all biallelic markers in linkage disequilibrium with the biallelic markers of the MGST-II gene. The term MGST-II-related biallelic marker includes both the genic and non-genic biallelic markers described in Table 2.

The term "non-genic" is used herein to describe MGST-II-related biallelic markers, as well as polynucleotides and primers which occur outside the nucleotide positions shown in the human MGST-II genomic sequence of SEQ ID No. 485. The term "genic" is used herein to describe MGST-II-related biallelic markers as well as polynucleotides and primers
5 which do occur in the nucleotide positions shown in the human MGST-II genomic sequence of SEQ ID No. 485.

The terms "agent acting on arachidonic acid metabolism" refers to a drug or a compound modulating the activity or concentration of one or several enzymes of the distinct enzyme systems contributing to arachidonate metabolism including particularly the
10 5-lipoxygenase pathway. "Agent acting on arachidonic acid metabolism" also refers to compounds modulating the formation and action of the eicosanoids including particularly the leukotrienes.

The terms "response to a drug" refer to drug efficacy, including but not limited to ability to metabolize a therapeutic compound, to the ability to convert a pro-drug to an
15 active drug, and to the pharmacokinetics (absorption, distribution, elimination) and the pharmacodynamics (receptor-related) of a drug in an individual.

The terms "response to an agent acting on arachidonic acid metabolism" refer to drug efficacy, including but not limited to ability to metabolize a compound, to the ability to convert a pro-drug to an active drug, and to the pharmacokinetics (absorption, distribution,
20 elimination) and the pharmacodynamics (receptor-related) of a drug in an individual.

The terms "side effects to a drug" refer to adverse effects of therapy resulting from extensions of the principal pharmacological action of the drug or to idiosyncratic adverse reactions resulting from an interaction of the drug with unique host factors. "Side effects to a drug" include, but are not limited to, adverse reactions such as dermatologic, hematologic
25 or hepatologic toxicities and further includes gastric and intestinal ulceration, disturbance in platelet function, renal injury, generalized urticaria, bronchoconstriction, hypotension, and shock.

The terms "side effects to an agent acting on arachidonic acid metabolism" refer to adverse effects of therapy resulting from extensions of the principal pharmacological action
30 of the drug or to idiosyncratic adverse reactions resulting from an interaction of the drug with unique host factors. The terms "side effects to an agent acting on arachidonic acid metabolism" include, but are not limited to, adverse reactions such as dermatologic, hematologic or hepatologic toxicities.

The term "sequence described in Figure 2" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 2. The SEQ ID that contains each "sequence described in Figure 2" is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which each
5 sequence consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF PREFERRED SEQUENCE". It should be noted that some of the Sequence ID numbers have multiple sequence ranges listed, because they contain multiple "sequences described in Figure 2." Unless otherwise noted the term "sequence described in Figure 2" is to be construed as encompassing sequences that contain either of the two alleles
10 listed in the columns labeled, "1ST ALLELE" and "2ND ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Figure 2.

The term "sequence described in Figure 3" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 3. Unless
15 otherwise noted, the "sequences described in Figure 3" consist of the entire sequence of each Sequence ID provided in the column labeled, "SEQ ID NO." Also unless otherwise noted the term "sequence described in Figure 3" is to be construed as encompassing sequences that contain either of the two alleles listed in the columns labeled, "ORIGINAL ALLELE" and "ALTERNATIVE ALLELE" at the position identified in field <222> of the
20 allele feature in the appended Sequence Listing for each Sequence ID number referenced in Figure 3.

The term "sequence described in Figure 4" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 4. Unless otherwise noted, the "sequences described in Figure 4" consist of the entire sequence of
25 each Sequence ID provided in the column labeled, "SEQ ID NO." Also unless otherwise noted the term "sequence described in Figure 4" is to be construed as encompassing sequences that contain either of the two alleles listed in the columns labeled, "1ST ALLELE" and "2ND ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Figure 4.

30 The term "sequence described in Figure 5" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 5. The SEQ ID that contains each "sequence described in Figure 5" is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled,

"POSITION RANGE OF PREFERRED SEQUENCE". It should be noted that some of the Sequence ID numbers have multiple sequence ranges listed, because they contain multiple "sequences described in Figure 5."

The term "sequence described in Figure 6" is used herein to refer to the entire
5 collection of nucleotide sequences or any individual sequence defined in Figure 6. The SEQ ID that contains each "sequence described in Figure 6 " is provided in the column labeled, "SEQ ID" The range of nucleotide positions within the Sequence ID of which half of the sequences consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF MICROSEQUENCING PRIMERS". The remaining half of the
10 sequences described in Figure 6 are complementary to the range of nucleotide positions within the Sequence ID provided in the same row as the Sequence ID in a column labeled, "COMPLEMENTARY POSITION RANGE OF MICROSEQUENCING PRIMERS".

The term "sequence described in Figure 7" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 7. The SEQ
15 ID that contains each "sequence described in Figure 7 " is provided in the column labeled, "SEQ ID" The range of nucleotide positions within the Sequence ID of which half of the sequences consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF AMPLIFICATION PRIMERS". The remaining half of the sequences described in Figure 7 are complementary to the range of nucleotide positions
20 within the Sequence ID provided in the same row as the Sequence ID in a column labeled, "COMPLEMENTARY POSITION RANGE OF AMPLIFICATION PRIMERS".

The term "sequence described in Figure 8" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 8. The SEQ
ID that contains each "sequence described in Figure 8 " is provided in the column labeled,
25 "SEQ ID". The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF PROBES". The sequences which are complementary to the ranges listed in the column labeled, "POSITION RANGE OF PROBES" are also encompassed by the term, "sequence described in Figure 8." Unless otherwise noted the term "sequence
30 described in Figure 8 " is to be construed as encompassing sequences that contain either of the two alleles listed in the allele feature in the sequence listing.

The terms "biallelic marker described in Figure" and "allele described in Figure" are used herein to refer to any or all alleles which are listed in the allele feature in the appended

Sequence Listing for each Sequence ID number referenced in the particular Figure being mentioned.

Variants and Fragments

The invention also relates to variants and fragments of the polynucleotides described
5 herein, particularly of a MGST-II gene containing one or more biallelic markers according to the invention.

Variants of polynucleotides, as the term is used herein, are polynucleotides that differ from a reference polynucleotide. A variant of a polynucleotide may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is
10 not known to occur naturally. Such non-naturally occurring variants of the polynucleotide may be made by mutagenesis techniques, including those applied to polynucleotides, cells or organisms. Generally, differences are limited so that the nucleotide sequences of the reference and the variant are closely similar overall and, in many regions, identical.

Variants of polynucleotides according to the invention include, without being limited to,
15 nucleotide sequences which are at least 95% identical, preferably at least 99% identical, more particularly at least 99.5% identical, and most preferably at least 99.8% identical to a polynucleotide selected from the group consisting of the polynucleotides of a sequence from any sequence in the Sequence Listing as well as sequences which are complementary thereto or to any polynucleotide fragment of at least 8 consecutive nucleotides of a sequence
20 from any sequence in the Sequence Listing. Nucleotide changes present in a variant polynucleotide may be silent, which means that they do not alter the amino acids encoded by the polynucleotide. However, nucleotide changes may also result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence. The substitutions, deletions or additions may involve one or more
25 nucleotides. The variants may be altered in coding or non-coding regions or both.

Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. In the context of the present invention, particularly preferred embodiments are those in which the polynucleotides encode polypeptides which retain substantially the same biological function or activity as the mature MGST-II protein,
30 or those in which the polynucleotides encode polypeptides which maintain or increase a particular biological activity, while reducing a second biological activity. A polynucleotide fragment is a polynucleotide having a sequence that is entirely the same as part but not all of a given nucleotide sequence, preferably the nucleotide sequence of a MGST-II gene, and variants thereof. The fragment can be a portion of an exon or of an intron of a MGST-II

gene. It can also be a portion of the regulatory regions of MGST-II, preferably of the promoter sequence of the MGST-II gene. Such fragments may be "free-standing", i.e. not part of or fused to other polynucleotides, or they may be comprised within a single larger polynucleotide of which they form a part or region. Indeed, several of these fragments may
5 be present within a single larger polynucleotide.

Identity Between Nucleic Acids or Polypeptides

The terms "percentage of sequence identity" and "percentage homology" are used interchangeably herein to refer to comparisons among polynucleotides and polypeptides, and are determined by comparing two optimally aligned sequences over a comparison
10 window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to
15 yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Homology is evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA,
20 and CLUSTALW (Pearson and Lipman, *Proc. Natl. Acad. Sci.* 85(8):2444-2448, 1988; Altschul et al., *J. Mol. Biol.* 215(3):403-410, 1990; Thompson et al., *Nucleic Acids Res.* 22(2):4673-4680, 1994; Higgins et al., *Methods Enzymol.* 266:383-402, 1996; Altschul et al., *Nature Genetics* 3:266-272, 1993). In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search
25 Tool ("BLAST") which is well known in the art (See, e.g., Karlin and Altschul, *Proc. Natl. Acad. Sci. USA* 87:2267-2268, 1990; Altschul et al., *J. Mol. Biol.* 215(3):403-410, 1990; Altschul et al., *Nature Genetics* 3:266-272, 1993; Altschul et al., *Nuc. Acids Res.* 25:3389-3402, 1997). In particular, five specific BLAST programs are used to perform the following task:

30 (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
(2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
- 5 (5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a

10 protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (i.e., aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al., *Science* 256:1443-1445, 1992; Henikoff and Henikoff, *Proteins* 17:49-61, 1993). Less preferably, the PAM or PAM250 matrices may also be used (See, e.g., Schwartz and Dayhoff, eds.,

15 *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation, 1978). The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-

20 scoring segment pair is evaluated using the statistical significance formula of Karlin (see, e.g., Karlin and Altschul, 1990).

Stringent Hybridization Conditions

By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h

25 to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Alternatively, the hybridization step can be performed at

30 65°C in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37°C for 1 h in a solution containing 2 x SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1 X SSC at 50°C for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68°C for 15

minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989; and Ausubel et al., 1989. These hybridization conditions are suitable for a nucleic acid molecule of about 20 nucleotides in length. There is no need to say that the hybridization conditions described above are to be adapted according to the length of the desired nucleic acid, following techniques well known to the one skilled in the art. The suitable hybridization conditions may for example be adapted according to the teachings disclosed in the book of Hames and Higgins (*Nucleic Acid Hybridization: A Practical Approach*, IRL Press, Oxford, 1985) or in Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2nd edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

I. Biallelic Markers and Polynucleotides Comprising Biallelic Markers

I.A. Polynucleotides of the Present Invention

The present invention encompasses polynucleotides for use as primers and probes in the methods of the invention. These polynucleotides may consist of, consist essentially of, or comprise a contiguous span of nucleotides of a sequence from any sequence in the Sequence Listing as well as sequences which are complementary thereto ("complements thereof"). The "contiguous span" may be at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular Sequence ID. It should be noted that the polynucleotides of the present invention are not limited to having the exact flanking sequences surrounding the polymorphic bases which, are enumerated in the Sequence Listing. Rather, it will be appreciated that the flanking sequences surrounding the biallelic markers, or any of the primers of probes of the invention which, are more distant from the markers, may be lengthened or shortened to any extent compatible with their intended use and the present invention specifically contemplates such sequences. It will be appreciated that the polynucleotides referred to in the Sequence Listing may be of any length compatible with their intended use. Also the flanking regions outside of the contiguous span need not be homologous to native flanking sequences which actually occur in human subjects. The addition of any nucleotide sequence, which is compatible with the nucleotides intended use is specifically contemplated. The contiguous span may optionally include the DME-related biallelic marker in said sequence. Biallelic markers generally consist of a polymorphism at one single base position. Each biallelic marker therefore corresponds to two forms of a polynucleotide sequence which, when compared with one another, present a nucleotide

modification at one position. Usually, the nucleotide modification involves the substitution of one nucleotide for another. Optionally either the original or the alternative allele of the biallelic markers disclosed in Figure 3, or the first or second allele disclosed in Figure 2 and 3 may be specified as being present at the DME-related biallelic marker. Optionally, the biallelic markers may be specified as 12-421-135, 12-442-133, 12-449-63, 12-454-242, 12-463-230, 12-462-199, 10-430-287, 12-718-432, 12-269-301, 2-13-398, 2-28-132, 2-39-27, 2-45-155, 2-4-391, 12-345-410, 10-358-353, 10-360-190, 10-365-374, 10-367-58, 12-468-424, 12-481-293, 12-499-86, 12-500-217, 12-511-101, 12-586-443, 12-593-287, 12-795-383, 10-494-332, 12-659-251, 12-912-419, 12-914-28, 12-624-307 which consist of more complex polymorphisms including insertions/deletions of at least one nucleotide.

Optionally either the original or the alternative allele of these biallelic markers may be specified as being present at the DME-related biallelic marker. Preferred polynucleotides may consist of, consist essentially of, or comprise a contiguous span of nucleotides of a sequence from SEQ ID No. 436-468 well as sequences which are complementary thereto. The "contiguous span" may be at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular Sequence ID. The contiguous span may optionally comprise a biallelic marker selected from the group consisting of biallelic markers 12-421-135, 12-442-133, 12-449-63, 12-454-242, 12-463-230, 12-462-199, 10-430-287, 12-718-432, 12-269-301, 2-13-398, 2-28-132, 2-39-27, 2-45-155, 2-4-391, 12-345-410, 10-358-353, 10-360-190, 10-365-374, 10-367-58, 12-468-424, 12-481-293, 12-499-86, 12-500-217, 12-511-101, 12-586-443, 12-593-287, 12-795-383, 10-494-332, 12-659-251, 12-912-419, 12-914-28, 12-624-307.

The preferred polynucleotides of the invention include the sequence ranges included in any one the sequence ranges of Figures 2, and 5 to 8 individually or in groups consisting of all the possible combinations of the ranges of included in Figures 2, and 5 to 8. The preferred polynucleotides of the invention also include fragments of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides of the sequence ranges included in any one of the sequence ranges of Figures 2, and 5 to 8 to the extent that fragments of these lengths are consistent with the lengths of the particular sequence range. The preferred polynucleotides of the invention also include fragments of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides of the sequence complementary to the sequence ranges included in any one of the sequence ranges

of Figures 2, and 5 to 8 to the extent that fragments of these lengths are consistent with the lengths of the particular sequence range.

Preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50,
5 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence selected from the group consisting of the sequences of SEQ ID Nos. 2-3, 5-30, 437-441, 472, 485-487, and 490-493 and the complements thereof.

Particularly preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30,
10 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 485, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of the following nucleotide positions of SEQ ID No. 485: 1 to 7667, 7726 to 20264, 20365 to 36918, 36991 to 45180, 45263 to 45741, and 45980 to 49327, and the complements thereof. Other particularly preferred polynucleotides of the present invention include isolated, purified or
15 recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 486, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 486 and the complements thereof. Other particularly preferred polynucleotides of the present invention include isolated, purified or recombinant
20 polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 487, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 487 and the complements thereof. Other particularly preferred polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a
25 contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 490, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 490 and the complements thereof. Other preferred polynucleotides of the present invention include polynucleotides comprising, consisting of, or consisting essentially of a nucleotide sequence
30 of SEQ ID No. 491.

Particularly preferred polynucleotides of the present invention include purified, isolated or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37,

38, 41, 323, 345, 351-353, 357, 377, and 380, or the complements thereof, wherein said span includes a MGST-II-related biallelic marker. Optionally either allele of the biallelic markers described above in the definition of MGST-II-related biallelic marker is specified as being present at the MGST-II-related biallelic marker.

- 5 Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36971, a C at position 45214 or a T at position 45741 of SEQ ID No. 485. Additional preferred
- 10 polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 486, wherein said contiguous span comprises a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486; or the complement thereof. Additional preferred polynucleotides of the
- 15 invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 487, wherein said contiguous span comprises a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487; or the complements thereof.
- 20 Table 2 contains a list of preferred MGST-II-related biallelic markers. Each marker is described by indicating its Marker ID, the position of the marker in the SEQ ID and the two most common alleles.

Table 2

BIALLELIC MARKER ID	ALLELES	POSITION OF BIALLELIC MARKER IN SEQ ID
Non-genic biallelic markers		
12-424-192	A/G	SEQ ID No. 2, position 501
12-424-198	G/T	SEQ ID No. 3, position 501
12-426-154	G/A	SEQ ID No. 5, position 461
12-429-198	C/T	SEQ ID No. 6, position 501
12-430-80	C/T	SEQ ID No. 7, position 501
12-433-215	A/G	SEQ ID No. 8, position 501
12-441-233	A/G	SEQ ID No. 9, position 501
12-441-343	G/A	SEQ ID No. 10, position 501
12-442-221	T/C	SEQ ID No. 11, position 501
12-447-58	G/C	SEQ ID No. 12, position 501
12-449-300	T/C	SEQ ID No. 472, position 501
12-453-429	C/T	SEQ ID No. 13, position 501
12-454-363	A/G	SEQ ID No. 14, position 501

12-455-326	T/C	SEQ ID No. 15, position 501
12-455-383	G/A	SEQ ID No. 16, position 501
12-456-269	A/G	SEQ ID No. 17, position 501
12-456-380	G/T	SEQ ID No. 18, position 501
12-457-204	A/G	SEQ ID No. 19, position 501
12-457-206	C/T	SEQ ID No. 20, position 501
12-458-196	A/T	SEQ ID No. 21, position 501
12-458-438	T/C	SEQ ID No. 22, position 501
12-460-274	A/G	SEQ ID No. 23, position 501
12-461-124	A/C	SEQ ID No. 24, position 501
12-461-299	C/T	SEQ ID No. 25, position 501
12-461-465	C/T	SEQ ID No. 26, position 501
12-462-280	C/T	SEQ ID No. 27, position 501
12-464-66	G/T	SEQ ID No. 28, position 501
12-465-234	G/T	SEQ ID No. 30, position 501
12-465-26	C/T	SEQ ID No. 29, position 501
12-442-133	Deletion G	SEQ ID No. 437, position 501
12-449-63	Insertion AT	SEQ ID No. 438, position 501
10-454-242	Deletion AT	SEQ ID No. 439, position 501
12-463-230	Deletion CAT	SEQ ID No. 440, position 501
12-426-199	Deletion	SEQ ID No. 441, position 501
Genic Biallelic markers		
Biallelic Markers in Genomic sequence (SEQ ID No. 485)		
10-286-289	G/C	7564
10-286-345	A/T	7619
10-286-375	A/G	7649
12-425-57	G/A	17258
12-421-135	insertion of a T	21590
12-421-140	A/G	21595
10-523-232	C/T	36971
10-289-201	C/T	45214
10-290-37	C/T	45741
10-290-326	A/G	46029
10-290-328	G/T	46032
Biallelic Markers in MGST-II cDNA (SEQ ID No. 486)		
10-286-289	G/C	98
10-286-345	A/T	153
10-286-375	A/G	183
10-289-201	C/T	478
10-290-37	C/T	526
Biallelic Markers in MGST-II cDNA (SEQ ID No. 487)		
10-286-289	G/C	98
10-286-345	A/T	153
10-286-375	A/G	183
10-289-201	C/T	378
10-290-37	C/T	426

The invention also relates to polynucleotides that hybridize, under conditions of high or intermediate stringency, to a polynucleotide of a sequence from any sequence in the Sequence Listing as well as sequences, which are complementary thereto. Preferably such

polynucleotides are at least 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that a polynucleotide of these lengths is consistent with the lengths of the particular Sequence ID. Preferred polynucleotides comprise a DME-related biallelic marker. Optionally either the original or the alternative allele of the biallelic markers

5 disclosed in Figure 3 may be specified as being present at the DME-related biallelic marker. Conditions of high and intermediate stringency are further described in III.C.4 "Methods of Genotyping DNA Samples for Biallelic Markers-Hybridization assay methods."

The present invention further embodies isolated, purified, and recombinant polynucleotides which encode MGST-II polypeptides comprising a contiguous span of at
10 least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode the variant MGST-II polypeptides of SEQ ID Nos. 488 and 489. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode a variant
15 MGST-II polypeptide comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 489. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15,
20 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488 wherein said contiguous span comprises a His residue at amino acid position 93. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of amino acid positions 1-
25 108 of SEQ ID No. 488.

The primers of the present invention may be designed from the disclosed sequences for any method known in the art. A preferred set of primers is fashioned such that the 3' end of the contiguous span of identity with the sequences of the Sequence Listing is present at the 3' end of the primer. Such a configuration allows the 3' end of the primer to hybridize to
30 a selected nucleic acid sequence and dramatically increases the efficiency of the primer for amplification or sequencing reactions. In a preferred set of primers the contiguous span is found in one of the sequences described in Figure 5. Allele specific primers may be designed such that a biallelic marker is at the 3' end of the contiguous span and the contiguous span is present at the 3' end of the primer. Such allele specific primers tend to

selectively prime an amplification or sequencing reaction so long as they are used with a nucleic acid sample that contains one of the two alleles present at a biallelic marker. The 3' end of primer of the invention may be located within or at least 2, 4, 6, 8, 10, 12, 15, 18, 20, 25, 50, 100, 250, 500, or 1000, to the extent that this distance is consistent with the particular Sequence ID, nucleotides upstream of a DME-related biallelic marker in said sequence or at any other location which is appropriate for their intended use in sequencing, amplification or the location of novel sequences or markers. A list of preferred amplification primers is disclosed in Figure 7. Primers with their 3' ends located 1 nucleotide upstream of a DME-related biallelic marker have a special utility as microsequencing assays. Preferred microsequencing primers are described in Figure 6.

The probes of the present invention may be designed from the disclosed sequences for any method known in the art, particularly methods which allow for testing if a particular sequence or marker disclosed herein is present. A preferred set of probes may be designed for use in the hybridization assays of the invention in any manner known in the art such that they selectively bind to one allele of a biallelic marker, but not the other under any particular set of assay conditions. Preferred hybridization probes may consists of, consist essentially of, or comprise a contiguous span which ranges in length from 8, 10, 12, 15, 18 or 20 to 25, 35, 40, 50, 60, 70, or 80 nucleotides, or be specified as being 12, 15, 18, 20, 25, 35, 40, or 50 nucleotides in length and including a DME-related biallelic marker of said sequence. Optionally the original allele or alternative allele disclosed in Figure 3 and 4 may be specified as being present at the biallelic marker site. Optionally, said biallelic marker may be within 6, 5, 4, 3, 2, or 1 nucleotides of the center of the hybridization probe or at the center of said probe. A particularly preferred set of hybridization probes is disclosed in Figure 8 or a sequence complementary thereto.

Any of the polynucleotides of the present invention can be labeled, if desired, by incorporating a label detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include radioactive substances, fluorescent dyes or biotin. Preferably, polynucleotides are labeled at their 3' and 5' ends. A label can also be used to capture the primer, so as to facilitate the immobilization of either the primer or a primer extension product, such as amplified DNA, on a solid support. A capture label is attached to the primers or probes and can be a specific binding member which forms a binding pair with the solid's phase reagent's specific binding member (e.g. biotin and streptavidin). Therefore depending upon the type of label carried by a polynucleotide or a probe, it may be employed to capture or to detect the target

DNA. Further, it will be understood that the polynucleotides, primers or probes provided herein, may, themselves, serve as the capture label. For example, in the case where a solid phase reagent's binding member is a nucleic acid sequence, it may be selected such that it binds a complementary portion of a primer or probe to thereby immobilize the primer or probe to the solid phase. In cases where a polynucleotide probe itself serves as the binding member, those skilled in the art will recognize that the probe will contain a sequence or "tail" that is not complementary to the target. In the case where a polynucleotide primer itself serves as the capture label, at least a portion of the primer will be free to hybridize with a nucleic acid on a solid phase. DNA Labeling techniques are well known to the skilled technician.

Any of the polynucleotides, primers and probes of the present invention can be conveniently immobilized on a solid support. Solid supports are known to those skilled in the art and include the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic beads, nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or other animal) red blood cells, duracytes® and others. The solid support is not critical and can be selected by one skilled in the art. Thus, latex particles, microparticles, magnetic or non-magnetic beads, membranes, plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red blood cells and duracytes are all suitable examples. Suitable methods for immobilizing nucleic acids on solid phases include ionic, hydrophobic, covalent interactions and the like. A solid support, as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid support can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid support and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid support material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, duracytes® and other configurations known to those of ordinary skill in the art. The

polynucleotides of the invention can be attached to or immobilized on a solid support individually or in groups of at least 2, 5, 8, 10, 12, 15, 20, or 25 distinct polynucleotides of the inventions to a single solid support. In addition, polynucleotides other than those of the invention may attached to the same solid support as one or more polynucleotides of the
5 invention.

Any polynucleotide provided herein may be attached in overlapping areas or at random locations on the solid support. Alternatively the polynucleotides of the invention may be attached in an ordered array wherein each polynucleotide is attached to a distinct region of the solid support which does not overlap with the attachment site of any other
10 polynucleotide. Preferably, such an ordered array of polynucleotides is designed to be "addressable" where the distinct locations are recorded and can be accessed as part of an assay procedure. Addressable polynucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. The knowledge of the precise location of each polynucleotides location
15 makes these "addressable" arrays particularly useful in hybridization assays. Any addressable array technology known in the art can be employed with the polynucleotides of the invention. One particular embodiment of these polynucleotide arrays is known as the Genechips™, and has been generally described in US Patent 5,143,854; PCT publications WO 90/15070 and 92/10092. These arrays may generally be produced using mechanical
20 synthesis methods or light directed synthesis methods, which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis (Fodor et al., Science, 251:767-777, 1991). The immobilization of arrays of oligonucleotides on solid supports has been rendered possible by the development of a technology generally identified as "Very Large Scale Immobilized Polymer Synthesis" (VLSIPS™) in which, typically, probes are
25 immobilized in a high density array on a solid surface of a chip. Examples of VLSIPS™ technologies are provided in US Patents 5,143,854 and 5,412,087 and in PCT Publications WO 90/15070, WO 92/10092 and WO 95/11995, which describe methods for forming oligonucleotide arrays through techniques such as light-directed synthesis techniques. In designing strategies aimed at providing arrays of nucleotides immobilized on solid supports,
30 further presentation strategies were developed to order and display the oligonucleotide arrays on the chips in an attempt to maximize hybridization patterns and sequence information. Examples of such presentation strategies are disclosed in PCT Publications WO 94/12305, WO 94/11530, WO 97/29212 and WO 97/31256.

Oligonucleotide arrays may comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides, to the extent that fragments of these
5 lengths is consistent with the lengths of the particular Sequence ID, for determining whether a sample contains one or more alleles of the biallelic markers of the present invention.

Oligonucleotide arrays may also comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50,
10 70, 80, 100, 250, 500 or 1000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for amplifying one or more alleles of the biallelic markers of Figure 1. In other embodiments, arrays may also comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a
15 fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for conducting microsequencing analyses to determine whether a sample contains one or more alleles of the biallelic markers of the invention. In still further embodiments, the oligonucleotide array may comprise at least one
20 of the sequences selecting from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for determining whether a sample contains one or more alleles of
25 the biallelic markers of the present invention.

The present invention also encompasses diagnostic kits comprising one or more polynucleotides of the invention, optionally with a portion or all of the necessary reagents and instructions for genotyping a test subject by determining the identity of a nucleotide at a DME-related biallelic marker. The polynucleotides of a kit may optionally be attached to a
30 solid support, or be part of an array or addressable array of polynucleotides. The kit may provide for the determination of the identity of the nucleotide at a marker position by any method known in the art including, but not limited to, a sequencing assay method, a microsequencing assay method, a hybridization assay method, or an allele specific amplification method. Optionally such a kit may include instructions for scoring the results

of the determination with respect to the test subjects' risk of contracting a diseases involving the metabolic conversion of xenobiotics, or likely response to a drug, or chances of suffering from side effects to a drug, including hepatotoxicity.

I.B. Genomic Sequences of the MGST-II Gene and Biallelic Markers

5 The present invention encompasses the genomic sequence of the MGST-II gene of SEQ ID No. 485. The MGST-II genomic sequences comprise exons and introns. Particularly preferred genomic sequences of the MGST-II gene of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of
10 SEQ ID No. 485, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of the following nucleotide positions of SEQ ID No. 485: 1 to 7667, 7726 to 20264, 20365 to 36918, 36991 to 45180, 45263 to 45741, and 45980 to 49327, and the complements thereof. The nucleic acids defining the MGST-II intronic polynucleotides may be used as oligonucleotide primers or probes in order to detect the presence of a copy of the MGST-II
15 gene in a test sample, or alternatively in order to amplify a target nucleotide sequence within the MGST-II sequences.

The present invention further provides MGST-II intron and exon polynucleotide sequences including biallelic markers. Particularly preferred polynucleotides of the present invention include purified, isolated or recombinant polynucleotides comprising a contiguous
20 span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence of SEQ ID No. 485; or the complements thereof; wherein said span includes a MGST-II-related biallelic marker. Preferred polynucleotides comprise at least one biallelic marker selected from the group consisting of biallelic markers 10-286-289, 10-287-116, 10-286-375, 12-425-57, 12-421-135, 12-421-140, 10-523-232, 10-289-201,
25 10-290-37, 10-290-326 and 10-290-328. The present invention also provides polynucleotides which, may be used as primers and probes in order to amplify fragments carrying biallelic markers or in order to detect biallelic marker alleles.

Regulatory sequences

The genomic sequence of the MGST-II gene contains regulatory sequences both in
30 the non-coding 5'- flanking region and in the non-coding 3'- flanking region that border the MGST-II transcribed region containing the 5 exons of this gene. 5'-regulatory sequences of the MGST-II gene comprise the polynucleotide sequences located between the nucleotide in position 1 and the nucleotide in position 7466 of the nucleotide sequence of SEQ ID No. 485. 3'-regulatory sequences of the MGST-II gene comprise the polynucleotide sequences

located between the nucleotide in position 45980 and the nucleotide in position 49327 of the nucleotide sequence of SEQ ID No. 485. Particularly preferred regulatory polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 485, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of the following nucleotide positions of SEQ ID No. 485: 1 to 7466 and 45966 to 49312; and the complements thereof.

The promoter activity of the regulatory regions contained in the MGST-II genomic sequence of polynucleotide sequence of SEQ ID No. 485 can be assessed by any method known in the art. Methods for identifying the polynucleotide fragments of SEQ ID No. 485 involved in the regulation of the expression of the MGST-II gene are well-known to those skilled in the art (see Sambrook et al., Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). An example of a typical method, that can be used, involves a recombinant vector carrying a reporter gene and genomic sequences from the MGST-II genomic sequence of SEQ ID No. 485. Briefly, the expression of the reporter gene (for example beta galactosidase or chloramphenicol acetyl transferase) is detected when placed under the control of a biologically active polynucleotide fragment. Genomic sequences located upstream of the first exon of the MGST-II gene may be cloned into any suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, p β gal-Basic, p β gal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech, or pGL2-basic or pGL3-basic promoterless luciferase reporter gene vector from Promega. Each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, luciferase, beta galactosidase, or green fluorescent protein. The sequences upstream the first MGST-II exon are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained with a vector lacking an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert.

Promoter sequences within the 5' non-coding regions of the MGST-II gene may be further defined by constructing nested 5' and/or 3' deletions using conventional techniques such as Exonuclease III or appropriate restriction endonuclease digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether

the deletion has reduced or obliterated promoter activity, such as described, for example, by Coles et al. (*Hum. Mol. Genet.*, 7:791-800, 1998). In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate
5 potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into cloning sites in promoter reporter vectors. This type of assays are well known to those skilled in the art and are further described in WO 97/17359, US 5 374 544, EP 582 796, US 5 698 389, US 5 643 746, US 5 502 176, and US 5 266 488.

10 The activity and the specificity of the promoter of the MGST-II gene can further be assessed by monitoring the expression level of a detectable polynucleotide operably linked to the MGST-II promoter in different types of cells and tissues. The detectable polynucleotide may be either a polynucleotide that specifically hybridizes with a predefined oligonucleotide probe, or a polynucleotide encoding a detectable protein, including a
15 MGST-II polypeptide or a fragment or a variant thereof. This type of assay is well known to those skilled in the art and is described in US 5 502 176 and US 5 266 488 for example.

Polynucleotides carrying the regulatory elements located both at the 5' end and at the 3' end of the MGST-II coding region may be advantageously used to control the transcriptional and translational activity of an heterologous polynucleotide of interest, said
20 polynucleotide being heterologous as regards to the MGST-II regulatory region.

Thus, the present invention also concerns a purified, isolated, and recombinant nucleic acid comprising a polynucleotide which, is selected from the group consisting of, the polynucleotide sequences located between the nucleotide in position 1 and the nucleotide in position 7466 of the nucleotide sequence of SEQ ID No. 485; or a sequence
25 complementary thereto or a biologically active fragment thereof.

By a "biologically active" fragment of SEQ ID No. 485 according to the present invention is intended a polynucleotide comprising or alternatively consisting of a fragment of said polynucleotide which is functional as a regulatory region for expressing a recombinant polypeptide or a recombinant polynucleotide in a recombinant cell host.

30 For the purpose of the invention, a nucleic acid or polynucleotide is "functional" as a regulatory region for expressing a recombinant polypeptide or a recombinant polynucleotide if said regulatory polynucleotide contains nucleotide sequences which contain transcriptional and translational regulatory information, and such sequences are "operably

linked" to nucleotide sequences which encode the desired polypeptide or the desired polynucleotide.

The regulatory polynucleotides according to the invention may be advantageously part of a recombinant expression vector that may be used to express a coding sequence in a
5 desired host cell or host organism.

I.C. MGST-II cDNA Comprising Biallelic Markers and Variant MGST-II cDNA

The present invention provides a MGST-II cDNA of SEQ ID No. 486. The Open Reading Frame encoding the MGST-II protein spans from the nucleotide in position 202 to the nucleotide in position 642 of the polynucleotide sequence of SEQ ID No. 486. The
10 cDNA of SEQ ID No. 486 also includes a 5'-UTR region and a 3'-UTR region.

Particularly preferred cDNA polynucleotides of the present invention include purified, isolated or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence of SEQ ID No. 486, or the complements thereof, wherein said span includes a
15 MGST-II-related biallelic marker. Preferred cDNA fragments comprise a biallelic marker selected from the group consisting of 10-286-289 (position 98), 10-286-345 (position 153), 10-286-375 (position 183), 10-523-232 (position 426), 10-289-201 (position 478) and 10-290-37 (position 526). Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least
20 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 486, wherein said contiguous span comprises a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486; or the complement thereof. Most biallelic polymorphism represent silent nucleotide substitutions but biallelic marker 10-289-201 is associated with an amino acid change in the
25 corresponding MGST-II polypeptide (TYR replaced by ARG in position 93 of the polypeptide). Moreover, one biallelic marker allele of marker 10-290-37 is associated with a stop codon and the corresponding variant cDNA encodes a truncated MGST-II polypeptide including amino acids 1 to 108.

The present invention further provides a variant MGST-II cDNA of SEQ ID No.
30 487, corresponding to an alternative splicing form which results in the deletion of exon 2. This alternative splicing of MGST-II yields the variant MGST-II polypeptide of SEQ ID No. 489. MGST-II polypeptides of the present invention are further described below. Preferred cDNAs of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90,

100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 487; or the complements thereof. Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides
5 from a sequence of SEQ ID No. 487, wherein said contiguous span comprises a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487; or the complements thereof. The new exon 1/exon 3 junction sequence of the splice variant MGST-II cDNA, more particularly the nucleotide sequence comprised between the nucleotide in position 106 and the nucleotide in position 374 of the nucleic acid of SEQ ID
10 No. 486 corresponds to the nucleotide sequence of an EST that has been obtained from a human cDNA library. Polynucleotides comprising this EST of a sequence from SEQ ID No. 490 are also part of the invention.

The above disclosed polynucleotides that contain the coding sequence of the MGST-II gene and of MGST-II variants may be expressed in a desired host cell or a desired host
15 organism, when this polynucleotide is placed under the control of suitable expression signals. The expression signals may be either the expression signals contained in the regulatory regions in the MGST-II gene of the invention or in contrast the signals may be exogenous regulatory nucleic sequences. Such a polynucleotide, when placed under the suitable expression signals, may also be inserted in a vector for its expression and/or
20 amplification.

Another preferred cDNA fragment comprises the 5'-UTR region (regulatory) beginning at position 1 and ending at position 201 of SEQ ID Nos. 486 and 487. Preferably said 5'-UTR region comprises a biallelic marker selected from the group consisting of biallelic markers 10-286-289, 10-286-345 and 10-286-375. Particularly preferred 5'-UTR
25 polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 486, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 486; and the complements thereof. The 5'-end sequence of the MGST-II cDNA,
30 more particularly the nucleotide sequence comprised between the nucleotide in position 1 and the nucleotide in position 357 of the nucleic acid of SEQ ID No. 486 corresponds to the nucleotide sequence of a 5'-EST that has been obtained from a human cDNA library. Polynucleotides comprising this 5'-EST of a sequence from SEQ ID No. 490 are also part of the invention.

The polynucleotide disclosed above that contains the coding sequence of the MGST-II gene of the invention may be expressed in a desired host cell or a desired host organism, when this polynucleotide is placed under the control of suitable expression signals. The expression signals may be either the expression signals contained in the regulatory regions 5 in the MGST-II gene of the invention or may be exogenous regulatory nucleic sequences. Such a polynucleotide, when placed under the suitable expression signals, may also be inserted in a vector for its expression.

A further object of the invention consists of an isolated polynucleotide comprising:

- a) a nucleic acid comprising a regulatory nucleotide sequence from a sequence of SEQ ID 10 No. 485;
- b) a polynucleotide encoding a desired polypeptide or a nucleic acid of interest, operably linked to the nucleic acid defined in (a) above;
- c) Optionally, a nucleic acid comprising a 5'-UTR regulatory polynucleotide, preferably a 5'-UTR regulatory polynucleotide sequence of a sequence of SEQ ID No. 486.

15 The polypeptide encoded by the nucleic acid described above may be of various nature or origin, encompassing proteins of prokaryotic or eukaryotic origin. Among the polypeptides expressed under the control of a MGST-II regulatory region, there may be cited bacterial, fungal or viral antigens. Also encompassed are eukaryotic proteins such as intracellular proteins, for example "house keeping" proteins, membrane-bound proteins, for 20 example receptors, and secreted proteins, for example cytokines. In a specific embodiment, the desired polypeptide may be the MGST-II protein, especially the proteins of the amino acid sequence of SEQ ID Nos. 488 and 489.

The desired nucleic acids encoded by the above described polynucleotide, usually a RNA molecule, may be complementary to a desired coding polynucleotide, for example to 25 the MGST-II coding sequence, and thus useful as an antisense polynucleotide.

Such a polynucleotide may be included in a recombinant expression vector in order to express the desired polypeptide or the desired nucleic acid in host cell or in a host organism.

I.D. Polynucleotide Constructs, Recombinant Vectors, Host Cells and Transgenic

30 Animals

Polynucleotide Constructs

The terms "polynucleotide construct" and "recombinant polynucleotide" are used interchangeably herein to refer to linear or circular, purified or isolated polynucleotides that

have been artificially designed and which comprise at least two nucleotide sequences that are not found as contiguous nucleotide sequences in their initial natural environment.

DNA constructs for expressing the MGST-II gene in recombinant host cells and in transgenic animals

5 In order to study the physiological and phenotype consequences of a lack of synthesis of the MGST-II protein, both at the cellular level and at the multicellular organism level, in particular as regards to disorders related to abnormal cell proliferation, notably cancers, the invention also encompasses DNA constructs and recombinant vectors enabling a conditional expression of a specific allele of the MGST-II genomic sequence or cDNA

10 A first preferred DNA construct is based on the tetracycline resistance operon *tet* from *E. coli* transposon Tn10 for controlling the MGST-II gene expression, such as described by Gossen et al. (*Science*, 268:1766-1769, 1995). Such a DNA construct contains seven *tet* operator sequences from Tn10 (*tetop*) that are fused to either a minimal promoter or a 5'-regulatory sequence of the MGST-II gene, said minimal promoter or said MGST-II
15 regulatory sequence being operably linked to a polynucleotide of interest that codes either for a sense or an antisense oligonucleotide or for a polypeptide, including a MGST-II polypeptide or a peptide fragment thereof. This DNA construct is functional as a conditional expression system for the nucleotide sequence of interest when the same cell also comprises a nucleotide sequence coding for either the wild type (tTA) or the mutant (rTA) repressor
20 fused to the activating domain of viral protein VP16 of herpes simplex virus, placed under the control of a promoter, such as the HCMVIE1 enhancer/promoter or the MMTV-LTR. Indeed, a preferred DNA construct of the invention will comprise both the polynucleotide containing the *tet* operator sequences and the polynucleotide containing a sequence coding for the tTA or the rTA repressor. In the specific embodiment wherein the conditional
25 expression DNA construct contains the sequence encoding the mutant tetracycline repressor rTA, the expression of the polynucleotide of interest is silent in the absence of tetracycline and induced in its presence.

DNA constructs allowing homologous recombination: replacement vectors

30 A second preferred DNA construct will comprise, from 5'-end to 3'-end : (a) a first nucleotide sequence that is comprised in the MGST-II genomic sequence; (b) a nucleotide sequence comprising a positive selection marker, such as the marker for neomycine resistance (*neo*); and (c) a second nucleotide sequence that is comprised in the MGST-II genomic sequence, and is located on the genome downstream the first MGST-II nucleotide sequence (a).

In a preferred embodiment, this DNA construct also comprises a negative selection marker located upstream the nucleotide sequence (a) or downstream the nucleotide sequence (c). Preferably, the negative selection marker consists of the thymidine kinase (*tk*) gene (Thomas et al., *Cell*, 44:419-428, 1986), the hygromycin beta gene (Te Riele et al., *Nature*, 348:649-651, 1990), the *hprt* gene (Van der Lugt et al., *Gene*, 105:263-267, 1991; Reid et al., *Proc. Natl. Acad. Sci. USA*, 87:4299-4303, 1990) or the Diphtheria toxin A fragment (*Dt-A*) gene (Nada et al., *Cell*, 73:1125-1135, 1993; Yagi et al., *Proc. Natl. Acad. Sci. USA*, 87:9918-9922, 1990). Preferably, the positive selection marker is located within a MGST-II exon sequence so as to interrupt the sequence encoding a MGST-II protein. These replacement vectors are further described by Mansour et al. (*Nature*, 336:348-352, 1988) and Koller et al. (*Ann. Rev. Immunol.*, 10:705-730, 1992). The first and second nucleotide sequences (a) and (c) may be indifferently located within a MGST-II regulatory sequence, an intronic sequence, an exon sequence or a sequence containing both regulatory and/or intronic and/or exon sequences. The size of the nucleotide sequences (a) and (c) is ranging from 1 to 50 kb, preferably from 1 to 10 kb, more preferably from 2 to 6 kb and most preferably from 2 to 4 kb.

DNA constructs allowing homologous recombination: Cre-loxP system

These new DNA constructs make use of the site specific recombination system of the P1 phage. The P1 phage possesses a recombinase called Cre which, interacts specifically with a 34 base pairs *loxP* site. The *loxP* site is composed of two palindromic sequences of 13 bp separated by a 8 bp conserved sequence (Hoess et al., *Nucleic Acids Res.*, 14:2287-2300, 1986). The recombination by the Cre enzyme between two *loxP* sites having an identical orientation leads to the deletion of the DNA fragment.

The Cre-*loxP* system used in combination with a homologous recombination technique has been first described by Gu et al. (*Cell*, 73:1155-1164, 1993). Briefly, a nucleotide sequence of interest to be inserted in a targeted location of the genome harbors at least two *loxP* sites in the same orientation and located at the respective ends of a nucleotide sequence to be excised from the recombinant genome. The excision event requires the presence of the recombinase (Cre) enzyme within the nucleus of the recombinant cell host. The recombinase enzyme may be brought at the desired time either by (a) incubating the recombinant cell hosts in a culture medium containing this enzyme, by injecting the Cre enzyme directly into the desired cell, such as described by Araki et al. (*Proc. Natl. Acad. Sci. USA*, 92: 160-164, 1995), or by lipofection of the enzyme into the cells, such as described by Baubonis et al. (*Nucleic Acids Res.*, 21:2025-2029, 1993); (b) transfecting the

- cell host with a vector comprising the *Cre* coding sequence operably linked to a promoter functional in the recombinant cell host, which promoter being optionally inducible, said vector being introduced in the recombinant cell host, such as described by Gu et al. (*Cell*, 73:1155-1164, 1993) and Sauer et al. (*Proc. Natl. Acad. Sci. USA*, 85:5166-5170, 1988); (c) introducing in the genome of the cell host a polynucleotide comprising the *Cre* coding sequence operably linked to a promoter functional in the recombinant cell host, which promoter is optionally inducible, and said polynucleotide being inserted in the genome of the cell host either by a random insertion event or an homologous recombination event, such as described by Gu et al. (*Science*, 265:103-106, 1994).
- 10 In the specific embodiment wherein the vector containing the sequence to be inserted in the MGST-II gene by homologous recombination is constructed in such a way that selectable markers are flanked by *loxP* sites of the same orientation, it is possible, by treatment by the Cre enzyme, to eliminate the selectable markers while leaving the MGST-II sequences of interest that have been inserted by an homologous recombination event.
- 15 Again, two selectable markers are needed: a positive selection marker to select for the recombination event and a negative selection marker to select for the homologous recombination event. Vectors and methods using the Cre-*loxP* system are further described by Zou et al. (*Curr. Biol.*, 4:1099-1103, 1994).

- Thus, a third preferred DNA construct of the invention comprises, from 5'-end to 3'-end: (a) a first nucleotide sequence that is comprised in the MGST-II genomic sequence; (b) a nucleotide sequence comprising a polynucleotide encoding a positive selection marker, said nucleotide sequence comprising additionally two sequences defining a site recognized by a recombinase, such as a *loxP* site, the two sites being placed in the same orientation; and (c) a second nucleotide sequence that is comprised in the MGST-II genomic sequence, and
- 20 is located on the genome downstream of the first MGST-II nucleotide sequence (a).

- The sequences defining a site recognized by a recombinase, such as a *loxP* site, are preferably located within the nucleotide sequence (b) at suitable locations bordering the nucleotide sequence for which the conditional excision is sought. In one specific embodiment, two *loxP* sites are located at each side of the positive selection marker
- 30 sequence, in order to allow its excision at a desired time after the occurrence of the homologous recombination event.

In a preferred embodiment of a method using the third DNA construct described above, the excision of the polynucleotide fragment bordered by the two sites recognized by a recombinase, preferably two *loxP* sites, is performed at a desired time. due to the presence

within the genome of the recombinant cell host of a sequence encoding the Cre enzyme operably linked to a promoter sequence, preferably an inducible promoter, more preferably a tissue-specific promoter sequence and most preferably a promoter sequence which is both inducible and tissue-specific, such as described by Gu et al. (*Science*, 265:103-106, 1994).

5 The presence of the Cre enzyme within the genome of the recombinant cell host may result of the breeding of two transgenic animals, the first transgenic animal bearing the MGST-II-derived sequence of interest containing the *loxP* sites as described above and the second transgenic animal bearing the *Cre* coding sequence operably linked to a suitable promoter sequence, such as described by Gu et al. (*Science*, 265:103-106, 1994).

10 Spatio-temporal control of the Cre enzyme expression may also be achieved with an adenovirus based vector that contains the Cre gene thus allowing infection of cells, or *in vivo* infection of organs, for delivery of the Cre enzyme, such as described by Anton et al. (*J. Virol.*, 69:4600-4606, 1995) and Kanegae et al. (*Nucleic Acids Res.*, 23:3816-3821, 1995).

15 The DNA constructs described above may be used to introduce a desired nucleotide sequence of the invention, preferably a MGST-II genomic sequence or a MGST-II cDNA sequence, and most preferably an altered copy of a MGST-II genomic or cDNA sequence, within a predetermined location of the targeted genome, leading either to the generation of an altered copy of a targeted gene (knock-out homologous recombination) or to the
20 replacement of a copy of the targeted gene by another copy sufficiently homologous to allow an homologous recombination event to occur (knock-in homologous recombination).

Recombinant Vectors

The term "vector" is used herein to designate either a circular or a linear DNA or RNA molecule, which is either double-stranded or single-stranded, and which comprise at
25 least one polynucleotide of interest that is sought to be transferred in a cell host or in a unicellular or multicellular host organism.

The present invention encompasses a family of recombinant vectors that comprise a regulatory polynucleotide derived from the MGST-II genomic sequence, or a coding polynucleotide from the MGST-II genomic sequence. Consequently, the present invention
30 further deals with a recombinant vector comprising either a regulatory polynucleotide comprised in the nucleic acid of SEQ ID Nos. 485 and 486 or a polynucleotide comprising the MGST-II coding sequence or both.

In a first preferred embodiment, a recombinant vector of the invention is used to amplify the inserted polynucleotide derived from a MGST-II genomic sequence selected

from the group consisting of the nucleic acids of SEQ ID No. 485 or a MGST-II cDNA, for example the cDNA of SEQ ID Nos. 486 and 487 in a suitable host cell, this polynucleotide being amplified each time the recombinant vector replicates. Generally, a recombinant vector of the invention may comprise any of the polynucleotides described herein, including
5 regulatory sequences and coding sequences, as well as any MGST-II primer or probe as defined above.

A second preferred embodiment of the recombinant vectors according to the invention consists of expression vectors comprising either a regulatory polynucleotide or a coding nucleic acid of the invention, or both. Within certain embodiments, expression
10 vectors are employed to express the MGST-II polypeptide which can be then purified and, for example be used in ligand screening assays or as an immunogen in order to raise specific antibodies directed against the MGST-II protein. In other embodiments, the expression vectors are used for constructing transgenic animals and also for gene therapy. Expression requires that appropriate signals are provided in the vectors, said signals including various
15 regulatory elements, such as enhancers/promoters from both viral and mammalian sources that drive expression of the genes of interest in host cells. Dominant drug selection markers for establishing permanent, stable cell clones expressing the products are generally included in the expression vectors of the invention, as they are elements that link expression of the drug selection markers to expression of the polypeptide.

20 More particularly, the present invention relates to expression vectors which include nucleic acids encoding a MGST-II protein, preferably the MGST-II protein of the amino acid sequence of SEQ ID Nos. 488 and 489, under the control of a regulatory sequence selected among the MGST-II regulatory polynucleotides of SEQ ID Nos. 485 and 486, or alternatively under the control of an exogenous regulatory sequence. Consequently,
25 preferred expression vectors of the invention are selected from the group consisting of : (a) the MGST-II regulatory sequence comprised therein drives the expression of a coding polynucleotide operably linked thereto; (b) the MGST-II coding sequence is operably linked to regulation sequences allowing its expression in a suitable cell host and/or host organism. Additionally, the recombinant expression vector described above may also comprise a
30 nucleic acid comprising a 5'-regulatory polynucleotide or a 3'-regulatory polynucleotide, preferably a 5'-regulatory polynucleotide or a 3'-regulatory polynucleotide of the MGST-II gene. The MGST-II 5'-regulatory polynucleotide may also comprise the 5'-UTR sequence contained in the nucleotide sequence of SEQ ID Nos. 486 and 487; or a biologically active fragment or variant thereof. The invention also pertains to a recombinant expression vector

useful for the expression of the MGST-II coding sequence, wherein said vector comprises any of the MGST-II cDNAs or cDNA variants described above; or fragments thereof.

Some of the elements which, can be found in the vectors of the present invention are described in further detail in the following sections.

5 1. General features of the expression vectors of the invention

- A recombinant vector according to the invention comprises, but is not limited to, a YAC (Yeast Artificial Chromosome), a BAC (Bacterial Artificial Chromosome), a phage, a phagemid, a cosmid, a plasmid or even a linear DNA molecule which may consist of a chromosomal, non-chromosomal, semi-synthetic and synthetic DNA. Such a recombinant
- 10 vector can comprise a transcriptional unit comprising an assembly of :
- (1) a genetic element or elements having a regulatory role in gene expression, for example promoters or enhancers. Enhancers are cis-acting elements of DNA, usually from about 10 to 300 bp in length that act on the promoter to increase the transcription.
 - (2) a structural or coding sequence which is transcribed into mRNA and eventually
 - 15 translated into a polypeptide, said structural or coding sequence being operably linked to the regulatory elements described in (1); and
 - (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, when a
 - 20 recombinant protein is expressed without a leader or transport sequence, it may include a N-terminal residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

Generally, recombinant expression vectors will include origins of replication, selectable markers permitting transformation of the host cell, and a promoter derived from a

25 highly expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably a leader sequence capable of directing secretion of the translated protein into the periplasmic space or the extracellular medium. In a specific embodiment wherein the vector is adapted for transfecting and expressing desired

30 sequences in mammalian host cells, preferred vectors will comprise an origin of replication in the desired host, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5'-flanking non-transcribed sequences. DNA sequences derived

from the SV40 viral genome, for example SV40 origin, early promoter, enhancer, splice and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

The *in vivo* expression of a MGST-II polypeptide of SEQ ID Nos. 488 and 489 may be useful in order to correct a genetic defect related to the expression of the native gene in a host organism or to the production of a biologically inactive MGST-II protein.

Consequently, the present invention also deals with recombinant expression vectors mainly designed for the *in vivo* production of the MGST-II polypeptide of SEQ ID Nos. 488 and 489 or fragments or variants thereof by the introduction of the appropriate genetic material in the organism of the patient to be treated. This genetic material may be introduced *in vitro* in a cell that has been previously extracted from the organism, the modified cell being subsequently reintroduced in the said organism, directly *in vivo* into the appropriate tissue.

2. Regulatory elements

Promoters:

The suitable promoter regions used in the expression vectors according to the present invention are chosen taking into account the cell host in which the heterologous gene has to be expressed. The particular promoter employed to control the expression of a nucleic acid sequence of interest is not believed to be important, so long as it is capable of directing the expression of the nucleic acid in the targeted cell. Thus, where a human cell is targeted, it is preferable to position the nucleic acid coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell, such as, for example, a human or a viral promoter.

A suitable promoter may be heterologous with respect to the nucleic acid for which it controls the expression or alternatively can be endogenous to the native polynucleotide containing the coding sequence to be expressed. Additionally, the promoter is generally heterologous with respect to the recombinant vector sequences within which the construct promoter/coding sequence has been inserted.

Promoter regions can be selected from any desired gene using, for example, CAT (chloramphenicol transferase) vectors and more preferably pKK232-8 and pCM7 vectors.

Preferred bacterial promoters are the LacI, LacZ, the T3 or T7 bacteriophage RNA polymerase promoters, the gpt, lambda PR, PL and trp promoters (EP 0036776), the polyhedrin promoter, or the p10 protein promoter from baculovirus (Kit Novagen) (Smith et al., 1983; O'Reilly et al., 1992), the lambda PR promoter or also the trc promoter.

Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-L. Selection of a convenient vector and promoter is well within the level of ordinary skill in the art.

The choice of a promoter is well within the ability of a person skilled in the field of genetic engineering. For example, one may refer to the book of Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2nd edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

Other regulatory elements:

Where a cDNA insert is employed, one will typically desire to include a polyadenylation signal to effect proper polyadenylation of the gene transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and any such sequence may be employed such as human growth hormone and SV40 polyadenylation signals. Also contemplated as an element of the expression cassette is a terminator. These elements can serve to enhance message levels and to minimize read through from the cassette into other sequences.

The vector containing the appropriate DNA sequence as described above, more preferably MGST-II gene regulatory polynucleotide, a polynucleotide encoding the MGST-II polypeptides of SEQ ID Nos. 488 and 489 or both of them, can be utilized to transform an appropriate host to allow the expression of the desired polypeptide or polynucleotide.

3. Selectable markers

Such markers would confer an identifiable change to the cell permitting easy identification of cells containing the expression construct. The selectable marker genes for selection of transformed host cells are preferably dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, TRP1 for *S. cerevisiae* or tetracycline, rifampicin or ampicillin resistance in *E. coli*, or levan saccharase for mycobacteria, this latter marker being a negative selection marker.

4. Preferred vectors

Bacterial vectors:

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and a bacterial origin of replication derived from commercially available plasmids comprising genetic elements of pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia, Uppsala, Sweden), and GEM1 (Promega Biotec, Madison, WI, USA). Large numbers of other suitable vectors are known to those of skill in the art, and commercially available, such as the following

bacterial vectors : pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16A, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene); pSVK3, pBPV, pMSG, pSVL (Pharmacia); pQE-30 (QIAexpress).

5 Bacteriophage vectors

The P1 bacteriophage vector may contain large inserts ranging from about 80 to about 100 kb. The construction of P1 bacteriophage vectors such as p158 or p158/neo8 have been described by Sternberg (*Mamm. Genome*, 5:397-404, 1994). Recombinant P1 clones comprising MGST-II nucleotide sequences may be designed for inserting large
 10 polynucleotides of more than 40 kb (Linton et al., *J. Clin. Invest.*, 92:3029-3037, 1993). To generate P1 DNA for transgenic experiments, a preferred protocol is the protocol described by McCormick et al. (*Genet. Anal. Tech. Appl.*, 11:158-164, 1994). Briefly, *E. coli* (preferably strain NS3529) harboring the P1 plasmid are grown overnight in a suitable broth medium containing 25 µg/ml of kanamycin. The P1 DNA is prepared from the *E. coli* by
 15 alkaline lysis using the Qiagen Plasmid Maxi kit (Qiagen, Chatsworth, CA, USA), according to the manufacturer's instructions. The P1 DNA is purified from the bacterial lysate on two Qiagen-tip 500 columns, using the washing and elution buffers contained in the kit. A phenol/chloroform extraction is then performed before precipitating the DNA with 70% ethanol. After solubilizing the DNA in TE (10 mM Tris-HCl, pH 7.4, 1 mM
 20 EDTA), the concentration of the DNA is assessed by spectrophotometry.

When the goal is to express a P1 clone comprising MGST-II nucleotide sequences in a transgenic animal, typically in transgenic mice, it is desirable to remove vector sequences from the P1 DNA fragment, for example by cleaving the P1 DNA at rare-cutting sites within the P1 polylinker (*SfiI*, *NotI* or *SalI*). The P1 insert is then purified from vector
 25 sequences on a pulsed-field agarose gel, using methods similar using methods similar to those originally reported for the isolation of DNA from YACs (Schedl et al., 1993a; Peterson et al., 1993). At this stage, the resulting purified insert DNA can be concentrated, if necessary, on a Millipore Ultrafree-MC Filter Unit (Millipore, Bedford, MA, USA – 30,000 molecular weight limit) and then dialyzed against microinjection buffer (10 mM
 30 Tris-HCl, pH 7.4; 250 µM EDTA) containing 100 mM NaCl, 30 µM spermine, 70 µM spermidine on a microdialysis membrane (type VS, 0.025 µM from Millipore). The intactness of the purified P1 DNA insert is assessed by electrophoresis on 1% agarose (Sea Kem GTG; FMC Bio-products) pulse-field gel and staining with ethidium bromide.

Baculovirus vectors:

A suitable vector for the expression of the MGST-II polypeptides of SEQ ID Nos. 488 and 489 is a baculovirus vector that can be propagated in insect cells and in insect cell lines. A specific suitable host vector system is the pVL1392/1393 baculovirus transfer vector (Pharmingen) that is used to transfect the SF9 cell line (ATCC N^oCRL 1711) which
5 is derived from *Spodoptera frugiperda*.

Other suitable vectors for the expression of the MGST-II polypeptides of SEQ ID Nos. 488 and 489 in a baculovirus expression system include those described by Chai et al. (*Biotech. Appl. Biochem.*, 18:259-273, 1993), Vlasak et al. (*Eur. J. Biochem.*, 135: 123-126, 1983) and Lenhard et al. (*Gene*, 169: 187-190, 1996).

10 Viral vectors

Retrovirus vectors and adeno-associated virus vectors are generally understood to be the recombinant gene delivery systems of choice for the transfer of exogenous polynucleotides *in vivo*, particularly to mammals, including humans. These vectors provide efficient delivery of genes into cells, and the transferred nucleic acids are stably integrated
15 into the chromosomal DNA of the host.

Particularly preferred retroviruses for the preparation or construction of retroviral *in vitro* or *in vivo* gene delivery vehicles of the present invention include retroviruses selected from the group consisting of Mink-Cell Focus Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis virus and Rous Sarcoma virus. Particularly preferred Murine
20 Leukemia Viruses include the 4070A and the 1504A viruses, Abelson (ATCC No VR-999), Friend (ATCC No VR-245), Gross (ATCC No. VR-590), Rauscher (ATCC No VR-998) and Moloney Murine Leukemia Virus (ATCC No VR-190; PCT Application No WO 94/24298). Particularly preferred Rous Sarcoma Viruses include Bryan high titer (ATCC Nos. VR-334, VR-657, VR-726, VR-659 and VR-728). Other preferred retroviral vectors
25 are those described in Roth et al. (*Nature Medicine*, 2:985-991, 1996), PCT Application No. WO 93/25234 and PCT Application No. WO 94/ 06920.

Yet another viral vector system that is contemplated by the invention consists in the adeno-associated virus (AAV). The adeno-associated virus is a naturally occurring defective virus that requires another virus, such as an adenovirus or a herpes virus, as a helper virus
30 for efficient replication and a productive life cycle (Muzyczka et al., *Current Topics in Microbiol. Immunol.*, 158:97-129, 1992). It is also one of the few viruses that may integrate its DNA into non-dividing cells, and exhibits a high frequency of stable integration (McLaughlin et al., *Am. J. Hum. Genet.*, 59: 561-569, 1989). One advantageous feature of

AAV derives from its reduced efficacy for transducing primary cells relative to transformed cells.

BAC vectors:

The bacterial artificial chromosome (BAC) cloning system (Shizuya et al., 1992) has been developed to stably maintain large fragments of genomic DNA (100-300 kb) in *E. coli*. A preferred BAC vector consists of pBeloBAC11 vector that has been described by Kim et al. (*Genomics*, 34:213-218,1996). BAC libraries are prepared with this vector using size-selected genomic DNA that has been partially digested using enzymes that permit ligation into either the *Bam* HI or *Hind*III sites in the vector. Flanking these cloning sites are T7 and SP6 RNA polymerase transcription initiation sites that can be used to generate end probes by either RNA transcription or PCR methods. After the construction of a BAC library in *E. coli*, BAC DNA is purified from the host cell as a supercoiled circle. Converting these circular molecules into a linear form precedes both size determination and introduction of the BACs into recipient cells. The cloning site is flanked by two *Not* I sites, permitting cloned segments to be excised from the vector by *Not* I digestion. Alternatively, the DNA insert contained in the pBeloBAC11 vector may be linearized by treatment of the BAC vector with the commercially available enzyme lambda terminase that leads to the cleavage at the unique *cos*N site, but this cleavage method results in a full length BAC clone containing both the insert DNA and the BAC sequences.

5. Delivery of the recombinant vectors

In order to effect expression of the polynucleotides and polynucleotide constructs of the invention, these constructs must be delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for transforming cell lines, or *in vivo* or *ex vivo*, as in the treatment of certain diseases states. One mechanism is viral infection where the expression construct is encapsidated in an infectious viral particle. Several non-viral methods for the transfer of polynucleotides into cultured mammalian cells are also contemplated by the present invention, and include, without being limited to, calcium phosphate precipitation (Chen et al., *Proc. Natl. Acad. Sci. USA*, 94:10756-10761, 1987), DEAE-dextran (Gopal, *Mol. Cell. Biol.*, 5:1188-1190, 1985), electroporation (Tur-Kaspa et al., *Mol. Cell. Biol.*, 6:716-718, 1986), direct microinjection (Harland et al., 1985), DNA-loaded liposomes (Nicolau et al., 1982; Fraley et al., 1979), and receptor-mediate transfection (Wu and Wu, 1987; 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

Once the expression polynucleotide has been delivered into the cell, it may be stably integrated into the genome of the recipient cell. This integration may be in the cognate location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further
5 embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle.

One specific embodiment for a method for delivering a protein or peptide to the
10 interior of a cell of a vertebrate *in vivo* comprises the step of introducing a preparation comprising a physiologically acceptable carrier and a naked polynucleotide operatively coding for the polypeptide of interest into the interstitial space of a tissue comprising the cell, whereby the naked polynucleotide is taken up into the interior of the cell and has a physiological effect. This is particularly applicable for transfer *in vitro* but it may be applied
15 to *in vivo* as well.

Compositions for use *in vitro* and *in vivo* comprising a "naked" polynucleotide are described in PCT application No. WO 90/11092 (Vical Inc.) and also in PCT application No. WO 95/11307.

In still another embodiment of the invention, the transfer of a naked polynucleotide
20 of the invention, including a polynucleotide construct of the invention, into cells may be proceeded with a particle bombardment (biolistic), said particles being DNA-coated microprojectiles accelerated to a high velocity allowing them to pierce cell membranes and enter cells without killing them, such as described by Klein et al. (*Nature* 327:70-73, 1987).

In a further embodiment, the polynucleotide of the invention may be entrapped in a
25 liposome (Ghosh and Bacchawat, *Targeting of liposomes to hepatocytes*, In: *Liver Diseases, Targeted diagnosis and therapy using specific receptors and ligands*, Marcel Dekeker, New York, 87-104, 1991; Wong et al., *Gene* 10:87-94, 1980; Nicolau et al., *Biochim. Biophys. Acta.* 721:185-190, 1982).

In a specific embodiment, the invention provides a composition for the *in vivo*
30 production of the MGST-II protein or polypeptide described herein. It comprises a naked polynucleotide operatively coding for this polypeptide, in solution in a physiologically acceptable carrier, and suitable for introduction into a tissue to cause cells of the tissue to express the said protein or polypeptide.

The amount of vector to be injected to the desired host organism varies according to the site of injection. As an indicative dose, it will be injected between 0.1 and 100 µg of the vector in an animal body, preferably a mammal body, for example a mouse body.

In another embodiment of the invention, the vector may be introduced *in vitro* in a
5 host cell, preferably in a host cell previously harvested from the animal to be treated and more preferably a somatic cell such as a muscle cell. In a subsequent step, the cell that has been transformed with the vector coding for the desired MGST-II polypeptide or the desired fragment thereof is reintroduced into the animal body in order to deliver the recombinant protein within the body either locally or systemically.

10 Host Cells

Another embodiment of the invention consists of a host cell that has been transformed or transfected with one of the polynucleotides described therein, and more precisely a polynucleotide either comprising a MGST-II regulatory polynucleotide or the coding sequence of the MGST-II polypeptide having the amino acid sequence of SEQ ID
15 Nos. 488 and 489. The embodiment includes host cells that are transformed (prokaryotic cells) or that are transfected (eukaryotic cells) with a recombinant vector such as one of those described above. Generally, a recombinant host cell of the invention comprises any one of the polynucleotides or the recombinant vectors described therein.

A preferred recombinant host cell according to the invention comprises a
20 polynucleotide selected from the following group of polynucleotides :
a) a purified or isolated nucleic acid encoding a MGST-II polypeptide, or a polypeptide fragment or variant thereof.
b) a purified or isolated nucleic comprising at least 8, preferably at least 15, more preferably at least 25, consecutive nucleotides of the nucleotide sequence SEQ ID No. 485, a
25 nucleotide sequence complementary thereto, or a variant thereof.
c) a purified or isolated nucleic acid comprising at least 8 consecutive nucleotides, preferably at least 15, more preferably at least 25 of the nucleotide sequence SEQ ID Nos. 486 and 487, a nucleotide sequence complementary thereto or a variant thereof.
d) a purified or isolated nucleic acid comprising an exon of the MGST-II gene, a sequence
30 complementary thereto or a fragment or a variant thereof.
e) a purified or isolated nucleic acid comprising a combination of at least two exons of the MGST-II gene, or the sequences complementary thereto wherein the polynucleotides are arranged within the nucleic acid, from the 5' end to the 3' end of said nucleic acid, in the same order than in SEQ ID No. 485.

- f) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof.
- g) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 486, or the sequence complementary thereto or a biologically active fragment thereof.
- 5 h) a polynucleotide consisting of:
- (1) a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof
 - (2) a polynucleotide encoding a desired polypeptide or nucleic acid.
 - (3) Optionally, a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 485, or
- 10 the sequence complementary thereto or a biologically active fragment thereof.
- i) a DNA construct as described previously in the present specification.

Another preferred recombinant cell host according to the present invention is characterized in that its genome or genetic background (including chromosome, plasmids) is modified by the nucleic acid coding for the MGST-II polypeptide of SEQ ID Nos. 488

15 and 489 or fragments or variants thereof.

Preferred host cells used as recipients for the expression vectors of the invention are the following:

- a) Prokaryotic host cells: *Escherichia coli* strains (I.E. DH5- α strain), *Bacillus subtilis*, *Salmonella typhimurium*, and strains from species like *Pseudomonas*, *Streptomyces* and
- 20 *Staphylococcus*.
- b) Eukaryotic host cells: HeLa cells (ATCC N°CCL2; N°CCL2.1; N°CCL2.2), Cv 1 cells (ATCC N°CCL70), COS cells (ATCC N°CRL1650; N°CRL1651), Sf-9 cells (ATCC N°CRL1711), C127 cells (ATCC N° CRL-1804), 3T3 (ATCC N° CRL-6361), CHO (ATCC N° CCL-61), human kidney 293.(ATCC N° 45504; N° CRL-1573) and BHK (ECACC N°
- 25 84100501; N° 84111301)
- c) Other mammalian host cells:

The MGST-II gene expression in mammalian, and typically human, cells may be rendered defective, or alternatively it may be proceeded with the insertion of a MGST-II genomic or cDNA sequence with the replacement of the MGST-II gene counterpart in the

30 genome of an animal cell by a MGST-II polynucleotide according to the invention. These genetic alterations may be generated by homologous recombination events using specific DNA constructs that have been previously described.

One kind of cell hosts that may be used are mammal zygotes, such as murine zygotes. For example, murine zygotes may undergo microinjection with a purified DNA

molecule of interest, for example a purified DNA molecule that has previously been adjusted to a concentration range from 1 ng/ml (for BAC inserts) 3 ng/ μ l (for P1 bacteriophage inserts) in 10 mM Tris-HCl, pH 7.4, 250 μ M EDTA containing 100 mM NaCl, 30 μ M spermine, and 70 μ M spermidine. When the DNA to be microinjected has a large size, polyamines and high salt concentrations can be used in order to avoid mechanical breakage of this DNA, as described by Schedl et al (*Nucleic Acids Res.* 21:4783-4787, 1993).

Anyone of the polynucleotides of the invention, including the DNA constructs described herein, may be introduced in an embryonic stem (ES) cell line, preferably a mouse ES cell line. ES cell lines are derived from pluripotent, uncommitted cells of the inner cell mass of pre-implantation blastocysts. Preferred ES cell lines are the following: ES-E14TG2a (ATCC n° CRL-1821), ES-D3 (ATCC n° CRL1934 and n° CRL-11632), YS001 (ATCC n° CRL-11776), 36.5 (ATCC n° CRL-11116). To maintain ES cells in an uncommitted state, they are cultured in the presence of growth inhibited feeder cells which, provide the appropriate signals to preserve this embryonic phenotype and serve as a matrix for ES cell adherence. Preferred feeder cells consist of primary embryonic fibroblasts that are established from tissue of day 13- day 14 embryos of virtually any mouse strain, that are maintained in culture, such as described by Abbondanzo et al. (*Methods in Enzymology*, Academic Press, New York, 803-823, 1993) and are inhibited in growth by irradiation, such as described by Robertson ("Embryo-Derived StemCell Lines," *E.J. Robertson Ed. Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*. IRL Press, Oxford, 71, 1987), or by the presence of an inhibitory concentration of LIF, such as described by Pease and Williams (*Exp. Cell. Res.* 190:09-211, 1990).

The constructs in the host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence.

Following transformation of a suitable host and growth of the host to an appropriate cell density, the selected promoter is induced by appropriate means, such as temperature shift or chemical induction, and cells are cultivated for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in the expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known by one skilled in the art.

Transgenic animals

The terms "transgenic animals" or "host animals" are used herein designate animals that have their genome genetically and artificially manipulated so as to include one of the nucleic acids according to the invention. Preferred animals are non-human mammals and
5 include those belonging to a genus selected from *Mus* (e.g. mice), *Rattus* (e.g. rats) and *Oryctogalus* (e.g. rabbits) which have their genome artificially and genetically altered by the insertion of a nucleic acid according to the invention.

The transgenic animals of the invention all include within a plurality of their cells a cloned recombinant or synthetic DNA sequence, more specifically one of the purified or
10 isolated nucleic acids comprising a MGST-II coding sequence, a MGST-II regulatory polynucleotide or a DNA sequence encoding an antisense polynucleotide such as described in the present specification.

Preferred transgenic animals according to the invention contains in their somatic cells and/or in their germ line cells a polynucleotide selected from the following group of
15 polynucleotides :

- a) a purified or isolated nucleic acid encoding a MGST-II polypeptide, or a polypeptide fragment or variant thereof.
- b) a purified or isolated nucleic comprising at least 8, preferably at least 15, more preferably at least 25, consecutive nucleotides of the nucleotide sequence SEQ ID No. 485, a
20 nucleotide sequence complementary thereto.
- c) a purified or isolated nucleic acid comprising at least 8 consecutive nucleotides, preferably at least 15, more preferably at least 25 of the nucleotide sequence SEQ ID Nos. 486 and 487, a nucleotide sequence complementary thereto.
- d) a purified or isolated nucleic acid comprising an exon of the MGST-II gene, a sequence
25 complementary thereto or a fragment or a variant thereof.
- e) a purified or isolated nucleic acid comprising a combination of at least two exons of the MGST-II gene, or the sequences complementary thereto wherein the polynucleotides are arranged within the nucleic acid, from the 5' end to the 3' end of said nucleic acid, in the same order than in SEQ ID No. 485.
- 30 f) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof.
- g) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 486, or the sequence complementary thereto or a biologically active fragment thereof.
- h) a polynucleotide consisting of :

- (1) a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof
- (2) a polynucleotide encoding a desired polypeptide or nucleic acid.
- (3) Optionally, a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 486, or
- 5 the sequence complementary thereto or a biologically active fragment thereof.
- i) a DNA construct as described previously in the present specification.

The transgenic animals of the invention thus contain specific sequences of exogenous genetic material such as the nucleotide sequences described above in detail.

In a first preferred embodiment, these transgenic animals may be good experimental

10 models in order to study the diverse pathologies related to cell differentiation, in particular concerning the transgenic animals within the genome of which has been inserted one or several copies of a polynucleotide encoding a native MGST-II protein, or alternatively a mutant MGST-II protein.

In a second preferred embodiment, these transgenic animals may express a desired

15 polypeptide of interest under the control of the regulatory polynucleotides of the MGST-II gene, leading to good yields in the synthesis of this protein of interest, and eventually a tissue specific expression of this protein of interest.

The design of the transgenic animals of the invention may be made according to the conventional techniques well known from the one skilled in the art. For more details

20 regarding the production of transgenic animals, and specifically transgenic mice, it may be referred to US Patents Nos. 4,873,191, issued October 10, 1989, 5,464,764 issued November 7, 1995 and 5,789,215, issued August 4, 1998, these documents being herein incorporated by reference to disclose methods producing transgenic mice.

Transgenic animals of the present invention are produced by the application of

25 procedures which result in an animal with a genome that has incorporated exogenous genetic material. The procedure involves obtaining the genetic material, or a portion thereof, which encodes either a MGST-II coding sequence, a MGST-II regulatory polynucleotide or a DNA sequence encoding a MGST-II antisense polynucleotide such as described in the present specification.

30 A recombinant polynucleotide of the invention is inserted into an embryonic or ES stem cell line. The insertion is preferably made using electroporation, such as described by Thomas et al. (*Cell* 51:503-512, 1987). The cells subjected to electroporation are screened (e.g. by selection via selectable markers, by PCR or by Southern blot analysis) to find positive cells which have integrated the exogenous recombinant polynucleotide into their

genome, preferably via an homologous recombination event. An illustrative positive-negative selection procedure that may be used according to the invention is described by Mansour et al. (*Nature* 336:348-352, 1988).

Then, the positive cells are isolated, cloned and injected into 3.5 days old blastocysts from mice, such as described by Bradley ("Production and Analysis of Chimaeric Mice," *E.J. Robertson (Ed.), Teratocarcinomas and embryonic stem cells: A practical approach* IRL Press, Oxford, 113, 1987). The blastocysts are then inserted into a female host animal and allowed to grow to term.

Alternatively, the positive ES cells are brought into contact with embryos at the 2.5 days old 8-16 cell stage (morulae) such as described by Wood et al. (*Proc. Natl. Acad. Sci. U.S.A.* 90:4582-4585, 1993) or by Nagy et al. (*Proc. Natl. Acad. Sci. USA.* 90: 8424-8428, 1993), the ES cells being internalized to colonize extensively the blastocyst including the cells which will give rise to the germ line.

The offspring of the female host are tested to determine which animals are transgenic e.g. include the inserted exogenous DNA sequence and which are wild-type.

Thus, the present invention also concerns a transgenic animal containing a nucleic acid, a recombinant expression vector or a recombinant host cell according to the invention.

A further object of the invention consists of recombinant host cells obtained from a transgenic animal described herein.

Recombinant cell lines may be established *in vitro* from cells obtained from any tissue of a transgenic animal according to the invention, for example by transfection of primary cell cultures with vectors expressing *onc*-genes such as SV40 large T antigen, as described by Chou (*Mol. Endocrinol.* 3:1511-1514, 1989) and Shay et al. (*Biochem. Biophys. Acta.* 1072:1-7, 1991).

I.E. MGST-II Polypeptides

The term "MGST-II polypeptides" is used herein to embrace all of the proteins and polypeptides of the present invention. Also forming part of the invention are polypeptides encoded by the polynucleotides of the invention, as well as fusion polypeptides comprising such polypeptides. The invention embodies MGST-II proteins from humans, including isolated or purified MGST-II proteins consisting, consisting essentially, or comprising the sequence of SEQ ID Nos. 488 and 489. It should be noted the MGST-II proteins of the invention are based on the naturally-occurring variants of the amino acid sequence of human MGST-II.

In a first embodiment, the present invention provides a variant MGST-II protein; wherein the Tyr residue of amino acid position 93 has been replaced with a His residue. Variant proteins and the fragments thereof which contain amino acid position 93 are collectively referred to herein as "93-His variants." More particularly, the present invention
5 embodies isolated, purified, and recombinant polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488, wherein said contiguous span comprises a His residue at amino acid position 93. In this amino acid substitution the original residue (Tyr) is replaced by a non-equivalent amino acid (His) presenting different
10 chemical properties.

The present invention further provides another naturally-occurring variant of the MGST-II protein that consists or consists essentially of amino acids 1-109 of SEQ ID No. 488. This variant MGST-II polypeptide corresponds to one allele of biallelic marker 10-290-37.

15 Another naturally-occurring variant of the MGST-II protein of the present invention is encoded by a cDNA obtained by alternative splicing. MGST-II cDNAs and cDNA variants are further described above. This variant polypeptide of a sequence from SEQ ID No. 489 is identical to the MGST-II protein of SEQ ID No. 488 from amino acid position 1 to amino acid position 19 but comprises 11 additional amino acids. The present invention
20 embodies isolated, purified, and recombinant polypeptides comprising, consisting of or consisting essentially of an amino acid sequence from SEQ ID No. 489. Moreover, the present invention embodies isolated, purified, and recombinant polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, or 30 amino acids of SEQ ID No. 489, wherein said
25 contiguous span comprises a least one of amino acid positions 20 to 30 of SEQ ID No. 489.

All the variant MGST-II polypeptides described above most probably show alterations in the activity, specificity and function of the MGST-II enzyme. In preferred embodiments the polypeptides of the present invention comprise the site of a mutation or functional mutation, including a deletion, substitution or truncation in the amino acid
30 sequence in the MGST-II protein.

MGST-II proteins are preferably isolated from human or mammalian tissue samples or expressed from human or mammalian genes. The MGST-II polypeptides of the invention can be made using routine expression methods known in the art. The polynucleotide encoding the desired polypeptide, is ligated into an expression vector suitable for any

convenient host. Both eukaryotic and prokaryotic host systems are used in forming recombinant polypeptides. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification is by any technique known in the art, for example, differential extraction, salt fractionation, chromatography, centrifugation, and the like. See, for example, Methods in Enzymology for a variety of methods for purifying proteins.

In addition, shorter protein fragments are produced by chemical synthesis. Alternatively the proteins of the invention are extracted from cells or tissues of humans or non-human animals. Methods for purifying proteins are known in the art, and include the use of detergents or chaotropic agents to disrupt particles followed by differential extraction and separation of the polypeptides by ion exchange chromatography, affinity chromatography, sedimentation according to density, and gel electrophoresis.

Any MGST-II cDNA of the invention is used to express MGST-II proteins and polypeptides. The nucleic acid encoding the MGST-II protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The MGST-II insert in the expression vector may comprise the full coding sequence for the MGST-II protein or a portion thereof. For example, the MGST-II derived insert may encode a polypeptide comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488, wherein said contiguous span comprises a His residue at amino acid position 93. The MGST-II derived insert may further encode a polypeptide comprising, consisting of or consisting essentially of an amino acid sequence from amino acid positions 1-108 of SEQ ID No. 488. The MGST-II derived insert may further encode a polypeptide comprising, consisting of or consisting essentially of an amino acid sequence from SEQ ID No. 489. The MGST-II derived insert may also encode a polypeptide comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, or 30 amino acids of SEQ ID No. 489, wherein said contiguous span comprises a least one of amino acid positions 20 to 30 of SEQ ID No. 489.

The expression vector is any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and

codon pairing of the sequence is optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767.

In one embodiment, the entire coding sequence of the MGST-II cDNA through the poly A signal of the cDNA is operably linked to a promoter in the expression vector.

- 5 Alternatively, if the nucleic acid encoding a portion of the MGST-II protein lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the insert from the MGST-II cDNA lacks a poly A signal, this sequence can be added to the construct by, for example, splicing out the Poly A signal from pSG5 (Stratagene) using BglI and SalI restriction
- 10 endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the gag gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex Thymidine Kinase promoter and the selectable neomycin gene. The nucleic acid encoding the MGST-II protein or a portion thereof is
- 15 obtained by PCR from a bacterial vector containing a MGST-II cDNA of the present invention using oligonucleotide primers complementary to the MGST-II cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5' primer and BglII at the 5' end of the corresponding cDNA 3' primer, taking care to ensure that the sequence encoding the MGST-II protein or a portion thereof is positioned properly with respect
- 20 to the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1, now containing a poly A signal and digested with BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product

25 specification. Positive transfectants are selected after growing the transfected cells in 600ug/ml G418 (Sigma, St. Louis, Missouri).

Alternatively, the nucleic acids encoding the MGST-II protein or a portion thereof is cloned into pED6dpc2 (Genetics Institute, Cambridge, MA). The resulting pED6dpc2 constructs is transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant

30 cells are selected and expanded.

The above procedures may also be used to express a mutant MGST-II protein responsible for a detectable phenotype or a portion thereof.

The expressed proteins are purified using conventional purification techniques such as ammonium sulfate precipitation or chromatographic separation based on size or charge. The

protein encoded by the nucleic acid insert may also be purified using standard immunochromatography techniques. In such procedures, a solution containing the expressed MGST-II protein or portion thereof, such as a cell extract, is applied to a column having antibodies against the MGST-II protein or portion thereof is attached to the chromatography matrix. The expressed protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound expressed protein is then released from the column and recovered using standard techniques.

To confirm expression of the MGST-II protein or a portion thereof, the proteins expressed from host cells containing an expression vector containing an insert encoding the MGST-II protein or a portion thereof can be compared to the proteins expressed in host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the MGST-II protein or a portion thereof is being expressed. Generally, the band will have the mobility expected for the MGST-II protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Antibodies capable of specifically recognizing the expressed MGST-II protein or a portion thereof, are described below.

If antibody production is not possible, the nucleic acids encoding the MGST-II protein or a portion thereof is incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the nucleic acid encoding the MGST-II protein or a portion thereof is inserted in frame with the gene encoding the other half of the chimera. The other half of the chimera is β -globin or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to β -globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites is engineered between the β -globin gene or the nickel binding polypeptide and the MGST-II protein or portion thereof. Thus, the two polypeptides of the chimera are separated from one another by protease digestion.

One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene), which encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques are well known to those skilled in the art of

molecular biology. Standard methods are published in methods texts such as Davis et al., (Basic Methods in Molecular Biology, L.G. Davis, M.D. Digner, and J.F. Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using in vitro translation systems such as the In vitro Express™ Translation Kit (Stratagene).

I.F. Production of Antibodies Against MGST-II Polypeptides

Any MGST-II polypeptide or whole protein may be used to generate antibodies capable of specifically binding to expressed MGST-II protein or fragments thereof or variants thereof. Preferably the antibody compositions of the invention are capable of specifically binding to the 93-His variant of the MGST-II protein. Alternatively the antibody compositions of the present invention are capable of specifically binding the variant MGST-II polypeptide of SEQ ID No. 489. A preferred embodiment of the invention encompasses isolated or purified antibody compositions capable of selectively binding, or which are capable of binding to an epitope-containing fragment of a polypeptide of the invention, wherein said epitope comprises at least one amino acid position selected from the group consisting of His residue at amino acid position 93 of SEQ ID No. 488 and of amino acid positions 20-30 of SEQ ID No. 489. For an antibody composition to specifically bind to these MGST-II variants it must demonstrate at least a 5%, 10%, 15%, 20%, 25%, 50%, or 100% greater binding affinity for full length MGST-II variants in an ELISA, RIA, or other antibody-based binding assay than to full length MGST-II protein described in SEQ ID No. 488. Affinity of the antibody composition for the epitope can further be determined by preparing competitive binding curves, as described, for example, by Fisher, D. (Chap. 42 in: Manual of Clinical Immunology, 2d Ed. (Rose and Friedman, Eds.) *Amer. Soc. For Microbiol.*, Washington, D.C., 1980).

The present invention also contemplates the use of variant MGST-II polypeptides in the manufacture of antibodies. In a preferred embodiment such polypeptides are useful in the manufacture of antibodies to detect the presence and absence of the 93-His variant and of the MGST-II variant of SEQ ID No. 489.

Non-human animals or mammals, whether wild-type or transgenic, which express a different species of MGST-II than the one to which antibody binding is desired, and animals which do not express MGST-II (i.e. an MGST-II knock out animal as described in herein) are particularly useful for preparing antibodies. MGST-II knock out animals will recognize all or most of the exposed regions of MGST-II as foreign antigens, and therefore produce antibodies with a wider array of MGST-II epitopes. Moreover, smaller polypeptides with

only 10 to 30 amino acids may be useful in obtaining specific binding to the 93-His variant and to the MGST-II variant of SEQ ID No. 489. In addition, the humoral immune system of animals which produce a species of MGST-II that resembles the antigenic sequence will preferentially recognize the differences between the animal's native MGST-II species and the antigen sequence, and produce antibodies to these unique sites in the antigen sequence. Such a technique will be particularly useful in obtaining antibodies that specifically bind to the 93-His variant and to the MGST-II variant of SEQ ID No. 489. The preparation of antibody compositions is further described in Example 6.

Antibody preparations prepared according to the present invention are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body. The antibodies of the invention may be labeled, either by a radioactive, a fluorescent or an enzymatic label. Consequently, the invention is also directed to a method for detecting specifically the presence of a variant MGST-II polypeptide according to the invention in a biological sample, said method comprising the following steps : a) bringing into contact the biological sample with a polyclonal or monoclonal antibody that specifically binds a variant MGST-II polypeptide or to a peptide fragment or variant thereof; and b) detecting the antigen-antibody complex formed. The invention also concerns a diagnostic kit for detecting *in vitro* the presence of a variant MGST-II polypeptide according to the present invention in a biological sample, wherein said kit comprises: a) a polyclonal or monoclonal antibody that specifically binds a variant MGST-II polypeptide or to a peptide fragment or variant thereof, optionally labeled; b) a reagent allowing the detection of the antigen-antibody complexes formed, said reagent carrying optionally a label, or being able to be recognized itself by a labeled reagent, more particularly in the case when the above-mentioned monoclonal or polyclonal antibody is not labeled by itself.

II. Methods for *De Novo* Identification of Biallelic Markers

Large fragments of human DNA, carrying genes of interest involved in the biotransformation of xenobiotics such as therapeutic drugs; were cloned, sequenced and screened for biallelic markers. Biallelic markers within the candidate genes themselves as well as markers located on the same genomic fragment were identified. It will be clear to one of skill in the art that large fragments of human genomic DNA may be obtained from any appropriate source and may be cloned into a number of suitable vectors.

In a preferred embodiment of the invention, BAC (Bacterial Artificial Chromosomes) vectors were used to construct DNA libraries covering the entire human genome. Specific amplification primers were designed for each candidate gene and the BAC library was screened by PCR until there was at least one positive BAC clone per candidate gene. Genomic sequence, screened for biallelic markers, was generated by sequencing ends of BAC subclones. Details of a preferred embodiment are provided in Example 1. As a preferred alternative to sequencing the ends of an adequate number of BAC subclones, high throughput deletion-based sequencing vectors, which allow the generation of a high quality sequence information covering fragments of about 6kb, may be used. Having sequence fragments longer than 2.5 or 3kb enhances the chances of identifying biallelic markers therein. Methods of constructing and sequencing a nested set of deletions are disclosed in the related U.S. Patent Application entitled "High Throughput DNA Sequencing Vector" (Serial No. 09/058,746).

In another embodiment of the invention, genomic sequences of candidate genes were available in public databases allowing direct screening for biallelic markers.

Any of a variety of methods can be used to screen a genomic fragment for single nucleotide polymorphisms such as differential hybridization with oligonucleotide probes, detection of changes in the mobility measured by gel electrophoresis or direct sequencing of the amplified nucleic acid. A preferred method for identifying biallelic markers involves comparative sequencing of genomic DNA fragments from an appropriate number of unrelated individuals.

In a first embodiment, DNA samples from unrelated individuals are pooled together, following which the genomic DNA of interest is amplified and sequenced. The nucleotide sequences thus obtained are then analyzed to identify significant polymorphisms. One of the major advantages of this method resides in the fact that the pooling of the DNA samples substantially reduces the number of DNA amplification reactions and sequencing reactions, which must be carried out. Moreover, this method is sufficiently sensitive so that a biallelic marker obtained thereby usually demonstrates a sufficient frequency of its less common allele to be useful in conducting association studies. Usually, the frequency of the least common allele of a biallelic marker identified by this method is at least 10%.

In a second embodiment, the DNA samples are not pooled and are therefore amplified and sequenced individually. This method is usually preferred when biallelic markers need to be identified in order to perform association studies within candidate genes. Preferably, highly relevant gene regions such as promoter regions or exon regions may be

screened for biallelic markers. A biallelic marker obtained using this method may show a lower degree of informativeness for conducting association studies, e.g. if the frequency of its less frequent allele may be less than about 10%. Such a biallelic marker will however be sufficiently informative to conduct association studies and it will further be appreciated that including less informative biallelic markers in the genetic analysis studies of the present invention, may allow in some cases the direct identification of causal mutations, which may, depending on their penetrance, be rare mutations.

The following is a description of the various parameters of a preferred method used by the inventors for the identification of the biallelic markers of the present invention.

10 II.A. Genomic DNA Samples

The genomic DNA samples from which the biallelic markers of the present invention are generated are preferably obtained from unrelated individuals corresponding to a heterogeneous population of known ethnic background. The number of individuals from whom DNA samples are obtained can vary substantially, preferably from about 10 to about 15 1000, more preferably from about 50 to about 200 individuals. Usually, DNA samples are collected from at least about 100 individuals in order to have sufficient polymorphic diversity in a given population to identify as many markers as possible and to generate statistically significant results.

As for the source of the genomic DNA to be subjected to analysis, any test sample 20 can be foreseen without any particular limitation. These test samples include biological samples, which can be tested by the methods of the present invention described herein, and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitourinary tracts, tears, saliva, milk, white blood cells, myelomas and the like; biological 25 fluids such as cell culture supernatants; fixed tissue specimens including tumor and non-tumor tissue and lymph node tissues; bone marrow aspirates and fixed cell specimens. The preferred source of genomic DNA used in the present invention is from peripheral venous blood of each donor. Techniques to prepare genomic DNA from biological samples are well known to the skilled technician. Details of a preferred embodiment are provided in 30 Example 1. The person skilled in the art can choose to amplify pooled or unpooled DNA samples.

II.B. DNA Amplification

The identification of biallelic markers in a sample of genomic DNA may be facilitated through the use of DNA amplification methods. DNA samples can be pooled or

unpooled for the amplification step. DNA amplification techniques are well known to those skilled in the art. Various methods to amplify DNA fragments carrying biallelic markers are further described hereinafter in III.B. The PCR technology is the preferred amplification technique used to identify new biallelic markers.

- 5 In a first embodiment, biallelic markers are identified using genomic sequence information generated by the inventors. Genomic DNA fragments, such as the inserts of the BAC clones described above, are sequenced and used to design primers for the amplification of 500 bp fragments. These 500 bp fragments are amplified from genomic DNA and are scanned for biallelic markers. Primers may be designed using the OSP
10 software (Hillier L. and Green P., 1991). All primers may contain, upstream of the specific target bases, a common oligonucleotide tail that serves as a sequencing primer. Those skilled in the art are familiar with primer extensions, which can be used for these purposes.

In another embodiment of the invention, genomic sequences of candidate genes are available in public databases allowing direct screening for biallelic markers. Preferred
15 primers, useful for the amplification of genomic sequences encoding the candidate genes, focus on promoters, exons and splice sites of the genes. A biallelic marker present in these functional regions of the gene have a higher probability to be a causal mutation.

Preferred primers include those disclosed in Figure 7.

II.C. Sequencing of Amplified Genomic DNA and Identification of Single Nucleotide

20 Polymorphisms

The amplification products generated as described above, are then sequenced using any method known and available to the skilled technician. Methods for sequencing DNA using either the dideoxy-mediated method (Sanger method) or the Maxam-Gilbert method are widely known to those of ordinary skill in the art. Such methods are for example
25 disclosed in Maniatis et al. (Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Second Edition, 1989). Alternative approaches include hybridization to high-density DNA probe arrays as described in Chee et al. (*Science* 274, 610, 1996).

Preferably, the amplified DNA is subjected to automated dideoxy terminator sequencing reactions using a dye-primer cycle sequencing protocol. The products of the
30 sequencing reactions are run on sequencing gels and the sequences are determined using gel image analysis. The polymorphism search is based on the presence of superimposed peaks in the electrophoresis pattern resulting from different bases occurring at the same position. Because each dideoxy terminator is labeled with a different fluorescent molecule, the two peaks corresponding to a biallelic site present distinct colors corresponding to two different

nucleotides at the same position on the sequence. However, the presence of two peaks can be an artifact due to background noise. To exclude such an artifact, the two DNA strands are sequenced and a comparison between the peaks is carried out. In order to be registered as a polymorphic sequence, the polymorphism has to be detected on both strands.

5 The above procedure permits those amplification products, which contain biallelic markers to be identified. The detection limit for the frequency of biallelic polymorphisms detected by sequencing pools of 100 individuals is approximately 0.1 for the minor allele, as verified by sequencing pools of known allelic frequencies. However, more than 90% of the biallelic polymorphisms detected by the pooling method have a frequency for the minor
10 allele higher than 0.25. Therefore, the biallelic markers selected by this method have a frequency of at least 0.1 for the minor allele and less than 0.9 for the major allele. Preferably at least 0.2 for the minor allele and less than 0.8 for the major allele, more preferably at least 0.3 for the minor allele and less than 0.7 for the major allele, thus a heterozygosity rate higher than 0.18, preferably higher than 0.32, more preferably higher
15 than 0.42.

In another embodiment, biallelic markers are detected by sequencing individual DNA samples, the frequency of the minor allele of such a biallelic marker may be less than 0.1.

The markers carried by the same fragment of genomic DNA, such as the insert in a
20 BAC clone, need not necessarily be ordered with respect to one another within the genomic fragment to conduct association studies. However, in some embodiments of the present invention, the order of biallelic markers carried by the same fragment of genomic DNA are determined.

II.D. Validation of the Biallelic Markers of the Present Invention

25 The polymorphisms are evaluated for their usefulness as genetic markers by validating that both alleles are present in a population. Validation of the biallelic markers is accomplished by genotyping a group of individuals by a method of the invention and demonstrating that both alleles are present. Microsequencing is a preferred method of genotyping alleles. The validation by genotyping step may be performed on individual
30 samples derived from each individual in the group or by genotyping a pooled sample derived from more than one individual. The group can be as small as one individual if that individual is heterozygous for the allele in question. Preferably the group contains at least three individuals, more preferably the group contains five or six individuals, so that a single validation test will be more likely to result in the validation of more of the biallelic markers

that are being tested. It should be noted, however, that when the validation test is performed on a small group it may result in a false negative result if as a result of sampling error none of the individuals tested carries one of the two alleles. Thus, the validation process is less useful in demonstrating that a particular initial result is an artifact, than it is at

- 5 demonstrating that there is a *bona fide* biallelic marker at a particular position in a sequence. For an indication of whether a particular biallelic marker has been validated see Figure 1. All of the genotyping, haplotyping, association, and interaction study methods of the invention may optionally be performed solely with validated biallelic markers.

II.E. Evaluation of the Frequency of the Biallelic Markers of the Present Invention

- 10 The validated biallelic markers are further evaluated for their usefulness as genetic markers by determining the frequency of the least common allele at the biallelic marker site. The determination of the least common allele is accomplished by genotyping a group of individuals by a method of the invention and demonstrating that both alleles are present. This determination of frequency by genotyping step may be performed on individual
- 15 samples derived from each individual in the group or by genotyping a pooled sample derived from more than one individual. The group must be large enough to be representative of the population as a whole. Preferably the group contains at least 20 individuals, more preferably the group contains at least 50 individuals, most preferably the group contains at least 100 individuals. Of course the larger the group the greater the
- 20 accuracy of the frequency determination because of reduced sampling error. For an indication of the frequency for the less common allele of a particular biallelic marker of the invention see Figure 1. A biallelic marker wherein the frequency of the less common allele is 30% or more is termed a "high quality biallelic marker." All of the genotyping, haplotyping, association, and interaction study methods of the invention may optionally be
- 25 performed solely with high quality biallelic markers.

III. Methods of Genotyping an Individual for Biallelic Markers

- Methods are provided to genotype a biological sample for one or more biallelic markers of the present invention, all of which may be performed *in vitro*. Such methods of genotyping comprise determining the identity of a nucleotide at a DME-related biallelic
- 30 marker by any method known in the art. These methods find use in genotyping case-control populations in association studies as well as individuals in the context of detection of alleles of biallelic markers which, are known to be associated with a given trait, in which case both copies of the biallelic marker present in individual's genome are determined so that an individual may be classified as homozygous or heterozygous for a particular allele.

These genotyping methods can be performed nucleic acid samples derived from a single individual or pooled DNA samples.

Genotyping can be performed using similar methods as those described above for the identification of the biallelic markers, or using other genotyping methods such as those
5 further described below. In preferred embodiments, the comparison of sequences of amplified genomic fragments from different individuals is used to identify new biallelic markers whereas microsequencing is used for genotyping known biallelic markers in diagnostic and association study applications.

III.A. Source of DNA for Genotyping

10 Any source of nucleic acids, in purified or non-purified form, can be utilized as the starting nucleic acid, provided it contains or is suspected of containing the specific nucleic acid sequence desired. DNA or RNA may be extracted from cells, tissues, body fluids and the like as described above in II.A. "Genomic DNA Samples." While nucleic acids for use in the genotyping methods of the invention can be derived from any mammalian source, the
15 test subjects and individuals from which nucleic acid samples are taken are generally understood to be human.

III.B. Amplification of DNA Fragments Comprising Biallelic Markers

Methods and polynucleotides are provided to amplify a segment of nucleotides comprising one or more biallelic marker of the present invention. It will be appreciated that
20 amplification of DNA fragments comprising biallelic markers may be used in various methods and for various purposes and is not restricted to genotyping. Nevertheless, many genotyping methods, although not all, require the previous amplification of the DNA region carrying the biallelic marker of interest. Such methods specifically increase the concentration or total number of sequences that span the biallelic marker or include that site
25 and sequences located either distal or proximal to it. Diagnostic assays may also rely on amplification of DNA segments carrying a biallelic marker of the present invention.

Amplification of DNA may be achieved by any method known in the art. The established PCR (polymerase chain reaction) method or by developments thereof or alternatives. Amplification methods which can be utilized herein include but are not limited
30 to Ligase Chain Reaction (LCR) as described in EP A 320 308 and EP A 439 182, Gap LCR (Wolcott, M.J., Clin. Microbiol. Rev. 5:370-386), the so-called "NASBA" or "3SR" technique described in Guatelli J.C. et al. (*Proc. Natl. Acad. Sci. USA* 87:1874-1878, 1990) and in Compton J. (*Nature* 350:91-92, 1991), Q-beta amplification as described in European Patent Application no 4544610, strand displacement amplification as described in

Walker et al. (*Clin. Chem.* 42:9-13, 1996) and EP A 684 315 and, target mediated amplification as described in PCT Publication WO 9322461.

LCR and Gap LCR are exponential amplification techniques, both depend on DNA ligase to join adjacent primers annealed to a DNA molecule. In Ligase Chain Reaction (LCR), probe pairs are used which include two primary (first and second) and two secondary (third and fourth) probes, all of which are employed in molar excess to target. The first probe hybridizes to a first segment of the target strand and the second probe hybridizes to a second segment of the target strand, the first and second segments being contiguous so that the primary probes abut one another in 5' phosphate-3'hydroxyl relationship, and so that a ligase can covalently fuse or ligate the two probes into a fused product. In addition, a third (secondary) probe can hybridize to a portion of the first probe and a fourth (secondary) probe can hybridize to a portion of the second probe in a similar abutting fashion. Of course, if the target is initially double stranded, the secondary probes also will hybridize to the target complement in the first instance. Once the ligated strand of primary probes is separated from the target strand, it will hybridize with the third and fourth probes which can be ligated to form a complementary, secondary ligated product. It is important to realize that the ligated products are functionally equivalent to either the target or its complement. By repeated cycles of hybridization and ligation, amplification of the target sequence is achieved. A method for multiplex LCR has also been described (WO 9320227). Gap LCR (GLCR) is a version of LCR where the probes are not adjacent but are separated by 2 to 3 bases.

For amplification of mRNAs, it is within the scope of the present invention to reverse transcribe mRNA into cDNA followed by polymerase chain reaction (RT-PCR); or, to use a single enzyme for both steps as described in U.S. Patent No. 5,322,770 or, to use Asymmetric Gap LCR (RT-AGLCR) as described by Marshall R.L. et al. (*PCR Methods and Applications* 4:80-84, 1994). AGLCR is a modification of GLCR that allows the amplification of RNA.

Some of these amplification methods are particularly suited for the detection of single nucleotide polymorphisms and allow the simultaneous amplification of a target sequence and the identification of the polymorphic nucleotide as it is further described in IIIC.

The PCR technology is the preferred amplification technique used in the present invention. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in *Methods*

in *Molecular Biology* 67: Humana Press, Totowa (1997) and the publication entitled "PCR Methods and Applications" (1991, Cold Spring Harbor Laboratory Press). In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable
5 polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between
10 the primer sites. PCR has further been described in several patents including US Patents 4,683,195, 4,683,202 and 4,965,188.

The identification of biallelic markers as described above allows the design of appropriate oligonucleotides, which can be used as primers to amplify DNA fragments comprising the biallelic markers of the present invention. Amplification can be performed
15 using the primers initially used to discover new biallelic markers which are described herein or any set of primers allowing the amplification of a DNA fragment comprising a biallelic marker of the present invention. Primers can be prepared by any suitable method. As for example, direct chemical synthesis by a method such as the phosphodiester method of Narang S.A. et al. (*Methods Enzymol.* 68:90-98, 1979), the phosphodiester method of
20 Brown E.L. et al. (*Methods Enzymol.* 68:109-151, 1979), the diethylphosphoramidite method of Beaucage et al. (*Tetrahedron Lett.* 22:1859-1862, 1981) and the solid support method described in EP 0 707 592.

In some embodiments the present invention provides primers for amplifying a DNA fragment containing one or more biallelic markers of the present invention. Preferred
25 amplification primers are listed in Figure 7. It will be appreciated that the primers listed are merely exemplary and that any other set of primers which produce amplification products containing one or more biallelic markers of the present invention.

The primers are selected to be substantially complementary to the different strands of each specific sequence to be amplified. The length of the primers of the present
30 invention can range from 8 to 100 nucleotides, preferably from 8 to 50, 8 to 30 or more preferably 8 to 25 nucleotides. Shorter primers tend to lack specificity for a target nucleic acid sequence and generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. Longer primers are expensive to produce and can sometimes self-hybridize to form hairpin structures. The formation of stable hybrids depends on the

melting temperature (T_m) of the DNA. The T_m depends on the length of the primer, the ionic strength of the solution and the G+C content. The higher the G+C content of the primer, the higher is the melting temperature because G:C pairs are held by three H bonds whereas A:T pairs have only two. The G+C content of the amplification primers of the
5 present invention preferably ranges between 10 and 75 %, more preferably between 35 and 60 %, and most preferably between 40 and 55 %. The appropriate length for primers under a particular set of assay conditions may be empirically determined by one of skill in the art.

The spacing of the primers determines the length of the segment to be amplified. In the context of the present invention amplified segments carrying biallelic markers can range
10 in size from at least about 25 bp to 35 kbp. Amplification fragments from 25-3000 bp are typical, fragments from 50-1000 bp are preferred and fragments from 100-600 bp are highly preferred. It will be appreciated that amplification primers for the biallelic markers may be any sequence which allow the specific amplification of any DNA fragment carrying the markers. Amplification primers may be labeled or immobilized on a solid support as
15 described in I.

III.C. Methods of Genotyping DNA samples for Biallelic Markers

Any method known in the art can be used to identify the nucleotide present at a biallelic marker site. Since the biallelic marker allele to be detected has been identified and specified in the present invention, detection will prove simple for one of ordinary skill in the
20 art by employing any of a number of techniques. Many genotyping methods require the previous amplification of the DNA region carrying the biallelic marker of interest. While the amplification of target or signal is often preferred at present, ultrasensitive detection methods which do not require amplification are also encompassed by the present genotyping methods. Methods well-known to those skilled in the art that can be used to detect biallelic
25 polymorphisms include methods such as, conventional dot blot analyzes, single strand conformational polymorphism analysis (SSCP) described by Orita et al. (*Proc. Natl. Acad. Sci. U.S.A* 86:27776-2770, 1989), denaturing gradient gel electrophoresis (DGGE), heteroduplex analysis, mismatch cleavage detection, and other conventional techniques as described in Sheffield, V.C. et al. (*Proc. Natl. Acad. Sci. USA* 49:699-706, 1991), White et
30 al. (*Genomics* 12:301-306, 1992), Grompe, M. et al. (*Proc. Natl. Acad. Sci. USA* 86:5855-5892, 1989) and Grompe, M. (*Nature Genetics* 5:111-117, 1993). Another method for determining the identity of the nucleotide present at a particular polymorphic site employs a specialized exonuclease-resistant nucleotide derivative as described in US patent 4,656,127.

Preferred methods involve directly determining the identity of the nucleotide present at a biallelic marker site by sequencing assay, enzyme-based mismatch detection assay, or hybridization assay. The following is a description of some preferred methods. A highly preferred method is the microsequencing technique. The term "sequencing assay" is used
5 herein to refer to polymerase extension of duplex primer/template complexes and includes both traditional sequencing and microsequencing.

1) Sequencing assays

The nucleotide present at a polymorphic site can be determined by sequencing methods. In a preferred embodiment, DNA samples are subjected to PCR amplification
10 before sequencing as described above. DNA sequencing methods are described in IIC.

Preferably, the amplified DNA is subjected to automated dideoxy terminator sequencing reactions using a dye-primer cycle sequencing protocol. Sequence analysis allows the identification of the base present at the biallelic marker site.

2) Microsequencing assays

15 In microsequencing methods, a nucleotide at the polymorphic site that is unique to one of the alleles in a target DNA is detected by a single nucleotide primer extension reaction. This method involves appropriate microsequencing primers which, hybridize just upstream of a polymorphic base of interest in the target nucleic acid. A polymerase is used to specifically extend the 3' end of the primer with one single ddNTP (chain terminator)
20 complementary to the selected nucleotide at the polymorphic site. Next the identity of the incorporated nucleotide is determined in any suitable way.

Typically, microsequencing reactions are carried out using fluorescent ddNTPs and the extended microsequencing primers are analyzed by electrophoresis on ABI 377 sequencing machines to determine the identity of the incorporated nucleotide as described in
25 EP 412 883. Alternatively capillary electrophoresis can be used in order to process a higher number of assays simultaneously. An example of a typical microsequencing procedure that can be used in the context of the present invention is provided in Example 2.

Different approaches can be used to detect the nucleotide added to the microsequencing primer. A homogeneous phase detection method based on fluorescence
30 resonance energy transfer has been described by Chen and Kwok (*Nucleic Acids Research* 25:347-353 1997) and Chen et al. (*Proc. Natl. Acad. Sci. USA* 94/20 10756-10761, 1997). In this method amplified genomic DNA fragments containing polymorphic sites are incubated with a 5'-fluorescein-labeled primer in the presence of allelic dye-labeled dideoxynucleoside triphosphates and a modified Taq polymerase. The dye-labeled

primer is extended one base by the dye-terminator specific for the allele present on the template. At the end of the genotyping reaction, the fluorescence intensities of the two dyes in the reaction mixture are analyzed directly without separation or purification. All these steps can be performed in the same tube and the fluorescence changes can be monitored in
5 real time. Alternatively, the extended primer may be analyzed by MALDI-TOF Mass Spectrometry. The base at the polymorphic site is identified by the mass added onto the microsequencing primer (see Haff L.A. and Smirnov I.P., *Genome Research*, 7:378-388, 1997).

Microsequencing may be achieved by the established microsequencing method or by
10 developments or derivatives thereof. Alternative methods include several solid-phase microsequencing techniques. The basic microsequencing protocol is the same as described previously, except that the method is conducted as a heterogenous phase assay, in which the primer or the target molecule is immobilized or captured onto a solid support. To simplify the primer separation and the terminal nucleotide addition analysis, oligonucleotides are
15 attached to solid supports or are modified in such ways that permit affinity separation as well as polymerase extension. The 5' ends and internal nucleotides of synthetic oligonucleotides can be modified in a number of different ways to permit different affinity separation approaches, e.g., biotinylation. If a single affinity group is used on the oligonucleotides, the oligonucleotides can be separated from the incorporated terminator
20 reagent. This eliminates the need of physical or size separation. More than one oligonucleotide can be separated from the terminator reagent and analyzed simultaneously if more than one affinity group is used. This permits the analysis of several nucleic acid species or more nucleic acid sequence information per extension reaction. The affinity group need not be on the priming oligonucleotide but could alternatively be present on the
25 template. For example, immobilization can be carried out via an interaction between biotinylated DNA and streptavidin-coated microtitration wells or avidin-coated polystyrene particles. In the same manner oligonucleotides or templates may be attached to a solid support in a high-density format. In such solid phase microsequencing reactions, incorporated ddNTPs can be radiolabeled (Syvänen, *Clinica Chimica Acta* 226:225-236,
30 1994) or linked to fluorescein (Livak and Hainer, *Human Mutation* 3:379-385, 1994). The detection of radiolabeled ddNTPs can be achieved through scintillation-based techniques. The detection of fluorescein-linked ddNTPs can be based on the binding of anti fluorescein antibody conjugated with alkaline phosphatase, followed by incubation with a chromogenic substrate (such as *p*-nitrophenyl phosphate). Other possible reporter-detection pairs include:

ddNTP linked to dinitrophenyl (DNP) and anti-DNP alkaline phosphatase conjugate (Harju et al., *Clin. Chem.* 39/11 2282-2287, 1993) or biotinylated ddNTP and horseradish peroxidase-conjugated streptavidin with *o*-phenylenediamine as a substrate (WO 92/15712). As yet another alternative solid-phase microsequencing procedure, Nyren et al. (*Analytical Biochemistry* 208:171-175, 1993) described a method relying on the detection of DNA polymerase activity by an enzymatic luminometric inorganic pyrophosphate detection assay (ELIDA).

Pastinen et al. (*Genome research* 7:606-614, 1997), describe a method for multiplex detection of single nucleotide polymorphism in which the solid phase minisequencing principle is applied to an oligonucleotide array format. High-density arrays of DNA probes attached to a solid support (DNA chips) are further described in III.C.5.

In one aspect the present invention provides polynucleotides and methods to genotype one or more biallelic markers of the present invention by performing a microsequencing assay. Preferred microsequencing primers include those being featured Figure 6. It will be appreciated that the microsequencing primers listed in Figure 6 are merely exemplary and that, any primer having a 3' end immediately adjacent to a polymorphic nucleotide may be used. Similarly, it will be appreciated that microsequencing analysis may be performed for any biallelic marker or any combination of biallelic markers of the present invention. One aspect of the present invention is a solid support which includes one or more microsequencing primers listed in Figure 6, or fragments comprising at least 8, at least 12, at least 15, or at least 20 consecutive nucleotides thereof and having a 3' terminus immediately upstream of the corresponding biallelic marker, for determining the identity of a nucleotide at biallelic marker site.

3) Mismatch detection assays based on polymerases and ligases

In one aspect the present invention provides polynucleotides and methods to determine the allele of one or more biallelic markers of the present invention in a biological sample, by mismatch detection assays based on polymerases and/or ligases. These assays are based on the specificity of polymerases and ligases. Polymerization reactions places particularly stringent requirements on correct base pairing of the 3' end of the amplification primer and the joining of two oligonucleotides hybridized to a target DNA sequence is quite sensitive to mismatches close to the ligation site, especially at the 3' end. The terms "enzyme based mismatch detection assay" are used herein to refer to any method of determining the allele of a biallelic marker based on the specificity of ligases and polymerases. Preferred methods are described below. Methods, primers and various

parameters to amplify DNA fragments comprising biallelic markers of the present invention are further described above in III.B.

Allele specific amplification

Discrimination between the two alleles of a biallelic marker can also be achieved by
5 allele specific amplification, a selective strategy, whereby one of the alleles is amplified without amplification of the other allele. This is accomplished by placing a polymorphic base at the 3' end of one of the amplification primers. Because the extension forms from the 3' end of the primer, a mismatch at or near this position has an inhibitory effect on
10 amplification. Therefore, under appropriate amplification conditions, these primers only direct amplification on their complementary allele. Designing the appropriate allele-specific primer and the corresponding assay conditions are well within the ordinary skill in the art.

Ligation/amplification based methods

The "Oligonucleotide Ligation Assay" (OLA) uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target
15 molecules. One of the oligonucleotides is biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate that can be captured and detected. OLA is capable of detecting biallelic markers and may be advantageously combined with PCR as described by Nickerson D.A. et al. (*Proc. Natl. Acad. Sci. U.S.A.*
20 87:8923-8927, 1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Other methods which are particularly suited for the detection of biallelic markers include LCR (ligase chain reaction), Gap LCR (GLCR) which are described above in III.B. As mentioned above LCR uses two pairs of probes to exponentially amplify a specific
25 target. The sequences of each pair of oligonucleotides, is selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependant ligase. In accordance with the present invention, LCR can be performed with oligonucleotides having the proximal and distal sequences of the same strand of a biallelic marker site. In one embodiment, either oligonucleotide will be
30 designed to include the biallelic marker site. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide(s) that is complementary to the biallelic marker on the oligonucleotide. In an alternative embodiment, the oligonucleotides will not include the biallelic marker, such that when they hybridize to the target molecule, a "gap" is

created as described in WO 90/01069. This gap is then "filled" with complementary dNTPs (as mediated by DNA polymerase), or by an additional pair of oligonucleotides. Thus at the end of each cycle, each single strand has a complement capable of serving as a target during the next cycle and exponential allele-specific amplification of the desired sequence is
5 obtained.

Ligase/Polymerase-mediated Genetic Bit AnalysisTM is another method for determining the identity of a nucleotide at a preselected site in a nucleic acid molecule (WO 95/21271). This method involves the incorporation of a nucleoside triphosphate that is complementary to the nucleotide present at the preselected site onto the terminus of a primer
10 molecule, and their subsequent ligation to a second oligonucleotide. The reaction is monitored by detecting a specific label attached to the reaction's solid phase or by detection in solution.

4) Hybridization assay methods

A preferred method of determining the identity of the nucleotide present at a biallelic
15 marker site involves nucleic acid hybridization. The hybridization probes, which can be conveniently used in such reactions, preferably include the probes defined herein. Any hybridization assay may be used including Southern hybridization, Northern hybridization, dot blot hybridization and solid-phase hybridization (see Sambrook et al., Molecular Cloning – A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., 1989).

20 Hybridization refers to the formation of a duplex structure by two single stranded nucleic acids due to complementary base pairing. Hybridization can occur between exactly complementary nucleic acid strands or between nucleic acid strands that contain minor regions of mismatch. Specific probes can be designed that hybridize to one form of a biallelic marker and not to the other and therefore are able to discriminate between different
25 allelic forms. Allele-specific probes are often used in pairs, one member of a pair showing perfect match to a target sequence containing the original allele and the other showing a perfect match to the target sequence containing the alternative allele. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response,
30 whereby a probe hybridizes to only one of the alleles. Stringent, sequence specific hybridization conditions, under which a probe will hybridize only to the exactly complementary target sequence are well known in the art (Sambrook et al., Molecular Cloning – A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., 1989). Stringent conditions are sequence dependent and will be different in different

circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 5 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Alternatively, the hybridization step can be performed at 65°C in the 10 presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37°C for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50°C for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68°C for 15 minute 15 intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60°C in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50°C and the 20 hybridized probes are detectable by autoradiography. Other conditions of high and intermediate stringency which may be used are well known in the art and as cited in Sambrook et al. (Molecular Cloning - A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., 1989) and Ausubel et al. (Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y., 1989).

25 Although such hybridizations can be performed in solution, it is preferred to employ a solid-phase hybridization assay. The target DNA comprising a biallelic marker of the present invention may be amplified prior to the hybridization reaction. The presence of a specific allele in the sample is determined by detecting the presence or the absence of stable hybrid duplexes formed between the probe and the target DNA. The detection of hybrid 30 duplexes can be carried out by a number of methods. Various detection assay formats are well known which utilize detectable labels bound to either the target or the probe to enable detection of the hybrid duplexes. Typically, hybridization duplexes are separated from unhybridized nucleic acids and the labels bound to the duplexes are then detected. Those skilled in the art will recognize that wash steps may be employed to wash away excess

target DNA or probe. Standard heterogeneous assay formats are suitable for detecting the hybrids using the labels present on the primers and probes.

Two recently developed assays allow hybridization-based allele discrimination with no need for separations or washes (see Landegren U. et al., *Genome Research*, 8:769-776, 1998). The TaqMan assay takes advantage of the 5' nuclease activity of Taq DNA polymerase to digest a DNA probe annealed specifically to the accumulating amplification product. TaqMan probes are labeled with a donor-acceptor dye pair that interacts via fluorescence energy transfer. Cleavage of the TaqMan probe by the advancing polymerase during amplification dissociates the donor dye from the quenching acceptor dye, greatly increasing the donor fluorescence. All reagents necessary to detect two allelic variants can be assembled at the beginning of the reaction and the results are monitored in real time (see Livak et al., *Nature Genetics*, 9:341-342, 1995). In an alternative homogeneous hybridization-based procedure, molecular beacons are used for allele discriminations. Molecular beacons are hairpin-shaped oligonucleotide probes that report the presence of specific nucleic acids in homogeneous solutions. When they bind to their targets they undergo a conformational reorganization that restores the fluorescence of an internally quenched fluorophore (Tyagi et al., *Nature Biotechnology*, 16:49-53, 1998).

The polynucleotides provided herein can be used in hybridization assays for the detection of biallelic marker alleles in biological samples. These probes are characterized in that they preferably comprise between 8 and 50 nucleotides, and in that they are sufficiently complementary to a sequence comprising a biallelic marker of the present invention to hybridize thereto and preferably sufficiently specific to be able to discriminate the targeted sequence for only one nucleotide variation. The GC content in the probes of the invention usually ranges between 10 and 75 %, preferably between 35 and 60 %, and more preferably between 40 and 55 %. The length of these probes can range from 10, 15, 20, or 30 to at least 100 nucleotides, preferably from 10 to 50, more preferably from 18 to 35 nucleotides. A particularly preferred probe is 25 nucleotides in length. Preferably the biallelic marker is within 4 nucleotides of the center of the polynucleotide probe. In particularly preferred probes the biallelic marker is at the center of said polynucleotide. Shorter probes may lack specificity for a target nucleic acid sequence and generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. Longer probes are expensive to produce and can sometimes self-hybridize to form hairpin structures. Methods for the synthesis of oligonucleotide probes have been described above and can be applied to the probes of the present invention.

Preferably the probes of the present invention are labeled or immobilized on a solid support. Labels and solid supports are further described in I. Detection probes are generally nucleic acid sequences or uncharged nucleic acid analogs such as, for example peptide nucleic acids which are disclosed in International Patent Application WO 92/20702, d,
5 morpholino analogs which are described in U.S. Patents Numbered 5,185,444; 5,034,506 and 5,142,047. The probe may have to be rendered "non-extendable" in that additional dNTPs cannot be added to the probe. In and of themselves analogs usually are non-extendable and nucleic acid probes can be rendered non-extendable by modifying the 3' end of the probe such that the hydroxyl group is no longer capable of participating in elongation.
10 For example, the 3' end of the probe can be functionalized with the capture or detection label to thereby consume or otherwise block the hydroxyl group. Alternatively, the 3' hydroxyl group simply can be cleaved, replaced or modified, U.S. Patent Application Serial No. 07/049,061 filed April 19, 1993 describes modifications, which can be used to render a probe non-extendable.

15 The probes of the present invention are useful for a number of purposes. They can be used in Southern hybridization to genomic DNA or Northern hybridization to mRNA. The probes can also be used to detect PCR amplification products. By assaying the hybridization to an allele specific probe, one can detect the presence or absence of a biallelic marker allele in a given sample.

20 High-Throughput parallel hybridizations in array format are specifically encompassed within "hybridization assays" and are described below.

Hybridization to addressable arrays of oligonucleotides

Hybridization assays based on oligonucleotide arrays rely on the differences in hybridization stability of short oligonucleotides to perfectly matched and mismatched target
25 sequence variants. Efficient access to polymorphism information is obtained through a basic structure comprising high-density arrays of oligonucleotide probes attached to a solid support (the chip) at selected positions. Each DNA chip can contain thousands to millions of individual synthetic DNA probes arranged in a grid-like pattern and miniaturized to the size of a dime.

30 The chip technology has already been applied with success in numerous cases. For example, the screening of mutations has been undertaken in the BRCA1 gene, in *S. cerevisiae* mutant strains, and in the protease gene of HIV-1 virus (Hacia et al., *Nature Genetics*, 14(4):441-447, 1996; Shoemaker et al., *Nature Genetics*, 14(4):450-456, 1996 ; Kozal et al., *Nature Medicine*, 2:753-759, 1996). Chips of various formats for use in

detecting biallelic polymorphisms can be produced on a customized basis by Affymetrix (GeneChip™), Hyseq (HyChip and HyGnostics), and Protogene Laboratories.

In general, these methods employ arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual which, target
5 sequences include a polymorphic marker. EP785280, describes a tiling strategy for the detection of single nucleotide polymorphisms. Briefly, arrays may generally be “tilled” for a large number of specific polymorphisms. By “tiling” is generally meant the synthesis of a defined set of oligonucleotide probes which is made up of a sequence complementary to the target sequence of interest, as well as preselected variations of that sequence, e.g.,
10 substitution of one or more given positions with one or more members of the basis set of monomers, i.e. nucleotides. Tiling strategies are further described in PCT application No. WO 95/11995. In a particular aspect, arrays are tiled for a number of specific, identified biallelic marker sequences. In particular the array is tiled to include a number of detection blocks, each detection block being specific for a specific biallelic marker or a set of biallelic
15 markers. For example, a detection block may be tiled to include a number of probes, which span the sequence segment that includes a specific polymorphism. To ensure probes that are complementary to each allele, the probes are synthesized in pairs differing at the biallelic marker. In addition to the probes differing at the polymorphic base, monosubstituted probes are also generally tiled within the detection block. These
20 monosubstituted probes have bases at and up to a certain number of bases in either direction from the polymorphism, substituted with the remaining nucleotides (selected from A, T, G, C and U). Typically the probes in a tiled detection block will include substitutions of the sequence positions up to and including those that are 5 bases away from the biallelic marker. The monosubstituted probes provide internal controls for the tiled array, to
25 distinguish actual hybridization from artefactual cross-hybridization. Upon completion of hybridization with the target sequence and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data from the scanned array is then analyzed to identify which allele or alleles of the biallelic marker are present in the sample. Hybridization and scanning may be carried
30 out as described in PCT application No. WO 92/10092 and WO 95/11995 and US patent No. 5,424,186, .

Thus, in some embodiments, the chips may comprise an array of nucleic acid sequences of fragments of about 15 nucleotides in length. In further embodiments, the chip may comprise an array including at least one of the sequences selected from the group

consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 and the sequences complementary thereto, or a fragment thereof at least about 8 consecutive nucleotides, preferably 10, 15, 20, more preferably 25, 30, 40, 47, or 50 consecutive nucleotides. In some embodiments, the chip may comprise an array of at least 2, 3, 4, 5, 6, 7, 8 or more of these polynucleotides of the invention. Solid supports and polynucleotides of the present invention attached to solid supports are further described in I. "Biallelic Markers and Polynucleotides Comprising Biallelic Markers."

5) Integrated Systems

Another technique, which may be used to analyze polymorphisms, includes multicomponent integrated systems, which miniaturize and compartmentalize processes such as PCR and capillary electrophoresis reactions in a single functional device. An example of such technique is disclosed in US patent 5,589,136, which describes the integration of PCR amplification and capillary electrophoresis in chips.

Integrated systems can be envisaged mainly when microfluidic systems are used. These systems comprise a pattern of microchannels designed onto a glass, silicon, quartz, or plastic wafer included on a microchip. The movements of the samples are controlled by electric, electroosmotic or hydrostatic forces applied across different areas of the microchip. For genotyping biallelic markers, the microfluidic system may integrate nucleic acid amplification, microsequencing, capillary electrophoresis and a detection method such as laser-induced fluorescence detection.

IV. Methods of Genetic Analysis Using the Biallelic Markers of the Present Invention

Different methods are available for the genetic analysis of complex traits (see Lander and Schork, *Science*, 265, 2037-2048, 1994). The search for disease-susceptibility genes is conducted using two main methods: the linkage approach in which evidence is sought for cosegregation between a locus and a putative trait locus using family studies, and the association approach in which evidence is sought for a statistically significant association between an allele and a trait or a trait causing allele (Khoury J. et al., *Fundamentals of Genetic Epidemiology*, Oxford University Press, NY, 1993). In general, the biallelic markers of the present invention find use in any method known in the art to demonstrate a statistically significant correlation between a genotype and a phenotype. The biallelic markers may be used in parametric and non-parametric linkage analysis methods. Preferably, the biallelic markers of the present invention are used to identify genes associated with detectable traits using association studies, an approach which does not

require the use of affected families and which permits the identification of genes associated with complex and sporadic traits.

The genetic analysis using the biallelic markers of the present invention may be conducted on any scale. The whole set of biallelic markers of the present invention or any
5 subset of biallelic markers of the present invention may be used. In some embodiments a subset of biallelic markers corresponding to one or several candidate genes of the present invention may be used. In other embodiments a subset of biallelic markers corresponding to candidate genes from a given metabolic pathway may be used. Such pathways include glucoronidation and glutathione conjugation. Alternatively, a subset of biallelic markers of
10 the present invention localised on a specific chromosome segment may be used. Further, any set of genetic markers including a biallelic marker of the present invention may be used. A set of biallelic polymorphisms that, could be used as genetic markers in combination with the biallelic markers of the present invention, has been described in WO 98/20165. As mentioned above, it should be noted that the biallelic markers of the present invention may
15 be included in any complete or partial genetic map of the human genome. These different uses are specifically contemplated in the present invention and claims.

IV.A. Linkage Analysis

Linkage analysis is based upon establishing a correlation between the transmission of genetic markers and that of a specific trait throughout generations within a family. Thus,
20 the aim of linkage analysis is to detect marker loci that show cosegregation with a trait of interest in pedigrees.

Parametric methods

When data are available from successive generations there is the opportunity to study the degree of linkage between pairs of loci. Estimates of the recombination fraction
25 enable loci to be ordered and placed onto a genetic map. With loci that are genetic markers, a genetic map can be established, and then the strength of linkage between markers and traits can be calculated and used to indicate the relative positions of markers and genes affecting those traits (Weir, B.S., *Genetic data Analysis II: Methods for Discrete population genetic Data*, Sinauer Assoc., Inc., Sunderland, MA, USA, 1996). The classical method for
30 linkage analysis is the logarithm of odds (lod) score method (see Morton N.E., *Am.J. Hum. Genet.*, 7:277-318, 1955; Ott J., *Analysis of Human Genetic Linkage*, John Hopkins University Press, Baltimore, 1991). Calculation of lod scores requires specification of the mode of inheritance for the disease (parametric method). Generally, the length of the candidate region identified using linkage analysis is between 2 and 20Mb. Once a candidate

region is identified as described above, analysis of recombinant individuals using additional markers allows further delineation of the candidate region. Linkage analysis studies have generally relied on the use of a maximum of 5,000 microsatellite markers, thus limiting the maximum theoretical attainable resolution of linkage analysis to about 600 kb on average.

- 5 Linkage analysis has been successfully applied to map simple genetic traits that show clear Mendelian inheritance patterns and have a high penetrance (i.e., the ratio between the number of trait positive carriers of allele a and the total number of a carriers in the population). However, parametric linkage analysis suffers from a variety of drawbacks. First, it is limited by its reliance on the choice of a genetic model suitable for each studied
- 10 trait. Furthermore, as already mentioned, the resolution attainable using linkage analysis is limited, and complementary studies are required to refine the analysis of the typical 2Mb to 20Mb regions initially identified through linkage analysis. In addition, parametric linkage analysis approaches have proven difficult when applied to complex genetic traits, such as those due to the combined action of multiple genes and/or environmental factors. It is very
- 15 difficult to model these factors adequately in a lod score analysis. In such cases, too large an effort and cost are needed to recruit the adequate number of affected families required for applying linkage analysis to these situations, as recently discussed by Risch, N. and Merikangas, K. (*Science*, 273:1516-1517, 1996).

Non-parametric methods

- 20 The advantage of the so-called non-parametric methods for linkage analysis is that they do not require specification of the mode of inheritance for the disease, they tend to be more useful for the analysis of complex traits. In non-parametric methods, one tries to prove that the inheritance pattern of a chromosomal region is not consistent with random Mendelian segregation by showing that affected relatives inherit identical copies of the
- 25 region more often than expected by chance. Affected relatives should show excess "allele sharing" even in the presence of incomplete penetrance and polygenic inheritance. In non-parametric linkage analysis the degree of agreement at a marker locus in two individuals can be measured either by the number of alleles identical by state (IBS) or by the number of alleles identical by descent (IBD). Affected sib pair analysis is a well-known special case
- 30 and is the simplest form of these methods.

The biallelic markers of the present invention may be used in both parametric and non-parametric linkage analysis. Preferably biallelic markers may be used in non-parametric methods which allow the mapping of genes involved in complex traits. The biallelic markers of the present invention may be used in both IBD- and IBS- methods to

map genes affecting a complex trait. In such studies, taking advantage of the high density of biallelic markers, several adjacent biallelic marker loci may be pooled to achieve the efficiency attained by multi-allelic markers (Zhao et al., *Am. J. Hum. Genet.*, 63:225-240, 1998).

- 5 However, both parametric and non-parametric linkage analysis methods analyse affected relatives, they tend to be of limited value in the genetic analysis of drug responses or in the analysis of side effects to treatments. This type of analysis is impractical in such cases due to the lack of availability of familial cases. In fact, the likelihood of having more than one individual in a family being exposed to the same drug at the same time is
10 extremely low.

IV.B. Population Association Studies

- The present invention comprises methods for identifying one or several genes among a set of candidate genes that are associated with a detectable trait using the biallelic markers of the present invention. In one embodiment the present invention comprises methods to
15 detect an association between a biallelic marker allele or a biallelic marker haplotype and a trait. Further, the invention comprises methods to identify a trait causing allele in linkage disequilibrium with any biallelic marker allele of the present invention.

- As described above, alternative approaches can be employed to perform association studies: genome-wide association studies, candidate region association studies and
20 candidate gene association studies. In a preferred embodiment, the biallelic markers of the present invention are used to perform candidate gene association studies. The candidate gene analysis clearly provides a short-cut approach to the identification of genes and gene polymorphisms related to a particular trait when some information concerning the biology of the trait is available. Further, the biallelic markers of the present invention may be
25 incorporated in any map of genetic markers of the human genome in order to perform genome-wide association studies. Methods to generate a high-density map of biallelic markers has been described in US Provisional Patent application serial number 60/082,614. The biallelic markers of the present invention may further be incorporated in any map of a specific candidate region of the genome (a specific chromosome or a specific chromosomal
30 segment for example).

As mentioned above, association studies may be conducted within the general population and are not limited to studies performed on related individuals in affected families. Association studies are extremely valuable as they permit the analysis of sporadic or multifactor traits. Moreover, association studies represent a powerful method for fine-

scale mapping enabling much finer mapping of trait causing alleles than linkage studies.

Studies based on pedigrees often only narrow the location of the trait causing allele.

Association studies using the biallelic markers of the present invention can therefore be used to refine the location of a trait causing allele in a candidate region identified by Linkage

- 5 Analysis methods. Moreover, once a chromosome segment of interest has been identified, the presence of a candidate gene such as a candidate gene of the present invention, in the region of interest can provide a shortcut to the identification of the trait causing allele.

Biallelic markers of the present invention can be used to demonstrate that a candidate gene is associated with a trait. Such uses are specifically contemplated in the present invention

- 10 and claims.

1) Determining the frequency of a biallelic marker allele or of a biallelic marker haplotype in a population

Association studies explore the relationships among frequencies for sets of alleles between loci.

15 Determining the frequency of an allele in a population

- Allelic frequencies of the biallelic markers in a population can be determined using one of the methods described above under the heading "Methods for genotyping an individual for biallelic markers", or any genotyping procedure suitable for this intended purpose. Genotyping pooled samples or individual samples can determine the frequency of
- 20 a biallelic marker allele in a population. One way to reduce the number of genotypings required is to use pooled samples. A major obstacle in using pooled samples is in terms of accuracy and reproducibility for determining accurate DNA concentrations in setting up the pools. Genotyping individual samples provides higher sensitivity, reproducibility and accuracy and; is the preferred method used in the present invention. Preferably, each
- 25 individual is genotyped separately and simple gene counting is applied to determine the frequency of an allele of a biallelic marker or of a genotype in a given population.

Determining the frequency of a haplotype in a population

- The gametic phase of haplotypes is unknown when diploid individuals are heterozygous at more than one locus. Using genealogical information in families gametic
- 30 phase can sometimes be inferred (Perlin et al., *Am. J. Hum. Genet.*, 55:777-787, 1994). When no genealogical information is available different strategies may be used. One possibility is that the multiple-site heterozygous diploids can be eliminated from the analysis, keeping only the homozygotes and the single-site heterozygote individuals, but this approach might lead to a possible bias in the sample composition and the underestimation of

low-frequency haplotypes. Another possibility is that single chromosomes can be studied independently, for example, by asymmetric PCR amplification (see Newton et al., *Nucleic Acids Res.*, 17:2503-2516, 1989; Wu et al., *Proc. Natl. Acad. Sci. USA*, 86:2757, 1989), or by isolation of single chromosome by limit dilution followed by PCR amplification (see Ruano et al., *Proc. Natl. Acad. Sci. USA*, 87:6296-6300, 1990). Further, a sample may be haplotyped for sufficiently close biallelic markers by double PCR amplification of specific alleles (Sarkar, G. and Sommer S.S., *Biotechniques*, 1991). These approaches are not entirely satisfying either because of their technical complexity, the additional cost they entail, their lack of generalisation at a large scale, or the possible biases they introduce. To overcome these difficulties, an algorithm to infer the phase of PCR-amplified DNA genotypes introduced by Clark A.G. (*Mol. Biol. Evol.*, 7:111-122, 1990), may be used. Briefly, the principle is to start filling a preliminary list of haplotypes present in the sample by examining unambiguous individuals, that is, the complete homozygotes and the single-site heterozygotes. Then other individuals in the same sample are screened for the possible occurrence of previously recognised haplotypes. For each positive identification, the complementary haplotype is added to the list of recognised haplotypes, until the phase information for all individuals is either resolved or identified as unresolved. This method assigns a single haplotype to each multiheterozygous individual, whereas several haplotypes are possible when there are more than one heterozygous site. Alternatively, one can use methods estimating haplotype frequencies in a population without assigning haplotypes to each individual. Preferably, a method based on an expectation-maximization (EM) algorithm (Dempster et al., *J. R. Stat. Soc.*, 39B: 1-38, 1977), leading to maximum-likelihood estimates of haplotype frequencies under the assumption of Hardy-Weinberg proportions (random mating) is used (see Excoffier L. and Slatkin M., *Mol. Biol. Evol.*, 12(5): 921-927, 1995). The EM algorithm is a generalised iterative maximum-likelihood approach to estimation that is useful when data are ambiguous and/or incomplete. The EM algorithm is used to resolve heterozygotes into haplotypes. Haplotype estimations are further described below under the heading "Statistical methods." Any other method known in the art to determine or to estimate the frequency of a haplotype in a population may also be used.

2) Linkage Disequilibrium analysis

Linkage disequilibrium is the non-random association of alleles at two or more loci and represents a powerful tool for mapping genes involved in disease traits (see Ajioka R.S. et al., *Am. J. Hum. Genet.*, 60:1439-1447, 1997). Biallelic markers, because they are

densely spaced in the human genome and can be genotyped in more numerous numbers than other types of genetic markers (such as RFLP or VNTR markers), are particularly useful in genetic analysis based on linkage disequilibrium. The biallelic markers of the present invention may be used in any linkage disequilibrium analysis method known in the art.

- 5 Briefly, when a disease mutation is first introduced into a population (by a new mutation or the immigration of a mutation carrier), it necessarily resides on a single chromosome and thus on a single "background" or "ancestral" haplotype of linked markers. Consequently, there is complete disequilibrium between these markers and the disease mutation: one finds the disease mutation only in the presence of a specific set of marker
- 10 alleles. Through subsequent generations recombinations occur between the disease mutation and these marker polymorphisms, and the disequilibrium gradually dissipates. The pace of this dissipation is a function of the recombination frequency, so the markers closest to the disease gene will manifest higher levels of disequilibrium than those that are further away. When not broken up by recombination, "ancestral" haplotypes and linkage
- 15 disequilibrium between marker alleles at different loci can be tracked not only through pedigrees but also through populations. Linkage disequilibrium is usually seen as an association between one specific allele at one locus and another specific allele at a second locus.

- The pattern or curve of disequilibrium between disease and marker loci is expected
- 20 to exhibit a maximum that occurs at the disease locus. Consequently, the amount of linkage disequilibrium between a disease allele and closely linked genetic markers may yield valuable information regarding the location of the disease gene. For fine-scale mapping of a disease locus, it is useful to have some knowledge of the patterns of linkage disequilibrium that exist between markers in the studied region. As mentioned above the mapping
- 25 resolution achieved through the analysis of linkage disequilibrium is much higher than that of linkage studies. The high density of biallelic markers combined with linkage disequilibrium analysis provides powerful tools for fine-scale mapping. Different methods to calculate linkage disequilibrium are described below under the heading "Statistical Methods."

30 3) Population-based case-control studies of trait-marker associations

As mentioned above, the occurrence of pairs of specific alleles at different loci on the same chromosome is not random and the deviation from random is called linkage disequilibrium. Association studies focus on population frequencies and rely on the phenomenon of linkage disequilibrium. If a specific allele in a given gene is directly

involved in causing a particular trait, its frequency will be statistically increased in an affected (trait positive) population, when compared to the frequency in a trait negative population or in a random control population. As a consequence of the existence of linkage disequilibrium, the frequency of all other alleles present in the haplotype carrying the trait-causing allele will also be increased in trait positive individuals compared to trait negative individuals or random controls. Therefore, association between the trait and any allele (specifically a biallelic marker allele) in linkage disequilibrium with the trait-causing allele will suffice to suggest the presence of a trait-related gene in that particular region. Case-control populations can be genotyped for biallelic markers to identify associations that narrowly locate a trait causing allele. As any marker in linkage disequilibrium with one given marker associated with a trait will be associated with the trait. Linkage disequilibrium allows the relative frequencies in case-control populations of a limited number of genetic polymorphisms (specifically biallelic markers) to be analysed as an alternative to screening all possible functional polymorphisms in order to find trait-causing alleles. Association studies compare the frequency of marker alleles in unrelated case-control populations, and represent powerful tools for the dissection of complex traits.

Case-control populations (inclusion criteria)

Population-based association studies do not concern familial inheritance but compare the prevalence of a particular genetic marker, or a set of markers, in case-control populations. They are case-control studies based on comparison of unrelated case (affected or trait positive) individuals and unrelated control (unaffected or trait negative or random) individuals. Preferably the control group is composed of unaffected or trait negative individuals. Further, the control group is ethnically matched to the case population. Moreover, the control group is preferably matched to the case-population for the main known confusion factor for the trait under study (for example age-matched for an age-dependent trait). Ideally, individuals in the two samples are paired in such a way that they are expected to differ only in their disease status. In the following "trait positive population", "case population" and "affected population" are used interchangeably.

An important step in the dissection of complex traits using association studies is the choice of case-control populations (see Lander and Schork, *Science*, 265, 2037-2048, 1994). A major step in the choice of case-control populations is the clinical definition of a given trait or phenotype. Any genetic trait may be analysed by the association method proposed here by carefully selecting the individuals to be included in the trait positive and trait negative phenotypic groups. Four criteria are often useful: clinical phenotype, age at onset,

family history and severity. The selection procedure for continuous or quantitative traits (such as blood pressure for example) involves selecting individuals at opposite ends of the phenotype distribution of the trait under study, so as to include in these trait positive and trait negative populations individuals with non-overlapping phenotypes. Preferably, case-
5 control populations consist of phenotypically homogeneous populations. Trait positive and trait negative populations consist of phenotypically uniform populations of individuals representing each between 1 and 98%, preferably between 1 and 80%, more preferably between 1 and 50%, and more preferably between 1 and 30%, most preferably between 1 and 20% of the total population under study, and selected among individuals exhibiting non-
10 overlapping phenotypes. The clearer the difference between the two trait phenotypes, the greater the probability of detecting an association with biallelic markers. The selection of those drastically different but relatively uniform phenotypes enables efficient comparisons in association studies and the possible detection of marked differences at the genetic level, provided that the sample sizes of the populations under study are significant enough.

15 In preferred embodiments, a first group of between 50 and 300 trait positive individuals, preferably about 100 individuals, are recruited according to their phenotypes. A similar number of trait negative individuals are included in such studies.

In the present invention, typical examples of inclusion criteria include a disease involving the metabolic conversion of xenobiotics or the evaluation of the response to a
20 drug or side effects to treatment with drugs.

Suitable examples of association studies using biallelic markers including the biallelic markers of the present invention, are studies involving the following populations:

a case population suffering from a disease involving the metabolic conversion of xenobiotics and a healthy unaffected control population, or

25 a case population treated with therapeutic agents suffering from side-effects resulting from the treatment and a control population treated with the same agents showing no side-effects, or

a case population treated with therapeutic agents showing a beneficial response and a control population treated with same agents showing no beneficial response.

30 In a preferred embodiment, the trait considered was a side-effect upon drug treatment, the study involved two populations derived from a clinical study of the anti-asthmatic drug zileuton. The case population was composed of asthmatic individuals treated with zileuton showing zileuton-associated hepatotoxicity monitored by the serum level of alanine aminotransferase (ALT) and the control population was composed of

asthmatic individuals treated with zileuton and having no increased serum level of ALT.

Inclusion criteria and association between the biallelic markers of the present invention and zileuton-associated hepatotoxicity are further described below and in Example 4.

Association analysis

5 The general strategy to perform association studies using biallelic markers derived from a region carrying a candidate gene is to scan two groups of individuals (case-control populations) in order to measure and statistically compare the allele frequencies of the biallelic markers of the present invention in both groups.

 If a statistically significant association with a trait is identified for at least one or
10 more of the analysed biallelic markers, one can assume that: either the associated allele is directly responsible for causing the trait (the associated allele is the trait causing allele), or more likely the associated allele is in linkage disequilibrium with the trait causing allele. The specific characteristics of the associated allele with respect to the candidate gene function usually gives further insight into the relationship between the associated allele and
15 the trait (causal or in linkage disequilibrium). If the evidence indicates that the associated allele within the candidate gene is most probably not the trait causing allele but is in linkage disequilibrium with the real trait causing allele, then the trait causing allele can be found by sequencing the vicinity of the associated marker.

 Association studies are usually run in two successive steps. In a first phase, the
20 frequencies of a reduced number of biallelic markers from one or several candidate genes are determined in the trait positive and trait negative populations. In a second phase of the analysis, the identity of the candidate gene and the position of the genetic loci responsible for the given trait is further refined using a higher density of markers from the relevant region. However, if the candidate gene under study is relatively small in length, as it is the
25 case for many of the candidate genes analysed included in the present invention, a single phase may be sufficient to establish significant associations.

Haplotype analysis

 As described above, when a chromosome carrying a disease allele first appears in a population as a result of either mutation or migration, the mutant allele necessarily resides
30 on a chromosome having a set of linked markers: the ancestral haplotype. This haplotype can be tracked through populations and its statistical association with a given trait can be analysed. Complementing single point (allelic) association studies with multi-point association studies also called haplotype studies increases the statistical power of association studies. Thus, a haplotype association study allows one to define the frequency

and the type of the ancestral carrier haplotype. A haplotype analysis is important in that it increases the statistical power of an analysis involving individual markers.

In a first stage of a haplotype frequency analysis, the frequency of the possible haplotypes based on various combinations of the identified biallelic markers of the invention is determined. The haplotype frequency is then compared for distinct populations of trait positive and control individuals. The number of trait positive individuals, which should be, subjected to this analysis to obtain statistically significant results usually ranges between 30 and 300, with a preferred number of individuals ranging between 50 and 150. The same considerations apply to the number of unaffected individuals (or random control) used in the study. The results of this first analysis provide haplotype frequencies in case-control populations, for each evaluated haplotype frequency a p-value and an odd ratio are calculated. If a statistically significant association is found, the relative risk for an individual carrying the given haplotype of being affected with the trait under study can be approximated.

The preferred 2, 3 and 4 marker haplotypes of the invention are listed in Table 3 below:

Table 3

GENE	MARKER 1	MARKER 2	MARKER 3	MARKER 4
MGST-II	12-455-326	12-453-429	12-424-198	
MGST-II	12-455-326	12-453-429	12-424-198	12-454-363
MGST-II	12-447-58	12-455-326	12-461-299	12-453-429
MGST-II	12-441-233	12-461-299	12-453-429	
MGST-II	12-441-233	12-461-299	12-453-429	12-426-154
MGST-II	12-426-154	12-424-198		
MGST-II	12-426-154	12-461-299	12-424-198	
ME1	10-428-219	12-724-225		
UGT1A7	12-128-225	12-156-91	12-139-380	12-140-134
UGT1A7	12-148-311	12-156-91	12-139-380	12-140-134
UGT2B4	10-470-25	12-652-203		
UGT2B4	10-470-25	12-637-219	12-652-203.	

The most preferred 2, 3 and 4 marker haplotypes of the invention are listed in Table 4 below:

Table 4

GENE	MARKER 1	MARKER 2	MARKER 3	MARKER 4
MGST-II	12-455-326	12-453-429	12-424-198	
MGST-II	12-455-326	12-453-429	12-424-198	12-454-363
MGST-II	12-447-58	12-455-326	12-461-299	12-453-429
MGST-II	12-426-154	12-424-198		
ME1	10-428-219	12-724-225		

UGT1A7	12-128-225	12-156-91	12-139-380	12-140-134
UGT2B4	10-470-25	12-652-203		

Interaction Analysis

The biallelic markers of the present invention may also be used to identify patterns of biallelic markers associated with detectable traits resulting from polygenic interactions.

- 5 The analysis of genetic interaction between alleles at unlinked loci requires individual genotyping using the techniques described herein. The analysis of allelic interaction among a selected set of biallelic markers with appropriate level of statistical significance can be considered as a haplotype analysis. Interaction analysis consists in stratifying the case-control populations with respect to a given haplotype for the first loci and performing a
- 10 haplotype analysis with the second loci with each subpopulation.

Statistical methods used in association studies are further described below in IV.C. "Statistical Methods."

4) Testing for linkage in the presence of association

- The biallelic markers of the present invention may further be used in TDT
- 15 (transmission/disequilibrium test). TDT tests for both linkage and association and is not affected by population stratification. TDT requires data for affected individuals and their parents or data from unaffected sibs instead of from parents (see Spielmann S. et al., *Am. J. Hum. Genet.*, 52:506-516, 1993; Schaid D.J. et al., *Genet. Epidemiol.*, 13:423-450, 1996, Spielmann S. and Ewens W.J., *Am. J. Hum. Genet.*, 62:450-458, 1998). Such combined
- 20 tests generally reduce the false-positive errors produced by separate analyses.

IV.C. Statistical Methods

In general, any method known in the art to test whether a trait and a genotype show a statistically significant correlation may be used.

1) Methods in linkage analysis

- 25 Statistical methods and computer programs useful for linkage analysis are well-known to those skilled in the art (see Terwilliger J.D. and Ott J., *Handbook of Human Genetic Linkage*, John Hopkins University Press, London, 1994; Ott J., *Analysis of Human Genetic Linkage*, John Hopkins University Press, Baltimore, 1991).

2) Methods to estimate haplotype frequencies in a population

- 30 As described above, when genotypes are scored, it is often not possible to distinguish heterozygotes so that haplotype frequencies cannot be easily inferred. When the gametic phase is not known, haplotype frequencies can be estimated from the multilocus genotypic data. Any method known to person skilled in the art can be used to estimate

haplotype frequencies (see Lange K., *Mathematical and Statistical Methods for Genetic Analysis*, Springer, New York, 1997; Weir, B.S., *Genetic data Analysis II: Methods for Discrete population genetic Data*, Sinauer Assoc., Inc., Sunderland, MA, USA, 1996).

Preferably, maximum-likelihood haplotype frequencies are computed using an Expectation-
 5 Maximization (EM) algorithm (see Dempster et al., *J. R. Stat. Soc.*, 39B:1-38, 1977; Excoffier L. and Slatkin M., *Mol. Biol. Evol.*, 12(5): 921-927, 1995). This procedure is an iterative process aiming at obtaining maximum-likelihood estimates of haplotype frequencies from multi-locus genotype data when the gametic phase is unknown. Haplotype estimations are usually performed by applying the EM algorithm using for example the EM-
 10 HAPLO program (Hawley M.E. et al., *Am. J. Phys. Anthropol.*, 18:104, 1994) or the Arlequin program (Schneider et al., *Arlequin: a software for population genetics data analysis*, University of Geneva, 1997). The EM algorithm is a generalised iterative maximum likelihood approach to estimation and is briefly described below.

In the following part of this text, phenotypes will refer to multi-locus genotypes with
 15 unknown phase. Genotypes will refer to known-phase multi-locus genotypes.

Suppose a sample of N unrelated individuals typed for K markers. The data observed are the unknown-phase K-locus phenotypes that can be categorised in F different phenotypes. Suppose that we have H underlying possible haplotypes (in case of K biallelic markers, $H=2^K$).

20 For phenotype j, suppose that c_j genotypes are possible. We thus have the following equation

$$P_j = \sum_{i=1}^{c_j} pr(genotype_i) = \sum_{i=1}^{c_j} pr(h_k, h_l) \quad \text{Equation 1}$$

where P_j is the probability of the phenotype j, h_k and h_l are the two haplotypes constituent the genotype i. Under the Hardy-Weinberg equilibrium, $pr(h_k, h_l)$ becomes :

25 $pr(h_k, h_l) = pr(h_k)^2$ if $h_k = h_l$, $pr(h_k, h_l) = 2pr(h_k).pr(h_l)$ if $h_k \neq h_l$. Equation 2

The successive steps of the E-M algorithm can be described as follows:

Starting with initial values of the of haplotypes frequencies, noted $p_1^{(0)}, p_2^{(0)}, \dots, p_H^{(0)}$, these initial values serve to estimate the genotype frequencies (Expectation step) and then estimate another set of haplotype frequencies (Maximisation step), noted $p_1^{(1)}, p_2^{(1)}, \dots, p_H^{(1)}$,
 30 these two steps are iterated until changes in the sets of haplotypes frequency are very small.

A stop criterion can be that the maximum difference between haplotype frequencies between two iterations is less than 10^{-7} . These values can be adjusted according to the desired precision of estimations.

In details, at a given iteration s , the Expectation step consists in calculating the
5 genotypes frequencies by the following equation:

$$\begin{aligned} pr(genotype_i)^{(s)} &= pr(phenotype_j) \cdot pr(genotype_i | phenotype_j)^{(s)} \\ &= \frac{n_j}{N} \cdot \frac{pr(h_k, h_l)^{(s)}}{p_j^{(s)}} \end{aligned} \quad \text{Equation 3}$$

where genotype i occurs in phenotype j , and where h_k and h_l constitute genotype i . Each probability is derived according to eq.1, and eq.2 described above.

Then the Maximisation step simply estimates another set of haplotype frequencies
10 given the genotypes frequencies. This approach is also known as gene-counting method (Smith, *Ann. Hum. Genet.*, 21:254-276, 1957).

$$p_i^{(s+1)} = \frac{1}{2} \sum_{j=1}^F \sum_{l=1}^{c_j} \delta_{il} \cdot pr(genotype_i)^{(s)} \quad \text{Equation 4}$$

Where δ_{il} is an indicator variable which count the number of time haplotype l in genotype i . It takes the values of 0, 1 or 2.

15 To ensure that the estimation finally obtained is the maximum-likelihood estimation several values of departures are required. The estimations obtained are compared and if they are different the estimations leading to the best likelihood are kept.

3) Methods to calculate linkage disequilibrium between markers

A number of methods can be used to calculate linkage disequilibrium between any
20 two genetic positions, in practice linkage disequilibrium is measured by applying a statistical association test to haplotype data taken from a population.

Linkage disequilibrium between any pair of biallelic markers comprising at least one of the biallelic markers of the present invention (M_i, M_j) having alleles (a_i/b_i) at marker M_i and alleles (a_j/b_j) at marker M_j can be calculated for every allele combination ($a_i, a_j, a_i, b_j, b_i, a_j$
25 and b_i, b_j), according to the Piazza formula :

$$\Delta_{aiaj} = \sqrt{\theta 4} - \sqrt{(\theta 4 + \theta 3)(\theta 4 + \theta 2)}, \text{ where :}$$

$\theta 4 = - - =$ frequency of genotypes not having allele a_i at M_i and not having allele a_j at M_j

$\theta 3 = - + =$ frequency of genotypes not having allele a_i at M_i and having allele a_j at M_j

30 $\theta 2 = + - =$ frequency of genotypes having allele a_i at M_i and not having allele a_j at M_j

Linkage disequilibrium (LD) between pairs of biallelic markers (M_i, M_j) can also be calculated for every allele combination ($a_i, a_j; a_i, b_j; b_i, a_j$ and b_i, b_j), according to the maximum-likelihood estimate (MLE) for delta (the composite genotypic disequilibrium coefficient), as described by Weir (Weir B.S., *Genetic Data Analysis, Sinauer Ass. Eds,*

5 1996). The MLE for the composite linkage disequilibrium is:

$$D_{aiaj} = (2n_1 + n_2 + n_3 + n_4/2)/N - 2(\text{pr}(a_i) \cdot \text{pr}(a_j))$$

Where $n_1 = \Sigma$ phenotype ($a_i/a_i, a_j/a_j$), $n_2 = \Sigma$ phenotype ($a_i/a_i, a_j/b_j$), $n_3 = \Sigma$ phenotype ($a_i/b_i, a_j/a_j$), $n_4 = \Sigma$ phenotype ($a_i/b_i, a_j/b_j$) and N is the number of individuals in the sample.

This formula allows linkage disequilibrium between alleles to be estimated when
10 only genotype, and not haplotype, data are available.

Another means of calculating the linkage disequilibrium between markers is as follows. For a couple of biallelic markers, $M_i (a/b_i)$ and $M_j (a/b_j)$, fitting the Hardy-Weinberg equilibrium, one can estimate the four possible haplotype frequencies in a given population according to the approach described above.

15 The estimation of gametic disequilibrium between a_i and a_j is simply:

$$D_{aiaj} = \text{pr}(\text{haplotype}(a_i, a_j)) - \text{pr}(a_i) \cdot \text{pr}(a_j).$$

Where $\text{pr}(a_i)$ is the probability of allele a_i and $\text{pr}(a_j)$ is the probability of allele a_j and where $\text{pr}(\text{haplotype}(a_i, a_j))$ is estimated as in Equation 3 above.

For a couple of biallelic marker only one measure of disequilibrium is necessary to
20 describe the association between M_i and M_j .

Then a normalised value of the above is calculated as follows:

$$D'_{aiaj} = D_{aiaj} / \max(-\text{pr}(a_i) \cdot \text{pr}(a_j), -\text{pr}(b_i) \cdot \text{pr}(b_j)) \text{ with } D_{aiaj} < 0$$

$$D'_{aiaj} = D_{aiaj} / \max(\text{pr}(b_i) \cdot \text{pr}(a_j), \text{pr}(a_i) \cdot \text{pr}(b_j)) \text{ with } D_{aiaj} > 0$$

The skilled person will readily appreciate that other LD calculation methods can be
25 used without undue experimentation.

Linkage disequilibrium among a set of biallelic markers having an adequate heterozygosity rate can be determined by genotyping between 50 and 1000 unrelated individuals, preferably between 75 and 200, more preferably around 100.

4) Testing for association

30 Methods for determining the statistical significance of a correlation between a phenotype and a genotype, in this case an allele at a biallelic marker or a haplotype made up of such alleles, may be determined by any statistical test known in the art and with any accepted threshold of statistical significance being required. The application of particular

methods and thresholds of significance are well within the skill of the ordinary practitioner of the art.

Testing for association is performed by determining the frequency of a biallelic marker allele in case and control populations and comparing these frequencies with a statistical test to determine if there is a statistically significant difference in frequency which would indicate a correlation between the trait and the biallelic marker allele under study. Similarly, a haplotype analysis is performed by estimating the frequencies of all possible haplotypes for a given set of biallelic markers in case and control populations, and comparing these frequencies with a statistical test to determine if there is a statistically significant correlation between the haplotype and the phenotype (trait) under study. Any statistical tool useful to test for a statistically significant association between a genotype and a phenotype may be used. Preferably the statistical test employed is a chi-square test with one degree of freedom. A P-value is calculated (the P-value is the probability that a statistic as large or larger than the observed one would occur by chance).

15 **Statistical significance**

In preferred embodiments, significance for diagnosis purposes, either as a positive basis for further diagnostic tests or as a preliminary starting point for early preventive therapy, the p value related to a biallelic marker association is preferably about 1×10^{-2} or less, more preferably about 1×10^{-4} or less, for a single biallelic marker analysis and about 1×10^{-3} or less, still more preferably 1×10^{-6} or less and most preferably of about 1×10^{-8} or less, for a haplotype analysis involving several markers. These values are believed to be applicable to any association studies involving single or multiple marker combinations.

The skilled person can use the range of values set forth above as a starting point in order to carry out association studies with biallelic markers of the present invention. In doing so, significant associations between the biallelic markers of the present invention and responses to drugs or side effects upon treatment with drugs or diseases involving the metabolic conversion of xenobiotics can be revealed and used for diagnosis and drug screening purposes.

Phenotypic permutation

30 In order to confirm the statistical significance of the first stage haplotype analysis described above, it might be suitable to perform further analyses in which genotyping data from case-control individuals are pooled and randomised with respect to the trait phenotype. Each individual genotyping data is randomly allocated to two groups, which contain the same number of individuals as the case-control populations used to compile the data

obtained in the first stage. A second stage haplotype analysis is preferably run on these artificial groups, preferably for the markers included in the haplotype of the first stage analysis showing the highest relative risk coefficient. This experiment is reiterated preferably at least between 100 and 10000 times. The repeated iterations allow the

5 determination of the percentage of obtained haplotypes with a significant p-value level.

Assessment of statistical association

To address the problem of false positives similar analysis may be performed with the same case-control populations in random genomic regions. Results in random regions and the candidate region are compared as described in US Provisional Patent Application

10 entitled "Methods, software and apparatus for identifying genomic regions harbouring a gene associated with a detectable trait".

5) Evaluation of risk factors

The association between a risk factor (in genetic epidemiology the risk factor is the presence or the absence of a certain allele or haplotype at marker loci) and a disease is

15 measured by the odds ratio (OR) and by the relative risk (RR). If $P(R^+)$ is the probability of developing the disease for individuals with R and $P(R^-)$ is the probability for individuals without the risk factor, then the relative risk is simply the ratio of the two probabilities, that is:

$$RR = P(R^+)/P(R^-)$$

20 In case-control studies, direct measures of the relative risk cannot be obtained because of the sampling design. However, the odds ratio allows a good approximation of the relative risk for low-incidence diseases and can be calculated:

$$OR = \left[\frac{F^+}{1 - F^+} \right] / \left[\frac{F^-}{(1 - F^-)} \right]$$

F^+ is the frequency of the exposure to the risk factor in cases and F^- is the frequency

25 of the exposure to the risk factor in controls. F^+ and F^- are calculated using the allelic or haplotype frequencies of the study and further depend on the underlying genetic model (dominant, recessive, additive...).

One can further estimate the attributable risk (AR) which describes the proportion of individuals in a population exhibiting a trait due to a given risk factor. This measure is

30 important in quantitating the role of a specific factor in disease etiology and in terms of the public health impact of a risk factor. The public health relevance of this measure lies in

estimating the proportion of cases of disease in the population that could be prevented if the exposure of interest were absent. AR is determined as follows:

$$AR = P_E (RR-1) / (P_E (RR-1)+1)$$

AR is the risk attributable to a biallelic marker allele or a biallelic marker haplotype.

- 5 P_E is the frequency of exposure to an allele or a haplotype within the population at large; and RR is the relative risk which, is approximated with the odds ratio when the trait under study has a relatively low incidence in the general population.

IV.D. Identification of Biallelic Markers in Linkage Disequilibrium with the Biallelic Markers of the Invention

- 10 Once a first biallelic marker has been identified in a genomic region of interest, the practitioner of ordinary skill in the art, using the teachings of the present invention, can easily identify additional biallelic markers in linkage disequilibrium with this first marker. As mentioned before any marker in linkage disequilibrium with a first marker associated with a trait will be associated with the trait. Therefore, once an association has been
15 demonstrated between a given biallelic marker and a trait, the discovery of additional biallelic markers associated with this trait is of great interest in order to increase the density of biallelic markers in this particular region. The causal gene or mutation will be found in the vicinity of the marker or set of markers showing the highest correlation with the trait.

- Identification of additional markers in linkage disequilibrium with a given marker
20 involves: (a) amplifying a genomic fragment comprising a first biallelic marker from a plurality of individuals; (b) identifying of second biallelic markers in the genomic region harboring said first biallelic marker; (c) conducting a linkage disequilibrium analysis between said first biallelic marker and second biallelic markers; and (d) selecting said second biallelic markers as being in linkage disequilibrium with said first marker.

- 25 Subcombinations comprising steps (b) and (c) are also contemplated.

- Methods to identify biallelic markers and to conduct linkage disequilibrium analysis are described herein and can be carried out by the skilled person without undue experimentation. The present invention then also concerns biallelic markers which are in linkage disequilibrium with the specific biallelic markers shown in Figure 1 and which are
30 expected to present similar characteristics in terms of their respective association with a given trait.

IV.E. Identification of Functional Mutations

Once a positive association is confirmed with a biallelic marker of the present invention, the associated candidate gene can be scanned for mutations by comparing the

sequences of a selected number of trait positive and trait negative or control individuals. In a preferred embodiment, functional regions such as exons and splice sites, promoters and other regulatory regions of the candidate gene are scanned for mutations. Preferably, trait positive individuals carry the haplotype shown to be associated with the trait and trait negative individuals do not carry the haplotype or allele associated with the trait. The mutation detection procedure is essentially similar to that used for biallelic site identification.

The method used to detect such mutations generally comprises the following steps: (a) amplification of a region of the candidate gene comprising a biallelic marker or a group of biallelic markers associated with the trait from DNA samples of trait positive patients and trait negative controls; (b) sequencing of the amplified region; (c) comparison of DNA sequences from trait-positive patients and trait-negative controls; and (d) determination of mutations specific to trait-positive patients. Subcombinations which comprise steps (b) and (c) are specifically contemplated.

It is preferred that candidate polymorphisms be then verified by screening a larger population of cases and controls by means of any genotyping procedure such as those described herein, preferably using a microsequencing technique in an individual test format. Polymorphisms are considered as candidate mutations when present in cases and controls at frequencies compatible with the expected association results.

Identification of mutations and low frequency polymorphisms in exons 3-5, in the 5'UTR region and in the 3' flanking region of the MGST-II gene is further described in Example 5. Eight polymorphisms were identified in the region of the MGST-II gene that was scanned. Three mutations were identified in the 3'UTR region. One mutation in exon 4 causes an amino acid substitution (Tyr→His) at the polypeptide level. A mutation in exon 5 introduces a stop codon into the ORF leading to the expression of a truncated MGST-II polypeptide. These mutations modify the specificity, activity and function of the MGST-II enzyme and therefore represent functional mutations of the MGST-II gene. Candidate polymorphisms and mutations suspected of being responsible for the detectable phenotype, such as hepatotoxicity to zileuton or asthma, can be confirmed by screening a larger population of affected and unaffected individuals using any of the genotyping procedures described herein. Preferably the microsequencing technique is used. In a preferred embodiment trait positive and trait negative populations are genotyped for the candidate polymorphisms identified in Example 5 (10-286-289, 10-286-345, 10-286-375, 10-523-232, 10-289-201, 10-290-37, 10-290-326 and 10-290-328) most preferably for the

mutations in exons 4 and 5 (10-289-201 and 10-290-37). Polymorphisms are considered as candidate "trait-causing" mutations when they exhibit a statistically significant correlation with the detectable phenotype.

V. Biallelic Markers of the Invention in Methods of Genetic Diagnostics

5 The biallelic markers of the present invention can also be used to develop diagnostics tests capable of identifying individuals who express a detectable trait as the result of a specific genotype or individuals whose genotype places them at risk of developing a detectable trait at a subsequent time. The trait analyzed using the present diagnostics may be any detectable trait, including a response to a drug or side effects to a
10 drug upon treatment or a disease involving the metabolic conversion of xenobiotics.

 The diagnostic techniques of the present invention may employ a variety of methodologies to determine whether a test subject has a biallelic marker pattern associated with an increased risk of developing a detectable trait or whether the individual suffers from a detectable trait as a result of a particular mutation, including methods which enable the
15 analysis of individual chromosomes for haplotyping, such as family studies, single sperm DNA analysis or somatic hybrids.

 The present invention provides diagnostic methods to determine whether an individual is at risk of developing a disease or suffers from a disease resulting from a mutation or a polymorphism in a candidate gene of the present invention. The present
20 invention also provides methods to determine whether an individual is likely to respond positively to a therapeutic agent or whether an individual is at risk of developing an adverse side effect to a therapeutic agent.

 These methods involve obtaining a nucleic acid sample from the individual and, determining, whether the nucleic acid sample contains at least one allele or at least one
25 biallelic marker haplotype, indicative of a risk of developing the trait or indicative that the individual expresses the trait as a result of possessing a particular candidate gene polymorphism or mutation (trait-causing allele).

 Preferably, in such diagnostic methods, a nucleic acid sample is obtained from the individual and this sample is genotyped using methods described above in III. "Methods of
30 Genotyping an Individual for Biallelic Markers." The diagnostics may be based on a single biallelic marker or a on group of biallelic markers.

 In each of these methods, a nucleic acid sample is obtained from the test subject and the biallelic marker pattern of one or more of the biallelic markers listed in Figure 1 is determined.

In one embodiment, a PCR amplification is conducted on the nucleic acid sample to amplify regions in which polymorphisms associated with a detectable phenotype have been identified. The amplification products are sequenced to determine whether the individual possesses one or more polymorphisms associated with a detectable phenotype. The primers
5 used to generate amplification products may comprise the primers listed in Figure 7. Alternatively, the nucleic acid sample is subjected to microsequencing reactions as described above to determine whether the individual possesses one or more polymorphisms associated with a detectable phenotype resulting from a mutation or a polymorphism in a candidate gene. The primers used in the microsequencing reactions may include the primers
10 listed in Figure 6. In another embodiment, the nucleic acid sample is contacted with one or more allele specific oligonucleotide probes which, specifically hybridize to one or more candidate gene alleles associated with a detectable phenotype. The probes used in the hybridization assay may include the probes listed in Figure 8. Diagnostic kits comprising polynucleotides of the present invention are further described in section I.

15 These diagnostic methods are extremely valuable as they can, in certain circumstances, be used to initiate preventive treatments or to allow an individual carrying a significant haplotype to foresee warning signs such as minor symptoms. For diseases in which attacks may be extremely violent and sometimes fatal if not treated on time, the knowledge of a potential predisposition, even if this predisposition is not absolute, might
20 contribute in a very significant manner to treatment efficacy. Similarly, a diagnosed predisposition to a potential side effect could immediately direct the physician toward a treatment for which such side effects have not been observed during clinical trials.

Diagnostics, which analyze and predict response to a drug or side effects to a drug, may be used to determine whether an individual should be treated with a particular drug.
25 For example, if the diagnostic indicates a likelihood that an individual will respond positively to treatment with a particular drug, the drug may be administered to the individual. Conversely, if the diagnostic indicates that an individual is likely to respond negatively to treatment with a particular drug, an alternative course of treatment may be prescribed. A negative response may be defined as either the absence of an efficacious
30 response or the presence of toxic side effects.

Clinical drug trials represent another application for the markers of the present invention. One or more markers indicative of response to a drug or to side effects to a drug may be identified using the methods described above. Thereafter, potential participants in clinical trials of such an agent may be screened to identify those individuals most likely to

respond favorably to the drug and exclude those likely to experience side effects. In that way, the effectiveness of drug treatment may be measured in individuals who respond positively to the drug, without lowering the measurement as a result of the inclusion of individuals who are unlikely to respond positively in the study and without risking
5 undesirable safety problems.

In a preferred embodiment the identity of the nucleotide present at, at least one, biallelic marker selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-
10 219, 12-721-440 and 10-420-284 is determined, and optionally wherein the detectable trait is asthma, or optionally the detectable trait is hepatotoxicity to the anti-asthmatic drug zileuton. In another preferred embodiment the identity of the nucleotide present at, at least one of the polymorphic sites selected from the group consisting of 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-716-295, 10-428-219, 12-720-80, 10-
15 420-248, 12-721-440, 12-653-423, 10-470-25, 10-471-84, 10-471-85, 12-637-219 and 12-652-203 is determined, and optionally wherein the detectable trait is asthma. In another preferred embodiment the identity of the nucleotide present at, at least one of the polymorphic sites selected from the group consisting of 12-453-429, 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-
20 219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284 is determined, and optionally wherein the detectable trait is hepatotoxicity to the anti-asthmatic drug zileuton. Diagnostic kits comprising polynucleotides of the present invention are further described in section I.
"Biallelic Markers and Polynucleotides Comprising Biallelic Markers."

25 **VI. Association of Biallelic Markers of the Invention With Asthma**

In the context of the present invention, an association between the MGST-II, ME1, UGT1A7 and UGT2B4 genes and asthma was established.

Asthma affects over 5% of the population in industrialized countries. It is increasing in prevalence and severity and has a rising mortality (Rang H.P., Ritter J.M. and
30 Dale M.M.; *Pharmacology*; Churchill Livingstone, NY, 1995). Bronchial asthma is a multifactorial syndrome rather than a single disease, defined as airway obstruction characterized by inflammatory changes in the airways and bronchial hyper-responsiveness. In addition to the evidenced impact of environmental factors on the development of asthma, patterns of clustering and segregation in asthmatic families have suggested a genetic

component to asthma. However the lack of a defined and specific asthma phenotype and of suitable markers for genetic analysis is proving to be a major hurdle for reliably identifying genes associated with asthma. The identification of genes implicated in asthma would represent a major step towards the identification of new molecular targets for the development of anti-asthma drugs. Moreover there is no straightforward physiological or biological blood test for the asthmatic state. As a result, adequate asthma treatment is often delayed, thereby allowing the inflammation process to better establish itself. Thus, there is a need for the identification of asthma susceptibility genes in order to develop an efficient and reliable asthma diagnostic test.

As mentioned above, products of arachidonic acid metabolism are important inflammatory mediators and have been involved in a number of inflammatory diseases, including asthma. More specifically, prostaglandins and leukotrienes are thought to play a major role in the inflammatory process observed in asthma patients.

In order to investigate and identify a genetic origin to asthma, a candidate gene scan was conducted. This approach comprised:

- selecting candidate genes potentially involved in the pathological pathway of interest, in this case arachidonic acid metabolism, and
- identifying biallelic markers in those genes, and finally
- conducting association studies to identify biallelic marker alleles or haplotypes associated with asthma.

Further details concerning this association study are provided in Example 3, results are briefly summarized below.

Two groups of independent individuals were used in this association study in accordance with the invention: the case-control populations. The two groups corresponded to 297 asthmatic individuals and 178 control individuals. The trait positive asthma population was mostly composed of individuals from Caucasian ethnic background (>90 %). The control population was composed of individuals from a random US Caucasian population.

In the association study described in Example 3, several biallelic marker haplotypes were shown to be significantly associated with asthma. A preferred haplotype consisting of three biallelic markers (12-455-326, 12-453-429 and 12-424-198) presented a p-value of $3.2 \cdot 10^{-5}$. Another preferred haplotype consisting of four biallelic markers (12-455-326, 12-453-429, 12-424-198 and 12-454-363) had a p-value of $1.2 \cdot 10^{-6}$. Phenotypic permutation

tests confirmed the statistical significance of these results. These haplotypes can therefore be considered to be significantly associated with asthma.

This information is extremely valuable. The knowledge of a potential genetic predisposition to asthma, even if this predisposition is not absolute, might contribute in a very significant manner to treatment efficacy of asthma patients and to the development of new therapeutic and diagnostic tools.

VII. Association of Biallelic Markers of the Invention with Hepatotoxicity to Anti-Asthma Drug Zileuton (Zyflo™)

In the context of the present invention, an association between the MGST-II gene and side effects related to treatment with the anti-asthmatic drug zileuton was discovered.

As mentioned above, bronchial asthma is a multifactorial syndrome rather than a single disease, defined as airway obstruction characterized by inflammatory changes in the airways and bronchial hyper-responsiveness. Although initially reversible with bronchodilators, airway obstruction becomes increasingly irreversible if treated poorly. Asthma management therefore relies on early and regular use of drugs that control the disease. As a consequence, there is a strong need for efficient and safe therapeutic opportunities for patients with asthma. There are two main categories of anti-asthmatic drugs— bronchodilators and anti-inflammatory agents. There is now general agreement on the need to implement early anti-inflammatory treatment rather than relying on symptomatic treatment with bronchodilators alone. The leukotrienes, a family of proinflammatory mediators arising via arachidonic acid metabolism, have been implicated in the inflammatory cascade that occurs in asthmatic airways. Of great relevance to the pathogenesis of asthma are the 5-lipoxygenase and the 5-lipoxygenase activating protein (FLAP), which catalyze the initial steps in the biosynthesis of leukotrienes from arachidonic acid. Given the significant role of the inflammatory process in asthma, pharmacological agents, such as leukotriene antagonists, FLAP inhibitors and 5-lipoxygenase inhibitors have been developed.

Zileuton (Zyflo™) is an active inhibitor of 5-lipoxygenase, the enzyme that catalyzes the formation of leukotrienes from arachidonic acid, indicated for prophylaxis and chronic treatment of asthma. A minority of zileuton-treated patients develop liver function abnormalities as close monitoring revealed that elevations of liver function tests may occur during treatment with zileuton. In the present invention the ALT test (serum level of alanine aminotransferase) was used, which is considered the most sensitive indicator of liver injury.

In order to investigate and identify a genetic origin to zileuton-associated hepatotoxicity, a candidate gene scan was conducted. This approach comprised:

- selecting candidate genes potentially involved in the pathological pathway of interest or in the metabolism of zileuton, and
- 5 - identifying biallelic markers in those genes, and finally
- conducting association studies to identify biallelic marker alleles or haplotypes associated with elevations of liver function tests upon treatment with zileuton.

Further details concerning this association study are provided in Example 4, results are briefly summarized below.

- 10 Two groups of unrelated individuals were used in this association study in accordance with the invention: the case-control populations. The case population was composed of 89 asthmatic individuals treated with zileuton showing zileuton-associated hepatotoxicity monitored by the serum level of alanine aminotransferase (ALT) and the control population was composed of 208 asthmatic individuals treated with zileuton and
- 15 having no increased serum ALT level.

The association study conducted with the biallelic markers derived from the MGST-II locus showed that several haplotypes were significantly associated with zileuton-associated hepatotoxicity. A preferred haplotype consisting of three biallelic markers (12-441-233, 12-461-299 and 12-453-429) presented a p-value of $1.5 \cdot 10^{-5}$ and an odd ratio of

20 3.63. A second preferred haplotype consisting of four biallelic markers (12-441-233, 12-461-299, 12-453-429 and 12-426-154) had a p-value of $5.2 \cdot 10^{-7}$ and an odd ratio of 5.75.

This information is extremely valuable. The knowledge of a potential genetic predisposition to hepatotoxicity upon treatment with zileuton, even if this predisposition is not absolute, might contribute in a very significant manner to the safety of asthma treatment and

25 to the development of diagnostic tools.

Similar association studies, with different case-control populations, can be routinely carried out by the skilled technician using the biallelic markers of the present invention in order to identify other association between traits and MGST-II-related biallelic marker alleles or haplotypes.

30 **VI. Computer-Related Embodiments**

As used herein the term "nucleic acid codes of the invention" encompass the nucleotide sequences comprising, consisting essentially of, or consisting of any one of the following: a) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500 or 1000 nucleotides, to the extent that a polynucleotide of these lengths

is consistent with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of the sequences described in Figure 2, and the complements thereof; b) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500 or 1000 nucleotides, to the extent that a polynucleotide of these lengths is consistent

5 with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of the sequences described in Figure 3, and the complements thereof; c) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, or 500 nucleotides, to the extent that a polynucleotide of these lengths is consistent with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of

10 the sequences described in Figure 6, more preferably a set of markers or sequences consisting of those markers or sequences found in SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, and 380, and the complements thereof, wherein said span includes an DME-related biallelic marker, preferably an DME-related biallelic marker described in Figure 1, preferably the biallelic markers found in Figures 9, 10, 11 and

15 12; or more preferably the biallelic markers found in SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, 380, in said sequence with the alternative allele present at said biallelic marker.

The "nucleic acid codes of the invention" further encompass nucleotide sequences homologous to a contiguous span of at least 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200,

20 500 or 1000 nucleotides, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of the sequences described in Figure 2, Figure 3 and Figure 6 and the complements thereof. Homologous sequences refer to a sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, or 75% homology to these contiguous spans. Homology

25 may be determined using any method described herein, including BLAST2N with the default parameters or with any modified parameters. Homologous sequences also may include RNA sequences in which uridines replace the thymines in the nucleic acid codes of the invention. It will be appreciated that the nucleic acid codes of the invention can be represented in the traditional single character format (See the inside back cover of Stryer, Lubert. *Biochemistry*,

30 3rd edition. W. H Freeman & Co., New York.) or in any other format or code which records the identity of the nucleotides in a sequence.

It will be appreciated by those skilled in the art that the nucleic acid codes of the invention, one or more of the polypeptide codes of SEQ ID Nos. 488 and 489 can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer. As

used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid codes of the invention and one or more of the polypeptide

5 codes of SEQ ID Nos. 488 and 489. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 nucleic acid codes of the invention, and the complements thereof. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 polypeptide codes of SEQ ID Nos. 488 and 489.

10 Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

15 Embodiments of the present invention include systems, particularly computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 17. As used herein, "a computer system" refers to the hardware components, software components, and data storage components used to analyze the nucleotide sequences of the nucleic acid codes of the invention

20 , or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489. In one embodiment, the computer system 100 is a Sun Enterprise 1000 server (Sun Microsystems, Palo Alto, CA). The computer system 100 preferably includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as the Pentium III from Intel Corporation, or similar processor

25 from Sun, Motorola, Compaq or International Business Machines. Preferably, the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data, and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently available computer systems are suitable. In one

30 particular embodiment, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (preferably implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some embodiments, the computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data

storage devices 110. The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, etc. In some embodiments, the internal data storage device 110 is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device. The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100. Software for accessing and processing the nucleotide sequences of the nucleic acid codes of the invention, or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489 (such as search tools, compare tools, and modeling tools etc.) may reside in main memory 115 during execution. In some embodiments, the computer system 100 may further comprise a sequence comparer for comparing the above-described nucleic acid codes of the invention or polypeptide codes of SEQ ID Nos. 488 and 489 stored on a computer readable medium to reference nucleotide or polypeptide sequences stored on a computer readable medium. A "sequence comparer" refers to one or more programs which are implemented on the computer system 100 to compare a nucleotide or polypeptide sequence with other nucleotide or polypeptide sequences and/or compounds including but not limited to peptides, peptidomimetics, and chemicals stored within the data storage means. For example, the sequence comparer may compare the nucleotide sequences of the nucleic acid codes of the invention, or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489 stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies, motifs implicated in biological function, or structural motifs. The various sequence comparer programs identified elsewhere in this patent specification are particularly contemplated for use in this aspect of the invention.

Figure 18 is a flow diagram illustrating one embodiment of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK, PIR OR SWISSPROT that is available through the Internet.

The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed

above, the memory could be any type of memory, including RAM or an internal storage device. The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then

5 performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the database. Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the

10 homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system. Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical.

15 Sequences that are within the homology parameters entered by the user will be marked as "same" in the process 200. If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is

20 displayed to the user, the process 200 moves to a decision state 218 wherein a determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this

25 manner, the new sequence is aligned and compared with every sequence in the database. It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison. Accordingly, one aspect of the present invention is a computer system

30 comprising a processor, a data storage device having stored thereon a nucleic acid code of the invention or a polypeptide code of SEQ ID Nos. 488 and 489, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to the nucleic acid code of the invention or polypeptide code of SEQ ID Nos. 488 and 489 and a sequence comparer for conducting the comparison. The sequence

comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code of the invention and polypeptide codes of SEQ ID Nos. 488 and 489 or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some embodiments, the data storage device may have stored thereon the sequences of at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of the invention or polypeptide codes of SEQ ID Nos. 488 and 489.

Another aspect of the present invention is a method for determining the level of homology between a nucleic acid code of the invention and a reference nucleotide sequence, comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through the use of a computer program which determines homology levels and determining homology between the nucleic acid code and the reference nucleotide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, including BLAST2N with the default parameters or with any modified parameters. The method may be implemented using the computer systems described above. The method may also be performed by reading 2, 5, 10, 15, 20, 25, 30, or 50 of the above described nucleic acid codes of the invention through use of the computer program and determining homology between the nucleic acid codes and reference nucleotide sequences .

Figure 19 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it should be in the single letter amino acid code so that the first and sequence sequences can be easily compared.

A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two

characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read. If there aren't any more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is
5 determined by calculating the proportion of characters between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%. Alternatively, the computer program may be a computer program which compares the nucleotide sequences of the nucleic acid codes of the present
10 invention, to reference nucleotide sequences in order to determine whether the nucleic acid code of SEQ ID Nos. 1-652 differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or the nucleic acid code of SEQ ID Nos. 1-652. In one embodiment, the computer program may
15 be a program which determines whether the nucleotide sequences of the nucleic acid codes of the invention contain a biallelic marker or single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence. This single nucleotide polymorphism may comprise a single base substitution, insertion, or deletion, while this biallelic marker may comprise about one to ten consecutive bases substituted, inserted or deleted.

20 Another aspect of the present invention is a method for determining the level of homology between a polypeptide code of SEQ ID Nos. 488 and 489 and a reference polypeptide sequence, comprising the steps of reading the polypeptide code of SEQ ID Nos. 488 and 489 and the reference polypeptide sequence through use of a computer program which determines homology levels and determining homology between the polypeptide code
25 and the reference polypeptide sequence using the computer program.

Accordingly, another aspect of the present invention is a method for determining whether a nucleic acid code of the invention differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies
30 differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some embodiments, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 19. The method may also be performed by

reading at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of the invention and the reference nucleotide sequences through the use of the computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program. In other embodiments the computer based system may further comprise
5 an identifier for identifying features within the nucleotide sequences of the nucleic acid codes of the invention or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489. An "identifier" refers to one or more programs which identifies certain features within the above-described nucleotide sequences of the nucleic acid codes of the invention or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and
10 489. In one embodiment, the identifier may comprise a program which identifies an open reading frame in the cDNAs codes of SEQ ID Nos. 486 and 487.

Figure 20 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features
15 is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG." Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA".
20 An example of such a database is produced by the University of Wisconsin Genetics Computer Group (www.gcg.com). Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the
25 feature was found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user. The process 300 then moves to a decision state 320 wherein a determination is made whether more features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the database, then the
30 process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence. It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database. In another embodiment, the identifier may comprise a

molecular modeling program which determines the 3-dimensional structure of the polypeptides codes of SEQ ID Nos. 488 and 489. In some embodiments, the molecular modeling program identifies target sequences that are most compatible with profiles representing the structural environments of the residues in known three-dimensional protein structures. (See, e.g., Eisenberg et al., U.S. Patent No. 5,436,850 issued July 25, 1995). In another technique, the known three-dimensional structures of proteins in a given family are superimposed to define the structurally conserved regions in that family. This protein modeling technique also uses the known three-dimensional structure of a homologous protein to approximate the structure of the polypeptide codes of SEQ ID Nos. 488 and 489. (See e.g., Srinivasan, et al., U.S. Patent No. 5,557,535 issued September 17, 1996).

Conventional homology modeling techniques have been used routinely to build models of proteases and antibodies. (Sowdhamini et al., Protein Engineering 10:207, 215 (1997)). Comparative approaches can also be used to develop three-dimensional protein models when the protein of interest has poor sequence identity to template proteins. In some cases, proteins fold into similar three-dimensional structures despite having very weak sequence identities. For example, the three-dimensional structures of a number of helical cytokines fold in similar three-dimensional topology in spite of weak sequence homology. The recent development of threading methods now enables the identification of likely folding patterns in a number of situations where the structural relatedness between target and template(s) is not detectable at the sequence level. Hybrid methods, in which fold recognition is performed using Multiple Sequence Threading (MST), structural equivalencies are deduced from the threading output using a distance geometry program DRAGON to construct a low resolution model, and a full-atom representation is constructed using a molecular modeling package such as QUANTA.

According to this 3-step approach, candidate templates are first identified by using the novel fold recognition algorithm MST, which is capable of performing simultaneous threading of multiple aligned sequences onto one or more 3-D structures. In a second step, the structural equivalencies obtained from the MST output are converted into interresidue distance restraints and fed into the distance geometry program DRAGON, together with auxiliary information obtained from secondary structure predictions. The program combines the restraints in an unbiased manner and rapidly generates a large number of low resolution model confirmations. In a third step, these low resolution model confirmations are converted into full-atom models and subjected to energy minimization using the

molecular modeling package QUANTA. (See e.g., Aszódi et al., *Proteins: Structure, Function, and Genetics*, Supplement 1:38-42 (1997)).

The results of the molecular modeling analysis may then be used in rational drug design techniques to identify agents which modulate the activity of the polypeptide codes of SEQ ID Nos. 488 and 489. Accordingly, another aspect of the present invention is a method of identifying a feature within the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 comprising reading the nucleic acid code(s) or the polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) or polypeptide code(s) with the computer program. In one embodiment, computer program comprises a computer program which identifies open reading frames. In a further embodiment, the computer program identifies structural motifs in a polypeptide sequence. In another embodiment, the computer program comprises a molecular modeling program. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program. The nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 may be stored as text in a word processing file, such as MicrosoftWORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE. In addition, many computer programs and databases may be used as sequence comparers, identifiers, or sources of reference nucleotide or polypeptide sequences to be compared to the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489. The following list is intended not to limit the invention but to provide guidance to programs and databases which are useful with the nucleic acid codes of the invention or the polypeptide codes of SEQ ID No. 488 and 489. The programs and databases which may be used include, but are not limited to: MacPattern (EMBL), DiscoveryBase (Molecular Applications Group), GeneMine (Molecular Applications Group), Look (Molecular Applications Group), MacLook (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al., *J. Mol. Biol.* 215: 403 (1990)), FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, 85: 2444 (1988)), FASTDB (Brutlag et al. *Comp. App. Biosci.* 6:237-245. 1990), Catalyst (Molecular Simulations Inc.), Catalyst/SHAPE

(Molecular Simulations Inc.), Cerius².DBAccess (Molecular Simulations Inc.), HypoGen (Molecular Simulations Inc.), Insight II, (Molecular Simulations Inc.), Discover (Molecular Simulations Inc.), CHARMm (Molecular Simulations Inc.), Felix (Molecular Simulations Inc.), DelPhi, (Molecular Simulations Inc.), QuanteMM, (Molecular Simulations Inc.),

5 Homology (Molecular Simulations Inc.), Modeler (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the EMBL/Swissprotein database, the MDL Available Chemicals Directory database, the MDL

10 Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwent's World Drug Index database, the BioByteMasterFile database, the Genbank database, and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure. Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites,

15 ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

It should be noted that the nucleic acid codes of the invention further encompass all

20 of the polynucleotides disclosed, described or claimed in the present invention. Also, it should be noted that the polypeptide codes of SEQ ID Nos. 488 and 489 further encompass all of the polypeptides disclosed, described or claimed in the present invention. Moreover, the present invention specifically contemplates the storage of such codes on computer readable media and computer systems individually or in combination, as well as the use of

25 such codes and combinations in the methods of section "VI. Computer-Related Embodiments."

EXAMPLES

Several of the methods of the present invention are described in the following examples, which are offered by way of illustration and not by way of limitation. Many

30 other modifications and variations of the invention as herein set forth can be made without departing from the spirit and scope thereof and therefore only such limitations should be imposed as are indicated by the appended claims.

Example 1**De Novo Identification Of Biallelic Markers**

The biallelic markers set forth in this application were isolated from human genomic sequences. To identify biallelic markers, genomic fragments were amplified, sequenced and
5 compared in a plurality of individuals.

DNA samples

Donors were unrelated and healthy. They represented a sufficient diversity for being representative of a French heterogeneous population. The DNA from 100 individuals was extracted and tested for the *de novo* identification of biallelic markers.

10 DNA samples were prepared from peripheral venous blood as follows. Thirty ml of peripheral venous blood were taken from each donor in the presence of EDTA. Cells (pellet) were collected after centrifugation for 10 minutes at 2000 rpm. Red cells were lysed in a lysis solution (50 ml final volume: 10 mM Tris pH7.6; 5 mM MgCl₂; 10 mM NaCl). The solution was centrifuged (10 minutes, 2000 rpm) as many times as necessary to
15 eliminate the residual red cells present in the supernatant, after resuspension of the pellet in the lysis solution. The pellet of white cells was lysed overnight at 42°C with 3.7 ml of lysis solution composed of: (a) 3 ml TE 10-2 (Tris-HCl 10 mM, EDTA 2 mM) / NaCl 0.4 M; (b) 200 µl SDS 10%; and (c) 500 µl proteinase K (2 mg proteinase K in TE 10-2 / NaCl 0.4 M).

For the extraction of proteins, 1 ml saturated NaCl (6M) (1/3.5 v/v) was added.

20 After vigorous agitation, the solution was centrifuged for 20 minutes at 10000 rpm. For the precipitation of DNA, 2 to 3 volumes of 100% ethanol were added to the previous supernatant, and the solution was centrifuged for 30 minutes at 2000 rpm. The DNA solution was rinsed three times with 70% ethanol to eliminate salts, and centrifuged for 20 minutes at 2000 rpm. The pellet was dried at 37°C, and resuspended in 1 ml TE 10-1 or 1
25 ml water. The DNA concentration was evaluated by measuring the OD at 260 nm (1 unit OD = 50 µg/ml DNA). To determine the presence of proteins in the DNA solution, the OD 260 / OD 280 ratio was determined. Only DNA preparations having a OD 260 / OD 280 ratio between 1.8 and 2 were used in the subsequent examples described below. DNA pools were constituted by mixing equivalent quantities of DNA from each individual.

30 Amplification of genomic DNA by PCR

Amplification of specific genomic sequences was carried out on pooled DNA samples obtained as described above.

Amplification primers

The primers used for the amplification of human genomic DNA fragments were defined with the OSP software (Hillier & Green, 1991). Preferably, primers included, upstream of the specific bases targeted for amplification, a common oligonucleotide tail useful for sequencing. Primers PU contain the following additional PU 5' sequence :

- 5 TGTAACACGACGGCCAGT; primers RP contain the following RP 5' sequence : CAGGAAACAGCTATGACC. Primers are listed in Figure 7.

Amplification

PCR assays were performed using the following protocol:

	Final volume	25 µl
10	DNA	2 ng/µl
	MgCl ₂	2 mM
	dNTP (each)	200 µM
	primer (each)	2.9 ng/µl
	Ampli Taq Gold DNA polymerase	0.05 unit/µl
15	PCR buffer (10x = 0.1 M TrisHCl pH8.3 0.5M KCl)	1x

DNA amplification was performed on a Genius II thermocycler. After heating at 94°C for 10 min, 40 cycles were performed. Cycling times and temperatures were: 30 sec at 94°C, 55°C for 1 min and 30 sec at 72°C. Holding for 7 min at 72°C allowed final elongation. The quantities of the amplification products obtained were determined on 96-
20 well microtiter plates, using a fluorometer and Picogreen as intercalant agent (Molecular Probes).

Sequencing of amplified genomic DNA and identification of biallelic polymorphisms

Sequencing of the amplified DNA was carried out on ABI 377 sequencers. The sequences of the amplification products were determined using automated dideoxy
25 terminator sequencing reactions with a dye terminator cycle sequencing protocol. The products of the sequencing reactions were run on sequencing gels and the sequences were determined using gel image analysis (ABI Prism DNA Sequencing Analysis software 2.1.2 version).

The sequence data were further evaluated to detect the presence of biallelic markers
30 within the amplified fragments. The polymorphism search was based on the presence of superimposed peaks in the electrophoresis pattern resulting from different bases occurring at the same position. However, the presence of two peaks can be an artifact due to background noise. To exclude such an artifact, the two DNA strands were sequenced and a comparison between the two strands was carried out. In order to be registered as a polymorphic

sequence, the polymorphism had to be detected on both strands. Further, some biallelic single nucleotide polymorphisms were confirmed by microsequencing as described below.

Biallelic markers were identified in the analyzed fragments and are shown in Figure 1 and Table 2.

5

Example 2

Genotyping Of Biallelic Markers

The biallelic markers identified as described above were further confirmed and their respective frequencies were determined through microsequencing. Microsequencing was carried out on individual DNA samples obtained as described herein.

10 Microsequencing primers

Amplification of genomic DNA fragments from individual DNA samples was performed as described in Example 1 using the same set of PCR primers (Figure 7). Microsequencing was carried out on the amplified fragments using specific primers. See Figure 6. The preferred primers used in microsequencing had about 19 nucleotides in length and hybridized just upstream of the considered polymorphic base.

The microsequencing reactions were performed as follows: 5 µl of PCR products were added to 5 µl purification mix (2U SAP (Shrimp alkaline phosphate) (Amersham E70092X)); 2U Exonuclease I (Amersham E70073Z); and 1 µl SAP buffer (200 mM Tris-HCl pH8, 100 mM MgCl₂) in a microtiter plate. The reaction mixture was incubated 20 minutes at 37°C, and denatured 10 minutes at 94°C afterwards. To each well was then added 20 µl of microsequencing reaction mixture containing: 10 pmol microsequencing oligonucleotide (19mers, GENSET, crude synthesis, 5 OD), 1 U Thermosequenase (Amersham E79000G), 1.25 µl Thermosequenase buffer (260 mM Tris HCl pH 9.5, 65 mM MgCl₂), and the two appropriate fluorescent ddNTPs complementary to the nucleotides at 25 the polymorphic site corresponding to both polymorphic bases (11.25 nM TAMRA-ddTTP ; 16.25 nM ROX-ddCTP ; 1.675 nM REG-ddATP ; 1.25 nM RHO-ddGTP ; Perkin Elmer, Dye Terminator Set 401095). After 4 minutes at 94°C, 20 PCR cycles of 15 sec at 55°C, 5 sec at 72°C, and 10 sec at 94°C were carried out in a Tetrad PTC-225 thermocycler (MJ Research). The microtiter plate was centrifuged 10 sec at 1500 rpm. The unincorporated 30 dye terminators were removed by precipitation with 19 µl MgCl₂ 2mM and 55 µl 100 % ethanol. After 15 minute incubation at room temperature, the microtiter plate was centrifuged at 3300 rpm 15 minutes at 4°C. After discarding the supernatants, the microplate was evaporated to dryness under reduced pressure (Speed Vac). Samples were resuspended in 2.5 µl formamide EDTA loading buffer and heated for 2 min at 95°C. 0.8 µl

microsequencing reaction were loaded on a 10 % (19:1) polyacrylamide sequencing gel. The data were collected by an ABI PRISM 377 DNA sequencer and processed using the GENESCAN software (Perkin Elmer).

Frequency of biallelic markers

- 5 Frequencies are reported for the less common allele only and are shown in Figure 1. The frequencies for both alleles are shown for the MGST-II, ME1, UGT1A7 and UGT2B4 genes in Figures 9, 10, 11, and 12, respectively.

Example 3

Association Between Asthma and the Biallelic Markers of the MGST-II Gene

10 Collection of DNA samples from trait positive and control individuals

- The disease trait followed in this association study was asthma, a disease involving the leukotriene pathway. The asthmatic population corresponded to 298 individuals that took part in a clinical study for the evaluation of the anti-asthmatic drug zileuton. More than 90 % of these 297 asthmatic individuals had a Caucasian ethnic background. The
15 control population corresponded to 178 individuals from a random US Caucasian population.

Genotyping of affected and control individuals

- The general strategy to perform the association studies was to individually scan the DNA samples from all individuals in each of the populations described above in order to
20 establish the allele frequencies of the above described biallelic markers in each of these populations.

- Allelic frequencies of the above-described biallelic marker alleles in each population were determined by performing microsequencing reactions on amplified fragments obtained by genomic PCR performed on the DNA samples from each individual. Genomic PCR and
25 microsequencing were performed as detailed above in Examples 1 and 2 using the described PCR and microsequencing primers.

Haplotype frequency analysis

- None of the single marker alleles showed a significant association with asthma however, significant results were obtained in haplotype studies. Allelic frequencies were
30 useful to check that the markers used in the haplotype studies meet the Hardy-Weinberg proportions (random mating).

The results of the haplotype analysis using 13 biallelic markers (12-421-135, 12-421-140, 12-430-80, 12-441-233, 12-442-133, 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-458-196 and 12-426-154) are shown in Figure 13.

Haplotype analysis for association of MGST-II biallelic markers and asthma was performed by estimating the frequencies of all possible 2, 3 and 4 marker haplotypes in the asthmatic and control populations described above. Haplotype estimations were performed by applying the Expectation-Maximization (EM) algorithm (Excoffier and Slatkin, *Mol. Biol. Evol.*, 12:921-927, 1995), using the EM-HAPLO program (Hawley et al., *Am. J. Phys. Anthropol.*, 18:104, 1994) as described above. Estimated haplotype frequencies in the asthmatic and control population were compared by means of a chi-square statistical test (one degree of freedom).

Figure 13 shows the most significant haplotypes obtained. Haplotype No. 6 consisting of three biallelic markers (12-455-326, 12-453-429 and 12-424-198) had a p-value of 3.2×10^{-5} and an odds ratio of 12.22. Estimated haplotype frequencies were 11.8 % in the cases and 1.1 % in the controls. Haplotype No. 18 consisting of four biallelic markers (12-455-326, 12-453-429, 12-424-198 and 12-454-363) had a p-value of 1.2×10^{-6} and an odds ratio of 100.00. Both haplotypes are related as three out of four biallelic marker alleles (G at 12-455-326, C at 12-453-429 and T and 12-454-363) are common to both haplotypes. Haplotype No. 19 consisting of four biallelic markers (12-447-58, 12-455-326, 12-461-299 and 12-453-429) had a p-value of 8.2×10^{-6} and an odds ratio of 100.00. Markers 12-455-326 and 12-453-429 are common in all three significant haplotypes; therefore, they represent preferred markers for the diagnosis of asthma. Haplotypes Nos. 6, 18 and 19 are strongly associated with asthma. Haplotypes Nos. 7-17 and 20-30 also showed very significant association (see Figure 13).

The statistical significance of the results obtained for the haplotype analysis was evaluated by a phenotypic permutation test reiterated 1000 or 10,000. For this computer simulation, data from the asthmatic and control individuals were pooled and randomly allocated to two groups which contained the same number of individuals as the case-control populations used to produce the data summarized in Figure 13. A haplotype analysis was then run on these artificial groups for the 3 markers included in haplotype No. 6 (haplotype GCT), the 4 markers included in haplotype No. 18 (haplotype GCTG) and the 4 markers included in haplotype No. 19 (haplotype CATT), all of which showed a strong association with asthma. This experiment was reiterated 1000 and 10,000 times and the results are shown in Figure 14. These results demonstrate that among 1000 iterations only 3 and among 10,000 iterations only 31 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 6 (haplotype GCT). These results demonstrate that among 1000 iterations 0 and among 10,000 iterations only 5 of the obtained haplotypes had a p-

value comparable to the one obtained for haplotype No. 18 (haplotype GCTG). These results further demonstrate that among 1000 iterations only 12 and among 10,000 iterations only 76 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 19 (haplotype CATT). These results clearly validate the statistical significance of the association between the haplotypes shown in Figure 13 and asthma.

Example 4

Association Between Side Effects Upon Treatment With the Anti-Asthmatic Drug Zileuton (Zyflo™) and the Biallelic Markers of the MGST-II Gene

Collection of DNA samples from trait positive and control individuals

10 The side effect examined in this study was the hepatotoxicity experienced by asthmatic individuals as a result of their treatment with Zileuton as part of a clinical study. Asthmatic individuals were unrelated and more than 90% of the individuals had a Caucasian ethnic background. Hepatotoxicity was monitored by measuring the serum levels of alanine aminotransferase (ALT), which is a sensitive indicator of liver cell damage.

15 More than 90% of the asthmatic individuals participating in this study did not experience Zileuton-associated ALT increase compared to their ALT levels prior to zileuton intake. As mentioned above, an association study is more informative if the populations considered present extreme phenotypes. Therefore, the asthmatic individuals, which were selected for the side effect positive trait (ALT+), corresponded to 89 individuals that
20 presented at least 3 times the upper limit of normal (ULN) level of ALT. On the other side, the asthmatic individuals that were selected for the side effect negative trait (ALT-) corresponded to 208 individuals that presented less than 1xULN of ALT. ALT+ and ALT- populations corresponded to 4% and 35% respectively of the total asthmatic individuals that participated in this study.

25 Genotyping of affected and control individuals

The general strategy to perform the Association studies was to individually scan the DNA samples from all individuals in each of the populations described above in order to establish the allele frequencies of the above described biallelic markers in each of these populations.

30 Allelic frequencies of the above-described biallelic marker alleles in each population were determined by performing microsequencing reactions on amplified fragments obtained by genomic PCR performed on the DNA samples from each individual. Genomic PCR and microsequencing were performed as detailed above in Examples 1 and 2 using the described PCR and microsequencing primers.

Haplotype frequency analysis

None of the single marker alleles showed a significant association with hepatotoxicity to zileuton however, significant results were obtained in haplotype studies.

The results of the haplotype analysis using 13 biallelic markers (12-421-135, 12-421-140, 12-430-80, 12-441-233, 12-442-133, 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-458-196 and 12-426-154) are shown in Figure 15.

Haplotype analysis for association of MGST-II biallelic markers and asthma was performed by estimating the frequencies of all possible 2, 3 and 4 marker haplotypes in the ALT+ and ALT- populations described above. Haplotype estimations were performed by applying the Expectation-Maximization (EM) algorithm (Excoffier and Slatkin, *Mol. Biol. Evol.*, 12:921-927, 1995), using the EM-HAPLO program (Hawley et al., *Am. J. Phys. Anthropol.*, 18:104, 1994) as described above. Estimated haplotype frequencies in the ALT+ and ALT- populations were compared by means of a chi-square statistical test (one degree of freedom).

Figure 15 shows the most significant haplotypes obtained. Haplotype No. 6 consisting of three biallelic markers (12-441-233, 12-461-299 and 12-453-429) presented a p-value of $1.5 \cdot 10^{-5}$ and an odd-ratio of 3.63. Estimated haplotype frequencies were 15.7 % in the cases and 4.9 % in the controls. Haplotype No. 19 consisting of four biallelic markers (12-441-233, 12-461-299, 12-453-429 and 12-426-154) had a p-value of $5.2 \cdot 10^{-7}$ and an odd ratio of 5.75. Estimated haplotype frequencies were 14.1 % in the cases and 2.8 % in the controls. Both haplotypes showed strong association with elevated serum ALT level upon treatment with zileuton. Both haplotypes are related as three out of four biallelic marker alleles (C at 12-441-233, T at 12-461-299 and T at 12-453-429) are common to both haplotypes. Haplotypes Nos. 7-18 and 20-31 of Figure 15 also showed very significant association.

The statistical significance of the results obtained for the haplotype analysis was evaluated by a phenotypic permutation test reiterated 1000 or 10,000 times on a computer. For this computer simulation, data from the ALT+ and ALT- populations were pooled and randomly allocated to two groups which contained the same number of individuals as the ALT+ and ALT- populations used to produce the data summarized in Figure 15. A haplotype analysis was then run on these artificial groups for the 3 markers included in haplotype No. 6 (haplotype CTT) and for the 4 markers included in haplotype No. 19 (haplotype CTTA) which, showed the strongest association with secondary effects to zileuton. This experiment was reiterated 1000 and 10,000 times and the results are shown in

Figure 16. These results demonstrate that among 1000 iterations only 1 and among 10,000 iterations only 12 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 6 (haplotype CTT). These results further demonstrate that among 1000 iterations only 1 and among 10,000 iterations only 7 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 19 (haplotype CTTA). These results clearly validate the statistical significance of the association between hepatotoxicity to Zylflo™ and the haplotypes shown in Figure 15.

Example 5

Identification of Mutations and of Low Frequency Alleles of the MGST-II Gene

Exons 3-5, the 5'UTR region and the 3'region of the MGST-II gene were screened for mutations by comparing their sequence in individuals exhibiting elevated ALT levels upon treatment with zileuton (ALT+) and in individuals showing normal ALT levels upon treatment with zileuton (ALT-). ALT + and ALT- individuals are further described in Example 4. Intron sequences immediately flanking the exons were also screened.

To identify mutations, fragments of the MGST-II gene were amplified, sequenced and compared in ALT+ and ALT- individuals. DNA samples from each individual were processed separately.

DNA samples

Individual DNA samples were obtained as described in Example 1.

Amplification of the MGST-II gene

Amplification primers are described in Table 5 and PCR assays were performed as described in Example 1.

Sequencing of amplified genomic DNA: identification of mutations and of low frequency polymorphisms

Sequencing of the amplified DNA was carried out on ABI 377 sequencers. The sequences of the amplification products were determined using automated dideoxy terminator sequencing reactions with a dye terminator cycle sequencing protocol. The products of the sequencing reactions were run on sequencing gels and the sequences were determined using gel image analysis (ABI Prism DNA Sequencing Analysis software 2.1.2 version).

The sequence data was further analyzed to detect the presence of mutations and of low frequency alleles. The sequences obtained with 79 ALT+ individuals and 105 ALT- individuals were compared. New polymorphisms/mutations were detected and the genotype of each individual for these markers was determined. Results are shown below:

Marker ID	Position in MGST-II gene	Least common allele/ mutation	Original allele	Genotype of ALT+ and ALT- individuals
10-286-289	5'UTR	G	C	79 ALT+ C/C 104 ALT- C/C 1 ALT- GC
10-286-345	5'UTR	T	A	65 ALT+ A/A 12 ALT+ A/T 2 ALT+ T/T 82 ALT- A/A 19 ALT- A/T 3 ALT- T/T
10-286-375	5'UTR	G	A	78 ALT+ A/A 1 ALT+ A/G 104 ALT- A/A
10-523-232	Exon 3	T	C	75 ALT+ C/C 100 ALT- C/C 1 ALT- C/T
10-289-201	Exon 4	C	T	76 ALT+ T/T 2 ALT+ C/T 100 ALT- T/T 1 ALT- C/T
10-290-37	Exon 5	T	C	78 ALT+ C/C 1 ALT+ C/T 104 ALT- C/C
10-290-326	3' region	A	G	79 ALT+ G/G 103 ALT- G/G 1 ALT- A/G
10-290-328	3' region	deletion	-	1 ALT+ deletion 78 ALT+ - 104 ALT- -

Eight polymorphisms were identified in the region of the MGST-II gene that was scanned. Three mutations were identified in the 3'UTR region. One mutation in exon 4 causes an amino acid substitution (Tyr→His) at the polypeptide level. A mutation in exon 5 introduces a stop codon into the ORF leading to the expression of a truncated MGST-II polypeptide. These mutations modify the specificity, activity and function of the MGST-II enzyme and therefore represent functional mutations of the MGST-II gene.

Example 6

Preparation of Antibody Compositions to MGST-II Variants

10 Preferably antibody compositions, specifically binding the 93-His variant or the SEQ ID No. 489 variant of MGST-II, are prepared.

Substantially pure protein or polypeptide is isolated from transfected or transformed cells containing an expression vector encoding the MGST-II protein or a portion thereof. The concentration of protein in the final preparation is adjusted, for example, by concentration on

an Amicon filter device, to the level of a few micrograms per ml. Monoclonal or polyclonal antibodies to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes in the MGST-II protein or a portion thereof can be
5 prepared from murine hybridomas according to the classical method of Kohler and Milstein (*Nature*, 256:495, 1975) or derivative methods thereof (see Harlow and Lane, *Antibodies A Laboratory Manual*, Cold Spring Harbor Laboratory, pp. 53-242, 1988).

Briefly, a mouse is repetitively inoculated with a few micrograms of the MGST-II protein or a portion thereof over a period of a few weeks. The mouse is then sacrificed, and the
10 antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by
15 detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol.* 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. *Basic Methods in Molecular Biology* Elsevier, New York. Section
20 21-2.

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes in the MGST-II protein or a portion thereof can be prepared by immunizing suitable non-human animal with the MGST-II protein or a portion thereof, which can be unmodified or modified to enhance
25 immunogenicity. A suitable non-human animal is preferably a non-human mammal is selected, usually a mouse, rat, rabbit, goat, or horse. Alternatively, a crude preparation which, has been enriched for MGST-II concentration can be used to generate antibodies. Such proteins, fragments or preparations are introduced into the non-human mammal in the presence of an appropriate adjuvant (e.g. aluminum hydroxide, RIBI, etc.) which is known
30 in the art. In addition the protein, fragment or preparation can be pretreated with an agent which will increase antigenicity, such agents are known in the art and include, for example, methylated bovine serum albumin (mBSA), bovine serum albumin (BSA), Hepatitis B surface antigen, and keyhole limpet hemocyanin (KLH). Serum from the immunized animal is collected, treated and tested according to known procedures. If the serum contains

polyclonal antibodies to undesired epitopes, the polyclonal antibodies can be purified by immunoaffinity chromatography.

Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. Techniques for producing and processing polyclonal antisera are known in the art, see for example, Mayer and Walker (1987). An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. (See, for example, Ouchterlony, O. et al., Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell, 1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum. Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., (Chap. 42: *Manual of Clinical Immunology*, 2d Ed. Rose and Friedman, Eds., *Amer. Soc. For Microbiol.*, Washington, D.C., 1980).

Antibody preparations prepared according to either the monoclonal or the polyclonal protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

It should be noted that in the accompanying Sequence Listing, all instances of the symbol "n" in the nucleic acid sequences mean that the nucleotide can be adenine, guanine, cytosine or thymine.

In some instances, the polymorphic bases of the biallelic markers alter the identity of amino acids in the encoded polypeptide. This is indicated in the accompanying Sequence Listing by use of the feature VARIANT, placement of a Xaa at the position of the polymorphic amino acid, and definition of Xaa as the two alternative amino acids. For example, if one allele of a biallelic marker is the codon CAC, which encodes histidine, while the other allele of the biallelic marker is CAA, which encodes glutamine, the

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Sequence Listing for the encoded polypeptide will contain an Xaa at the location of the polymorphic amino acid. In this instance, Xaa would be defined as being histidine or glutamine.

- In other instances, Xaa may indicate an amino acid whose identity is unknown
- 5 because of nucleotide sequence ambiguity. In this instance, the feature UNSURE is used, Xaa is placed at the position of the unknown amino acid, and Xaa is defined as being any of the 20 amino acids or a limited number of amino acids suggested by the genetic code.

SEQUENCE LISTING FREE TEXT

The following free text appears in the accompanying sequence listing:

- biallelic
- marker
- 5 drug metabolism
- Homo Sapiens
- allele
- polymorphic base
- misc_binding
- 10 potential
- complement
- potential complement
- primer_bind
- upstream amplification primer
- 15 upstream amplification primer, complement
- downstream amplification primer
- potential probe
- misc_feature
- 5' regulatory region
- 20 exon
- 5'UTR
- CDS
- 3'UTR
- polyA_signal
- 25 PRT
- VARIANT
- Stop
- Artificial Sequence
- sequencing oligonucleotide PrimerPU
- 30 sequencing oligonucleotide PrimerRP

WHAT IS CLAIMED IS:

1. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 2 and the complements thereof.
2. A polynucleotide according to claim 1, wherein said span includes a DME-related biallelic marker in said sequence.
3. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 3 and the complements thereof, wherein said span includes a DME-related biallelic marker in said sequence with the alternative allele present at said biallelic marker.
4. An isolated, purified or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 3 and the complements thereof, wherein said span includes a DME-related biallelic marker in said sequence with the original allele present at said biallelic marker.
5. An isolated, purified or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 4 and the complements thereof, wherein said span includes a DME-related biallelic marker in said sequence.
6. A polynucleotide according to any one of claims 2 to 5, wherein said contiguous span is 18 to 35 nucleotides in length and said biallelic marker is within 4 nucleotides of the center of said polynucleotide.
7. A polynucleotide according to claim 6, wherein said polynucleotide consists of said contiguous span and said contiguous span is 25 nucleotides in length and said biallelic marker is at the center of said polynucleotide.

8. A polynucleotide according to claim 1, wherein the 3' end of said contiguous span is present at the 3' end of said polynucleotide.
9. A polynucleotide according to any one of claims 2 to 5, wherein the 3' end of said
5 contiguous span is located at the 3' end of said polynucleotide and said biallelic marker is present at the 3' end of said polynucleotide.
10. A polynucleotide according to claim 8, wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a DME-related biallelic marker in said sequence.
10
11. An isolated, purified or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides in a sequence selected from the group consisting of the sequences described in Figure 3, the sequences described in Figure 4, and the complements thereof, wherein the 3' end of said contiguous span is located at the 3' end of
15 said polynucleotide, and wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a DME-related biallelic marker in said sequence.
12. A polynucleotide according to either claim 10 or 11, wherein the 3' end of said polynucleotide is located 1 nucleotide upstream of a DME-related biallelic marker in said
20 sequence.
13. A polynucleotide according to claim 1, wherein said polynucleotide consists essentially of a sequence selected from the sequences described in Figure 6.
- 25 14. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the sequences described in Figure 5.
15. A polynucleotide consisting essentially of a sequence selected from the sequences described in Figure 7.
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16. A polynucleotide consisting essentially of a sequence selected from the sequences described in Figure 8.

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17. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 wherein said contiguous span comprises at least 15 contiguous nucleotides in said sequence.
18. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 wherein
5 said contiguous span comprises at least 20 contiguous nucleotides in said sequence.
19. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 wherein said contiguous span comprises at least 25 contiguous nucleotides in said sequence.
- 10 20. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 attached to a solid support.
21. An array of polynucleotides comprising at least one polynucleotide according to claim 20.
- 15 22. An array according to claim 21, wherein said array is addressable.
23. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16, further comprising a label.
- 20 24. A method of genotyping comprising determining the identity of a nucleotide at a DME-related biallelic marker or MGST-II-related biallelic marker in a biological sample.
- 25 25. A method according to claim 24, wherein said DME-related biallelic marker is selected from the biallelic markers described in Figure 1.
26. A method according to claim 25, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.
- 30 27. A method according to claim 25, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

28. A method according to claim 24, wherein said biological sample is derived from a single subject.
- 5 29. A method according to claim 28, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said subject's genome.
30. A method according claim 24, wherein said biological sample is derived from
10 multiple subjects.
31. A method according to claim 24, further comprising amplifying a portion of said sequence comprising the biallelic marker prior to said determining step.
- 15 32. A method according to claim 31, wherein said amplifying is performed by PCR.
33. A method according to claim 24, wherein said determining is performed by a hybridization assay.
- 20 34. A method according to claim 24, wherein said determining is performed by a sequencing assay.
35. A method according to claim 24, wherein said determining is performed by a microsequencing assay.
- 25 36. A method according to claim 24, wherein said determining is performed by an enzyme-based mismatch detection assay.
37. A method of determining the frequency in a population of an allele of a DME-
30 related biallelic marker or MGST-II-related biallelic marker, comprising:
a) genotyping individuals from said population for said biallelic marker according to the method of claim 24; and
b) determining the proportional representation of said biallelic marker in said population.

38. A method according to claim 37, wherein said DME-related biallelic marker is selected from the biallelic markers described in Figure 1.
- 5 39. A method according to claim 38, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.
40. A method according to claim 38, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233,
10 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.
41. A method according to claim 37, wherein said genotyping of step a) is performed on
15 each individual of said population.
42. A method according to claim 37, wherein said genotyping is performed on a single biological sample derived from said population.
- 20 43. A method of detecting an association between an allele and a phenotype, comprising the steps of:
- a) determining the frequency of at least one DME-related biallelic marker or MGST-II-related biallelic marker allele in a trait positive population according to the method of claim 37;
 - 25 b) determining the frequency of said DME-related biallelic marker or MGST-II-related biallelic marker allele in a control population according to the method of claim 37; and
 - c) determining whether a statistically significant association exists between said allele and said phenotype.
- 30 44. A method of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising:
- a) genotyping each individual in said population for at least one DME-related biallelic marker or MGST-II-related biallelic marker according to claim 24;

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b) genotyping each individual in said population for a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome; and

5 c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

45. A method according to claim 44, wherein said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark method, and an expectation maximization
10 algorithm.

46. A method according to claim 44, wherein said DME-related biallelic marker is selected from the biallelic markers described in Figure 1.

15 47. A method according to claim 46, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

48. A method according to claim 46, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233,
20 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

49. A method according to claim 46, wherein said haplotype comprises one of the
25 following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;

12-455-326, 12-453-429, 12-424-198 and 12-454-363;

12-447-58, 12-455-326, 12-461-299 and 12-453-429;

12-441-233, 12-461-299 and 12-453-429;

30 12-441-233, 12-461-299, 12-453-429 and 12-426-154;

12-426-154, and 12-424-198;

12-426-154, 12-461-299, and 12-424-198;

10-428-219, and 12-724-225;

12-128-225, 12-156-91, 12-139-380, and 12-140-134;

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12-148-311, 12-156-91, 12-139-380, 12-140-134;
10-470-25, and 12-652-203; and
10-470-25, 12-637-219, and 12-652-203.

- 5 50. A method according to claim 46, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;
12-455-326, 12-453-429, 12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
10 12-426-154, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134; and
10-470-25, and 12-652-203.

- 15 51. A method of detecting an association between a haplotype and a phenotype, comprising the steps of:

a) estimating the frequency of at least one haplotype in a trait positive population according to the method of claim 44;
b) estimating the frequency of said haplotype in a control population
20 according to the method of claim 44; and
c) determining whether a statistically significant association exists between said haplotype and said phenotype.

52. A method according to either claim 43 or 51, wherein said control population is a
25 trait negative population.

53. A method according to either claim 43 or 51, wherein said case control population is a random population.

- 30 54. A method according to claim 51, wherein said haplotype is selected from the group of DME-related biallelic marker consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

55. A method according to claim 51, wherein said haplotype is selected from the group of DME-related biallelic marker consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

56. A method according to claim 51, wherein said haplotype comprises one of the following sets of DME-related biallelic preferred markers:

12-455-326, 12-453-429 and 12-424-198;
10 12-455-326, 12-453-429, 12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-441-233, 12-461-299 and 12-453-429;
12-441-233, 12-461-299, 12-453-429 and 12-426-154;
12-426-154, and 12-424-198;
15 12-426-154, 12-461-299, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134;
12-148-311, 12-156-91, 12-139-380, 12-140-134;
10-470-25, and 12-652-203; and
20 10-470-25, 12-637-219, and 12-652-203.

57. A method according to claim 51, wherein said haplotype comprises one of the following sets of DME-related biallelic markers:

12-455-326, 12-453-429 and 12-424-198;
25 12-455-326, 12-453-429, 12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-426-154, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134; and
30 10-470-25, and 12-652-203.

58. A method according to claim 43, wherein each of said determining of steps a) and b) is performed on a single pooled biological sample derived from each of said populations.

59. A method according to claim 43, wherein said genotyping of steps a) and b) is performed separately on biological samples derived from each individual in said populations.
- 5 60. A method according to either claim 43 or 51, wherein said phenotype is a response to a drug.
61. A method according to either claim 43 or 51, wherein said phenotype is a side effect to a drug.
- 10 62. A method according to either claim 43 or 51, wherein said phenotype is a disease involving the metabolic conversion of xenobiotics.
63. A method according to claim 43, wherein the identity of the nucleotides at all of the
15 biallelic markers described in Figure 1 is determined in steps a) and b).
64. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising a contiguous span of at least 12 nucleotides of a sequence described in Figure 2, Figure 3, Figure 5 and the complements
20 thereof; wherein said contiguous span of a sequence described in Figure 3 comprises a DME-related biallelic marker with the alternative allele present at said biallelic marker.
65. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a
25 nucleic acid code comprising a contiguous span of at least 12 nucleotides of a sequence described in Figure 2, Figure 3, Figure 5 and the complements thereof; wherein said contiguous span of a sequence described in Figure 3 comprises a DME-related biallelic marker with the alternative allele present at said biallelic marker.
- 30 66. The computer system of Claim 53 further comprising a sequence comparer and a data storage device having reference sequences stored thereon.
67. The computer system of Claim 54 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

68. A method for comparing a first sequence to a reference sequence, comprising the steps of:

5 a) reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

b) determining differences between said first sequence and said reference sequence with said computer program;

wherein said first sequence is selected from the group consisting of a nucleic acid comprising a contiguous span of at least 12 nucleotides of a sequence described in Figure 2,
10 Figure 3, Figure 5 and the complements thereof; wherein said contiguous span of a sequence described in Figure 3 comprises a DME-related biallelic marker with the alternative allele present at said biallelic marker.

69. The method of Claim 68, wherein said step b) comprises identifying polymorphisms.
15

70. A method of administering a drug or treatment comprising:

a) obtaining a nucleic acid sample from an individual;

20 b) determining the identity of the polymorphic base of at least one DME-related biallelic marker or MGST-II-related biallelic marker according to the method of claim 24 which is associated with a positive response to said drug or treatment, or at least one DME-related biallelic marker or MGST-II-related biallelic marker or which is associated with a negative response to said drug or treatment; and

25 c) administering said drug or treatment to said individual if said nucleic acid sample contains at least one biallelic marker associated with a positive response to said drug or treatment, or if said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

71. A method of selecting an individual for inclusion in a clinical trial of a drug or treatment comprising:

30 a) obtaining a nucleic acid sample from an individual;

b) determining the identity of the polymorphic base of at least one DME-related biallelic marker or MGST-II-related biallelic marker according to the method of claim 24 which is associated with a positive response to said drug or treatment, or

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at least one biallelic marker associated with a negative response to said drug or treatment in said nucleic acid sample; and

5 c) including said individual in said clinical trial if said nucleic acid sample contains at least one biallelic marker which is associated with a positive response to said drug or treatment, or if said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

72. A method according to claim 70, wherein said administering step comprises administering said drug or treatment to said individual if said nucleic acid sample contains
10 at least one biallelic marker associated with a positive response to said drug treatment, and said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

73. The method according to either claim 70 or 71, wherein said DME-related biallelic
15 marker is selected from the group consisting of the biallelic markers found in Figure 1.

74. A method according to claim 73, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

20 75. A method according to claim 73, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

25

76. A method according to claim 73, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;

12-455-326, 12-453-429, 12-424-198 and 12-454-363;

30 12-447-58, 12-455-326, 12-461-299 and 12-453-429;

12-441-233, 12-461-299 and 12-453-429;

12-441-233, 12-461-299, 12-453-429 and 12-426-154;

12-426-154, and 12-424-198;

12-426-154, 12-461-299, and 12-424-198;

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- 10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134;
12-148-311, 12-156-91, 12-139-380, 12-140-134;
10-470-25, and 12-652-203; and
5 10-470-25, 12-637-219, and 12-652-203.

77. A method according to claim 73, wherein said haplotype comprises one of the following sets of biallelic markers:

- 12-455-326, 12-453-429 and 12-424-198;
10 12-455-326, 12-453-429, 12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-426-154, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134; and
15 10-470-25, and 12-652-203.

78. A diagnostic kit comprising a polynucleotide according to any one of claims 2, 3, 4, 5, 10, 11, 13, 14, 15, and 16.

20 79. A polynucleotide for use in a hybridization assay for determining the identity of a nucleotide at a DME-related biallelic marker or MGST-II-related biallelic marker.

80. A polynucleotide for use in a sequencing assay for determining the identity of a nucleotide at a DME-related biallelic marker or MGST-II-related biallelic marker.

25

81. A polynucleotide for use in an allele specific amplification assay for determining the identity of a DME-related biallelic marker or MGST-II-related biallelic marker.

82. A polynucleotide for use in amplifying a segment of nucleotides comprising a DME-
30 related biallelic marker or MGST-II-related biallelic marker.

83. A use according to any one of claims 79 to 82. wherein said polynucleotide is selected from the sequences described in Figure 1.

84. A method according to claim 83, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

5 85. A method according to claim 83, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

10

86. A method according to claim 83, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;

12-455-326, 12-453-429, 12-424-198 and 12-454-363;

15

12-447-58, 12-455-326, 12-461-299 and 12-453-429;

12-441-233, 12-461-299 and 12-453-429;

12-441-233, 12-461-299, 12-453-429 and 12-426-154;

12-426-154, and 12-424-198;

12-426-154, 12-461-299, and 12-424-198;

20

10-428-219, and 12-724-225;

12-128-225, 12-156-91, 12-139-380, and 12-140-134;

12-148-311, 12-156-91, 12-139-380, 12-140-134;

10-470-25, and 12-652-203; and

10-470-25, 12-637-219, and 12-652-203.

25

87. A method according to claim 83, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;

12-455-326, 12-453-429, 12-424-198 and 12-454-363;

30

12-447-58, 12-455-326, 12-461-299 and 12-453-429;

12-426-154, and 12-424-198;

10-428-219, and 12-724-225;

12-128-225, 12-156-91, 12-139-380, and 12-140-134; and

10-470-25, and 12-652-203.

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88. An isolated, purified or recombinant, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7466, 7726-20255, 20356-36904,
5 36976-45166, 45249-45727 and 45966-49312.

89. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at
10 position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485.

90. An isolated, purified, or recombinant polynucleotides comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID
15 No. 486.

91. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at
20 position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486.

92. An isolated, purified, or recombinant polynucleotides comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID
25 No. 487.

93. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at
30 position 326, a C at position 378 or a T at position 426 of SEQ ID No. 487.

94. An isolated, purified, or recombinant polynucleotides comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 1-30, 436-441, 469-472, 474-477 and 484.

95. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos. 1-30, 436-441, 469-472, 474-477 and 484-487, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.

96. A polynucleotide according to claim 95, wherein said MGST-II-related biallelic marker is selected from the group consisting of the biallelic markers described in Table 1; and the complements thereof.

10

97. A polynucleotide according to claim 95, wherein said MGST-II-related biallelic marker is selected from the group consisting of biallelic markers: 12-421-135, 12-421-140, 12-430-80, 12-441-233, 12-442-133, 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-458-196 and 12-426-154; and the complements thereof.

15

98. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 in SEQ ID No. 488.

99. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488.

100. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

101. A recombinant vector comprising a polynucleotide according to any one of claims 88-95 and 98-100.

102. A host cell comprising a recombinant vector according to claim 101.

103. A non-human host animal or mammal comprising a recombinant vector according to claim 101.

104. A mammalian host cell comprising an MGST-II gene disrupted by homologous recombination with a knock out vector, comprising a polynucleotide according to any one of claims 88-95 and 98-100.
- 5 105. A non-human host mammal comprising a MGST-II gene disrupted by homologous recombination with a knock out vector, comprising a polynucleotide according to any one of claims 88-95 and 98-100.
106. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at
10 least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488.
107. An isolated or purified antibody composition capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 106, wherein said epitope
15 comprises a histidine residue at amino acid position 93 in SEQ ID No. 488.
108. An isolated, purified, or recombinant polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488.
- 20 109. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.
110. An isolated or purified antibody composition capable of selectively binding to an
25 epitope-containing fragment of a polypeptide according to claim 109, wherein said epitope comprises at least one of amino acid positions 20-30 of SEQ ID No. 489.
111. A method of determining whether an individual is at risk of developing asthma, or whether said individual suffers from asthma, comprising:
- 30 a) genotyping said individual for at least one MGST-II-related biallelic marker according to the method of claim 24; and
- b) correlating the result of step a) with a risk of developing asthma.

112. A method of determining whether an individual is at risk of developing hepatotoxicity upon treatment with zileuton, comprising:

a) genotyping said individual for at least one MGST-II-related biallelic marker according to the method of claim 24; and

5 b) correlating the result of step a) with a risk of developing asthma.

113. A method according to any one of claims 111 and 112, wherein said MGST-II-related biallelic marker is selected from the group consisting of biallelic markers: 12-455-326, 12-453-429, 12-424-198, 12-454-363, 12-447-58, 12-461-299, 12-441-233, and 12-10 426-154.

114. A diagnostic kit comprising a polynucleotide according to any one of claims 20, 23 and 88-97.

15 115. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising one of the following:

a) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7667, 7726-20264, 20365-36918, 20 36991-45180, 45263-45741 and 45980-49327;

b) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485;

25 c) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 486;

d) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide 30 selected from the group consisting of a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486;

e) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 487;

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- f) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487;
- 5 g) contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2, 3, 5-30, 437-441, 472;
- h) a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos 1 to 3 and 8 to 44, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.
- 10 i) a nucleotide sequence complementary to any one of the contiguous spans of a), b), c), d), e), f), g) and h).

116. A computer readable medium having stored thereon a sequence consisting of a polypeptide code comprising one of the following:

- 15 a) a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488;
- b) a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488;
- 20 c) a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

117. A computer system comprising a processor and a data storage device wherein said
25 data storage device a computer readable medium according to with claim 115 or 116.

118. A computer system according to claim 117, further comprising a sequence comparer and a data storage device having reference sequences stored thereon.

30 119. A computer system of claim 118 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

120. A computer system of claim 118 further comprising an identifier which identifies features in said sequence.

121. A method for comparing a first sequence to a reference sequence, comprising the steps of:

a) reading said first sequence and said reference sequence through use of a computer
5 program which compares sequences; and

b) determining differences between said first sequence and said reference sequence with said computer program,

wherein said first sequence is selected from the group consisting of a nucleic acid code comprising one of the following:

10 1) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7667, 7726-20264, 20365-36918, 36991-45180, 45263-45741 and 45980-49327;

15 2) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485;

20 3) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 486;

4) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486;

25 5) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 487;

30 6) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487;

7) contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2, 3, 5-30, 437-441, 472;

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8) a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos. 1 to 3 and 8 to 44, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.

5 9) a nucleotide sequence complementary to any one of the contiguous spans of 1-8.

and a polypeptide code comprising one of the following:

10 10) a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488;

11) a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488;

12) a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

15

122. A method according to Claim 121, wherein said step of determining differences between the first sequence and the reference sequence comprises identifying at least one polymorphism.

20 123. A method for identifying a feature in a sequence, comprising the steps of:

a) reading said sequence through the use of a computer program which identifies features in sequences; and

b) identifying features in said sequence with said computer program;

wherein said sequence is selected from the group consisting of a nucleic acid code

25 comprising one of the following:

1) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7667, 7726-20264, 20365-36918, 36991-45180, 45263-45741 and 45980-49327;

30

2) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485;

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3) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 486;

5 4) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486;

10 5) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 487;

6) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487;

15 7) contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos 2, 3, 5-30, 437-441, 472;

8) a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos. 1 to 3 and 8 to 44, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.

20 9) a nucleotide sequence complementary to any one of the contiguous spans of 1-8.

and a polypeptide code comprising one of the following:

25 10) a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488;

11) a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488;

30 12) a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

Fig. 1

GENE	BIALLELIC MARKER ID	SEQ ID NO.	BIALLELIC MARKER POSITION IN SEQ ID NO.	VALIDATION MICRO- SEQUENCING	GENOTYPING LEAST COMMON ALLELE FREQUENCY %	
MGST2	12-421-140	1	501	N		
MGST2	12-424-192	2	501	N		
MGST2	12-424-198	3	501	N		
MGST2	12-425-57	4	501	N		
MGST2	12-426-154	5	461	N		
MGST2	12-429-198	6	501	N		
MGST2	12-430-80	7	501	Y	T	5.38
MGST2	12-433-215	8	501	N		
MGST2	12-441-233	9	501	Y	G	34.48
MGST2	12-441-343	10	501	N		
MGST2	12-442-221	11	501	N		
MGST2	12-447-58	12	501	Y	G	34.27
MGST2	12-453-429	13	501	Y	T	42.55
MGST2	12-454-363	14	501	N		
MGST2	12-455-326	15	501	Y	C	41.94
MGST2	12-455-383	16	501	N		
MGST2	12-456-269	17	501	N		
MGST2	12-456-380	18	501	N		
MGST2	12-457-204	19	501	N		
MGST2	12-457-206	20	501	N		
MGST2	12-458-196	21	501	N		
MGST2	12-458-438	22	501	N		
MGST2	12-460-274	23	501	N		
MGST2	12-461-124	24	501	N		
MGST2	12-461-299	25	501	Y	C	42.39
MGST2	12-461-465	26	501	N		
MGST2	12-462-280	27	501	N		
MGST2	12-464-66	28	501	N		
MGST2	12-465-26	29	501	N		
MGST2	12-465-234	30	501	N		
ME1	10-428-219	31	501	N		
ME1	10-429-84	32	501	N		
ME1	10-420-284	33	501	N		
ME1	10-423-411	34	501	N		
ME1	12-713-95	35	232	Y	C	31.18
ME1	12-713-149	36	286	N		
ME1	12-716-295	37	500	Y	T	32.8
ME1	12-720-80	38	480	Y	C	33.69
ME1	12-721-281	40	426	N		
ME1	12-721-440	41	501	Y	A	1.6
ME1	12-723-293	42	503	Y	T	0.54
ME1	12-724-195	43	501	N		
ME1	12-724-225	44	501	Y	T	25.86
CYP1A2	10-153-329	45	330	Y	G	2.69

Fig. 1 (following)

CYP1A2	10-95-342	46	342	Y	A	0.54
CYP1A2	10-100-277	47	277	Y	C	2.33
CYP1A2	10-102-294	48	297	Y	C	30.85
CYP2C8	10-413-394	49	501	Y	A	38.07
CYP2C8	10-414-243	50	501	N		
CYP2C8	10-416-273	51	501	Y	T	39.25
CYP2C8	10-418-177	52	501	Y	G	11.41
CYP2C8	12-665-315	53	501	Y	T	22.58
CYP2C8	12-666-324	54	501	Y	C	10.87
CYP2C9	10-76-177	56	178	N		
CYP2C9	10-76-217	57	218	N		
CYP2C9	10-76-333	58	334	Y	G	13.04
CYP2C9	10-77-316	59	501	N		
CYP2C9	10-155-78	60	78	N		
CYP2C9	10-155-104	61	104	N		
CYP2C9	10-156-52	62	52	Y	A	4.79
CYP2C9	10-157-39	63	39	Y	C	30.65
CYP2C9	10-157-131	64	131	Y		
CYP2C9	10-157-166	65	166	N		
CYP2C9	10-157-246	66	246	N		
CYP2C9	10-159-161	67	161	Y	A	11.29
CYP2C9	10-159-162	68	162	N		
CYP2C18	10-83-169	69	169	Y	T	12.9
CYP2C18	10-84-152	70	152	N		
CYP2C18	10-84-243	71	243	Y	T	32.56
CYP2C18	10-84-277	72	277	N		
CYP2C18	10-84-295	73	295	Y		
CYP2C18	10-85-43	74	43	Y		
CYP2C18	10-85-117	75	117	Y	T	12.35
CYP2C18	10-85-320	76	320	N		
CYP2C18	10-86-121	77	121	Y		
CYP3A4- CYP3A7	12-244-275	78	501	N		
CYP3A4- CYP3A7	12-251-153	79	450	Y		
CYP3A4- CYP3A7	12-254-115	80	246	N		
CYP3A4- CYP3A7	12-254-180	81	311	Y		
CYP3A4- CYP3A7	12-265-300	82	499	N		
CYP3A4- CYP3A7	12-271-118	83	501	N		
CYP3A4- CYP3A7	12-272-112	84	501	Y		
CYP3A7	10-216-182	85	503	Y	A	6.59
CYP3A7	10-217-91	86	501	Y	T	12.64
CYP3A7	10-213-292	87	503	Y	G	12.9
CYP3A7	10-214-279	88	501	Y	C	13.3
CYP3A7	10-214-380	89	501	Y	G	13.44
FMO	2-1-216	90	216	N		

Fig. 1 (following)

FMO	2-1-397	91	397	N		
FMO	2-3-232	92	232	N		
FMO	2-4-51	93	51	N		
FMO	2-4-126	94	126	N		
FMO	2-5-202	95	202	N		
FMO	2-5-275	96	275	N		
FMO	2-5-346	97	346	N		
FMO	2-8-171	98	171	N		
FMO	2-9-188	99	188	N		
FMO	2-9-223	100	223	N		
FMO	2-10-107	101	107	N		
FMO	2-10-378	102	377	N		
FMO	2-11-284	103	284	N		
FMO	2-11-156	104	156	N		
FMO	2-11-379	105	379	N		
FMO	2-12-223	106	223	N		
FMO	2-14-239	107	239	N		
FMO	2-14-370	108	370	N		
FMO	2-17-104	109	104	N		
FMO	2-17-396	110	395	N		
FMO	2-22-43	111	43	N		
FMO	2-22-138	112	138	N		
FMO	2-23-82	113	82	N		
FMO	2-23-166	114	166	N		
FMO	2-23-244	115	244	N		
FMO	2-24-115	116	115	N		
FMO	2-25-36	117	36	N		
FMO	2-27-185	118	185	N		
FMO	2-27-378	119	378	N		
FMO	2-29-142	120	142	N		
FMO	2-29-166	121	166	N		
FMO	2-29-205	122	204	N		
FMO	2-29-206	123	205	N		
FMO	2-29-314	124	313	N		
FMO	2-32-68	125	68	N		
FMO	2-35-357	126	357	N		
FMO	2-36-256	127	256	N		
FMO	2-36-354	128	353	N		
FMO	2-42-236	129	236	N		
FMO	2-43-139	130	139	N		
FMO	2-44-215	131	213	N		
FMO	2-45-38	132	38	N		
FMO	2-45-183	133	183	N		
FMO	2-45-335	134	335	N		
FMO	2-45-394	135	394	N		
FMO	2-48-39	136	39	N		
FMO	2-48-72	137	72	N		
FMO	2-48-156	138	156	N		
FMO	2-48-285	139	285	N		
FMO	2-49-167	140	167	N		
GSHR	10-436-43	141	501	Y	C	19.44

Fig. 1 (following)

GSHR	10-436-376	142	501	Y	A	32.76
GSHR	10-431-51	143	501	Y	A	20.21
GSHR	10-432-93	144	477	Y		
GSHR	12-631-208	145	433	Y	G	17.39
GSHS	10-260-282	146	501	N		
GSHS	10-263-26	147	503	N		
GSHS	10-258-408	148	501	N		
GSHS	12-317-259	149	501	N		
GSHS	12-323-385	150	501	Y	T	47.85
GSHS	12-324-219	151	357	N		
GSHS	12-324-335	152	473	Y	C	35.16
GSHS	12-324-380	153	501	N		
GSHS	12-325-30	154	501	N		
GSHS	12-327-31	155	479	Y	G	47.87
GSHS	12-327-415	156	500	N		
GSHS	12-331-270	157	501	N		
GSHS	12-331-275	158	501	N		
GSHS	12-334-320	159	503	N		
GSHS	12-334-391	160	503	N		
GSHS	12-335-417	161	501	N		
GSHS	12-337-189	162	501	N		
GSHS	12-340-130	163	381	N		
GSHS	12-340-210	164	461	Y	T	46.81
GSHS	12-340-222	165	473	N		
GSHS	12-340-240	166	491	N		
GSHS	12-341-99	167	501	Y	A	17.2
GSHS	12-342-32	168	501	N		
GSHS	12-344-349	169	501	Y	G	43.75
GSHS	12-345-453	170	501	N		
GSHS	12-346-204	171	501	N		
GLCL	10-364-55	172	501	N		
GLCL	10-364-108	173	501	N		
GLCL	10-364-267	174	501	N		
GLCL	10-367-20	175	497	N		
GLCL	10-351-389	176	501	N		
GLCL	10-353-102	177	501	N		
GLCL	12-474-346	178	501	Y	A	25.28
GLCL	10-354-320	179	501	N		
GLCL	10-354-360	180	501	N		
GLCL	10-355-87	181	501	N		
GLCL	10-358-60	182	501	N		
GLCL	12-468-63	183	501	Y	C	46.24
GLCL	12-468-388	184	501	N		
GLCL	12-468-491	185	501	N		
GLCL	12-469-132	186	501	N		
GLCL	12-469-245	187	501	N		
GLCL	12-472-435	188	501	N		
GLCL	12-473-311	189	501	N		
GLCL	12-473-483	190	501	N		
GLCL	12-475-85	191	501	N		
GLCL	12-475-446	192	485	N		

Fig. 1 (following)

GLCL	12-477-100	193	501	N		
GLCL	12-477-331	194	501	N		
GLCL	12-477-332	195	501	N		
GLCL	12-477-44	196	501	N		
GLCL	12-478-223	197	501	N		
GLCL	12-478-320	198	501	N		
GLCL	12-479-289	199	501	N		
GLCL	12-482-237	200	501	N		
GLCL	12-482-285	201	501	N		
GLCL	12-482-482	202	501	N		
GLCL	12-483-322	203	499	N		
GLCL	12-484-46	204	501	N		
GLCL	12-490-312	205	501	N		
GLCL	12-491-295	206	501	N		
GLCL	12-493-417	207	501	N		
GLCL	12-494-373	208	501	N		
GLCL	12-495-166	209	501	N		
GLCL	12-495-272	210	501	N		
GLCL	12-495-424	211	501	N		
GLCL	12-500-220	212	501	N		
GLCL	12-501-155	213	501	N		
GLCL	12-503-52	214	501	N		
GLCL	12-503-62	215	501	N		
GLCL	12-504-54	216	499	N		
GLCL	12-504-96	217	501	N		
GLCL	12-504-428	218	501	Y	C	47.22
GLCL	12-507-53	219	474	Y	C	47.78
GLCL	12-507-92	220	501	N		
GLCL	12-507-159	221	500	N		
GLCL	12-507-177	222	501	N		
GLCL	12-508-29	223	501	N		
GLCL	12-509-42	224	501	N		
GLCL	12-509-126	225	501	N		
GLCL	12-510-59	226	501	N		
GLCL	12-511-74	227	501	Y	C	11.45
GGT5	10-325-311	228	501	N		
GGT5	10-327-120	229	501	N		
GGT5	10-331-179	230	501	N		
GGT5	10-331-357	231	501	N		
GGT5	10-334-263	232	501	N		
GGT5	10-321-226	233	501	N		
GGT5	12-183-98	234	501	N		
GGT5	12-185-78	235	501	N		
GGT5	12-186-154	236	501	Y	A	6.99
GGT5	12-186-397	237	501	Y	C	28.08
GGT5	12-187-65	238	501	Y	C	23.37
GGT5	12-187-66	239	501	N		
GGT5	12-189-348	240	501	Y	A	26.09
GGT5	12-192-63	241	501	N		
GGT5	12-192-64	242	502	N		
GGT5	12-192-268	243	501	N		

Fig. 1 (following)

GGT5	12-192-334	244	501	N		
GGT5	12-192-352	245	501	N		
GGT5	12-194-135	246	501	N		
GGT5	12-194-325	247	501	N		
GGT5	12-194-337	248	501	N		
GGT5	12-194-479	249	501	N		
DP	10-442-133	250	501	Y	C	7.06
DP	10-444-248	251	484	Y	G	42.78
DP	10-445-281	252	501	Y	T	13.3
DP	12-668-362	253	501	N		
DP	12-670-48	254	501	N		
DP	12-670-91	255	501	N		
DP	12-670-157	256	501	Y	T	47.83
DP	12-671-148	257	501	Y	C	41.49
DP	12-679-245	258	253	N		
DP	12-679-371	259	379	N		
DP	12-679-426	260	434	N		
DP	12-680-331	261	503	N		
G6PDH	10-151-154	262	154	Y	A	0.54
G6PDH	10-138-206	263	205	Y	T	8.51
G6PDH	10-138-352	264	351	Y	C	14.04
PGDH	12-586-414	265	501	Y	A	28.33
PGDH	12-587-379	266	499	N		
PGDH	12-588-103	267	501	Y	A	48.88
PGDH	12-589-152	268	501	N		
PGDH	12-592-118	269	501	Y	A	49.46
PGDH	12-593-174	270	501	Y	C	34.71
PGDH	12-596-124	271	501	Y	A	26.7
PGDH	12-602-196	272	501	Y	C	31.72
PGDH	12-602-350	273	501	N		
PGDH	12-603-191	274	501	Y	C	27.42
PGDH	12-783-73	275	501	N		
PGDH	12-783-421	276	501	N		
PGDH	12-785-200	277	501	N		
PGDH	12-785-393	278	501	N		
PGDH	12-787-103	279	501	N		
PGDH	12-790-396	280	501	N		
PGDH	12-791-211	281	501	N		
PGDH	12-792-233	282	501	N		
PGDH	12-793-383	283	505	N		
PGDH	12-803-125	284	501	N		
PGDH	12-805-115	285	501	N		
PGDH	12-808-52	286	501	N		
PGDH	12-808-75	287	501	N		
PGDH	12-809-119	288	501	N		
PGDH	12-810-77	289	501	N		
PGDH	10-265-178	290	501	N		
PGDH	10-266-203	291	503	N		
UGT1A7	10-403-312	292	501	N		
UGT1A7	10-405-54	293	501	N		
UGT1A7	10-408-356	294	501	N		

Fig. 1 (following)

UGT1A7	10-409-148	295	501	N		
UGT1A7	10-409-249	296	501	N		
UGT1A7	10-410-274	297	501	N		
UGT1A7	10-410-280	298	501	N		
UGT1A7	10-410-337	299	501	N		
UGT1A7	12-121-326	300	501	Y	A	26.88
UGT1A7	12-122-341	301	501	N		
UGT1A7	12-122-381	302	501	N		
UGT1A7	12-124-169	303	501	N		
UGT1A7	12-124-194	304	501	Y	C	19.41
UGT1A7	12-124-300	305	501	N		
UGT1A7	12-124-58	306	501	N		
UGT1A7	12-126-222	307	501	N		
UGT1A7	12-126-297	308	501	N		
UGT1A7	12-128-225	309	501	Y	G	47.44
UGT1A7	12-129-176	310	501	N		
UGT1A7	12-130-203	311	501	N		
UGT1A7	12-130-260	312	501	N		
UGT1A7	12-131-112	313	501	N		
UGT1A7	12-132-157	314	255	N		
UGT1A7	12-132-437	315	501	N		
UGT1A7	12-133-153	316	666	N		
UGT1A7	12-133-318	317	501	N		
UGT1A7	12-136-238	318	249	N		
UGT1A7	12-138-141	319	501	N		
UGT1A7	12-138-42	320	501	N		
UGT1A7	12-138-67	321	501	N		
UGT1A7	12-139-380	322	501	Y	A	21.24
UGT1A7	12-140-134	323	501	Y	T	41.01
UGT1A7	12-140-329	324	501	N		
UGT1A7	12-140-385	325	501	N		
UGT1A7	12-141-159	326	501	Y	T	37.5
UGT1A7	12-141-392	327	501	N		
UGT1A7	12-142-315	328	501	N		
UGT1A7	12-142-321	329	501	Y	G	45.56
UGT1A7	12-143-453	330	501	Y	G	49.39
UGT1A7	12-144-169	331	501	N		
UGT1A7	12-144-33	332	501	N		
UGT1A7	12-146-174	333	501	N		
UGT1A7	12-146-47	334	501	N		
UGT1A7	12-148-283	335	501	N		
UGT1A7	12-148-311	336	501	Y	T	43.17
UGT1A7	12-149-320	337	501	N		
UGT1A7	12-151-174	338	501	N		
UGT1A7	12-151-196	339	501	N		
UGT1A7	12-151-270	340	501	N		
UGT1A7	12-152-453	341	501	N		
UGT1A7	12-153-116	342	501	Y	T	37.78
UGT1A7	12-154-480	343	501	N		
UGT1A7	12-155-403	344	501	N		
UGT1A7	12-156-91	345	501	Y	A	50

Fig. 1 (following)

UGT1A7	12-157-437	346	501	N		
UGT1A7	12-158-213	347	501	N		
UGT1A7	12-158-450	348	480	N		
UGT1A7	12-161-157	349	501	N		
UGT1A7	12-162-21	350	498	N		
UGT2B4	10-470-25	351	503	Y	T	44.44
UGT2B4	10-471-84	352	503	Y	A	27.17
UGT2B4	10-471-85	353	503	Y		
UGT2B4	10-472-202	354	503	Y	C	9.68
UGT2B4	10-473-333	355	503	N		
UGT2B4	10-494-284	356	503	N		
UGT2B4	12-637-219	357	499	Y	G	36.17
UGT2B4	12-639-95	358	499	Y	G	34.95
UGT2B4	12-639-241	359	499	N		
UGT2B4	12-640-151	360	499	N		
UGT2B4	12-640-296	361	499	N		
UGT2B4	12-640-325	362	499	Y		
UGT2B4	12-640-413	363	499	N		
UGT2B4	12-641-120	364	499	N		
UGT2B4	12-641-122	365	499	N		
UGT2B4	12-641-223	366	432	N		
UGT2B4	12-641-267	367	388	N		
UGT2B4	12-642-387	368	503	N		
UGT2B4	12-642-417	369	503	Y	G	26.51
UGT2B4	12-646-429	370	434	N		
UGT2B4	12-646-433	371	438	N		
UGT2B4	12-647-145	372	503	N		
UGT2B4	12-648-123	373	251	N		
UGT2B4	12-648-300	374	428	Y	T	37.91
UGT2B4	12-648-402	375	501	N		
UGT2B4	12-652-115	376	298	N		
UGT2B4	12-652-203	377	386	Y	C	42.47
UGT2B4	12-652-274	378	457	N		
UGT2B4	12-652-371	379	501	N		
UGT2B4	12-653-423	380	499	N		
UGT2B4	12-654-115	381	499	N		
UGT2B4	12-654-207	382	499	N		
UGT2B4	12-657-396	383	503	N		
UGT2B4	12-658-120	384	503	N		
UGT2B4	12-659-382	385	501	N		
UGT2B4	12-660-134	386	306	N		
UGT2B4	12-662-80	387	497	N		
UGT2B7	12-906-149	388	501	Y		
UGT2B7	12-906-154	389	501	N		
UGT2B7	12-906-251	390	501	N		
UGT2B7	12-906-451	391	501	N		
UGT2B7	12-907-199	392	244	Y	G	3.23
UGT2B7	12-907-482	393	501	N		
UGT2B7	12-909-36	394	53	N		
UGT2B7	12-909-176	395	193	N		
UGT2B7	12-909-484	396	501	N		

Fig. 1 (following)

UGT2B7	12-910-76	397	347	Y	A	23.91
UGT2B7	12-910-295	398	503	N		
UGT2B7	12-911-22	399	240	Y	C	43.96
UGT2B7	12-912-65	400	501	N		
UGT2B7	12-914-106	401	384	Y	C	44.62
UGT2B7	12-914-252	402	503	N		
UGT2B10	10-448-266	403	503	N		
UGT2B10	10-453-330	404	503	N		
UGT2B10	10-455-367	405	503	N		
UGT2B10	12-5-158	406	503	Y	T	11.8
UGT2B10	12-9-367	407	499	Y	A	14.67
UGT2B10	12-10-303	408	501	Y	T	14.67
UGT2B10	12-14-264	409	501	Y	T	14.29
UGT2B10	12-17-86	410	499	Y	A	44.02
UGT2B10	12-19-163	411	501	Y	G	29.89
UGT2B15	10-457-284	412	503	N		
UGT2B15	10-460-221	413	503	N		
UGT2B15	10-460-232	414	503	N		
UGT2B15	10-460-235	415	503	N		
UGT2B15	10-460-236	416	503	N		
UGT2B15	10-460-285	417	503	N		
UGT2B15	12-605-58	418	501	Y	T	47.67
UGT2B15	12-607-207	419	501	N		
UGT2B15	12-609-119	420	499	Y	T	45.11
UGT2B15	12-609-180	421	499	N		
UGT2B15	12-609-233	422	499	N		
UGT2B15	12-611-294	423	501	Y	A	43.26
UGT2B15	12-612-41	424	501	Y	C	28.65
UGT2B15	12-613-302	425	499	N		
UGT2B15	12-614-471	426	501	Y	T	39.44
UGT2B15	12-620-192	427	503	Y	T	30.36
UGT2B15	12-621-49	428	503	N		
UGT2B15	12-622-325	429	364	N		
UGT2B15	12-624-82	430	501	N		
UGT2B15	12-624-83	431	501	N		
UGT2B15	12-624-107	432	489	N		
UGT2B15	12-624-146	433	501	N		
UGT2B15	12-624-288	434	501	N		
UGT2B15	12-624-293	435	501	N		
MGST2	12-421-135	436	501	N		
MGST2	12-442-133	437	501	Y	C	5.85
MGST2	12-449-63	438	501	N		
MGST2	12-454-242	439	501	N		
MGST2	12-463-250	440	501	N		
MGST2	12-462-199	441	501	N		
DME	10-430-287	442	501	N		
DME	12-718-432	443	501	N		
CYP3A4- CYP3A7	12-269-301	444	501	Y		
FMO	2-13-398	445	501	N		
FMO	2-28-132	446	501	N		

Fig. 1 (following)

FMO	2-39-27	447	501	N		
FMO	2-45-155	448	501	N		
FMO	2-4-391	14	501	N		
GSHS	12-345-410	450	501	N		
GLCL	10-358-353	451	501	N		
GLCL	10-360-190	452	501	N		
GLCL	10-365-374	453	501	N		
GLCL	10-367-58	454	501	N		
GLCL	12-468-424	455	501	N		
GLCL	12-481-293	456	501	N		
GLCL	12-499-86	457	501	N		
GLCL	12-500-217	458	501	N		
GLCL	12-511-101	459	501	N		
6PGD	12-586-443	460	501	N		
6PGD	12-593-287	461	501	N		
6PGD	12-795-383	462	501	N		
UGT2B4	10-494-332	463	501	N		
UGT2B4	12-659-251	465	429	N		
UGT2B7	12-912-419	466	501	N		
UGT2B7	12-914-28	467	306	N		
UGT2B15	12-624-307	468	501	N		
MGST2	10-290-326	469	501	N		
MGST2	10-290-37	470	501	N		
MGST2	10-523-232	471	501	N		
MGST2	12-449-300	472	501	N		
G6PDH	10-186-212	473	212	N		
MGST2	10-286-289	474	501	N		
MGST2	10-286-345	475	501	N		
MGST2	10-286-375	476	501	N		
MGST2	10-289-201	477	501	N		
GGT5	10-321-28	478	501	N		
CYP1A2	10-98-265	479	265	N		
UGT1A7	12-157-115	480	501	N		
GLCL	12-472-48	481	501	N		
GLCL	12-477-151	482	501	N		
GLCL	12-479-214	483	501	N		
MGST2	10-290-328	484	501	N		

FIG. 2

SEQ ID NO.	BIALLELIC MARKER ID	1 ST ALLELE	2 ND ALLELE	POSITION RANGE OF PREFERRED SEQUENCES
1	12-421-140	A	G	1-1001
2	12-424-192	A	G	190-801; 865-999
3	12-424-198	G	T	184-795; 859-993
4	12-425-57	G	A	208-225; 266-478
5	12-426-154	A	G	152-961
6	12-429-198	C	T	260-784; 822-1001
7	12-430-80	T	C	1-996
8	12-433-215	A	G	1-1001
12	12-447-58	G	C	1-36; 390-914
13	12-453-429	C	T	1-1001
14	12-454-363	A	G	1-315; 377-466; 598-619
15	12-455-326	T	C	1-357; 391-594; 760-827
16	12-455-383	G	A	1-414; 448-651; 817-884
17	12-456-269	A	G	1-536
19	12-457-204	A	G	437-527; 761-1001
20	12-457-206	C	T	435-525; 759-1001
21	12-458-196	T	A	1-727
22	12-458-438	T	C	1-21; 298-1001
23	12-460-274	A	G	1-499; 563-1001
24	12-461-124	A	C	1-203; 259-644; 687-773; 807-833
25	12-461-299	C	T	1-28; 84-469; 512-591
26	12-461-465	C	T	1-303; 346-432
27	12-462-280	C	T	1-1001
28	12-464-66	G	T	1-215; 261-1001
29	12-465-26	C	T	1-61; 99-1001
30	12-465-234	G	T	1-1001
31	10-428-219	A	G	1-398; 506-1000
33	10-420-284	C	T	1-302; 472-772
34	10-423-411	C	T	1-227; 333-821
35	12-713-95	C	T	1-668
36	12-713-149	G	C	1-668
37	12-716-295	C	T	1-902
38	12-720-80	G	C	1-982
40	12-721-281	A	C	1-926
41	12-721-440	A	G	1-1000
42	12-723-293	C	T	1-1001
43	12-724-195	C	T	277-1001
44	12-724-225	C	T	245-1001
49	10-413-394	A	G	1-139; 831-1001
51	10-416-273	A	T	1-258; 855-1001
53	12-665-315	T	C	180-1001
54	12-666-324	A	C	338-375; 414-501; 581-611

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FIG. 2 (following)

78	12-244-275	A	G	
79	12-251-153	A	C	1-111; 158-950
82	12-265-300	T	C	1-999
84	12-272-112	A	C	396-416
85	10-216-182	A	G	77-151; 186-235; 320-488; 733-761
86	10-217-91	C	T	1-189; 434-462; 810-871; 925-1001
101	2-10-107	C	T	260-450
102	2-10-378	A	G	260-450
104	2-11-156	A	C	369-387
105	2-11-379	A	G	369-387
121	2-29-166	C	T	
141	10-436-43	G	C	1-630; 794-1001
142	10-436-376	A	G	1-297; 461-642; 977-1001
143	10-431-51	A	C	329-534; 682-860
144	10-432-93	A	G	1-40; 374-559; 705-885
146	10-260-282	G	T	1-24; 95-324; 482-1001
147	10-263-26	A	C	1-632; 754-1001
148	10-258-408	A	G	337-668
149	12-317-259	G	A	1-44; 116-150; 181-241; 281-673; 968-1001
150	12-323-385	T	C	340-1001
152	12-324-335	G	C	1-176; 395-906
153	12-324-380	A	G	1-159; 378-889
154	12-325-30	C	T	272-837; 977-1001
155	12-327-31	G	T	1-570; 655-821; 875-922; 973-999
156	12-327-415	A	G	1-208; 293-459; 513-1001
157	12-331-270	G	A	1-531; 834-1001
158	12-331-275	T	G	125-536; 839-1001
159	12-334-320	A	G	68-705
160	12-334-391	A	G	1-634; 982-1001
161	12-335-417	G	C	239-1001
162	12-337-189	A	G	1-1001
163	12-340-130	A	G	196-881
164	12-340-210	C	T	196-961
165	12-340-222	G	T	196-973
166	12-340-240	C	T	196-975
167	12-341-99	A	G	1-1001
168	12-342-32	T	C	238-397; 859-960
169	12-344-349	G	T	365-1001
170	12-345-453	G	C	1-606
192	12-475-446	G	A	
228	10-325-311	A	G	41-312; 421-891
231	10-331-357	G	T	76-218; 373-730; 938-1001
232	10-334-263	A	G	1-359; 481-604; 781-893
235	12-185-78	C	T	1-1001
236	12-186-154	A	G	335-876
237	12-186-397	C	T	92-633; 967-1001

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FIG. 2 (following)

238	12-187-65	C	T	345-846
239	12-187-66	A	G	344-845
240	12-189-348	G	A	281-358; 407-1001
246	12-194-135	G	T	543-1001
247	12-194-325	A	G	351-1001
248	12-194-337	A	G	339-1001
249	12-194-479	C	T	197-1001
251	10-444-248	A	G	
254	12-670-48	G	C	1-961
255	12-670-91	C	T	1-918
256	12-670-157	C	T	1-852
257	12-671-148	C	T	1-908
258	12-679-245	A	G	96-465
259	12-679-371	A	G	96-465
260	12-679-426	C	T	96-465
265	12-586-414	A	G	1-71; 149-929
268	12-589-152	T	G	164-1001
269	12-592-118	A	T	353-1001
270	12-593-174	T	C	342-815
271	12-596-124	A	G	1-742
272	12-602-196	C	T	1-240; 436-641
274	12-603-191	T	C	1-709
275	12-783-73	G	C	1-769; 981-1001
277	12-785-200	C	T	351-510
279	12-787-103	G	A	1-47; 232-324; 401-1001
280	12-790-396	G	A	47-64; 393-1001
281	12-791-211	A	G	1-379; 467-818
284	12-803-125	T	A	125-1001
285	12-805-115	G	A	1-66; 278-838; 959-1001
286	12-808-52	A	G	400-1001
287	12-808-75	G	C	377-1001
289	12-810-77	G	A	99-1001
293	10-405-54	C	T	1-492
297	10-410-274	A	C	643-805
301	12-122-341	C	T	1-23; 150-282; 324-435; 593-620
302	12-122-381	A	C	110-242; 284-395; 553-580
303	12-124-169	G	T	1-727; 788-1001
304	12-124-194	C	T	1-702; 763-1001
305	12-124-300	G	T	1-596; 657-1001
306	12-124-58	A	C	1-837; 898-1001
308	12-126-297	T	C	1-508; 944-1001
310	12-129-176	G	T	163-1001
313	12-131-112	T	C	254-422
315	12-132-437	A	C	258-991
316	12-133-153	T	C	1-515; 607-666; 775-918; 976-1001
317	12-133-318	T	A	1-515; 607-666; 775-918; 976-1001

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FIG. 2 (following)

318	12-136-238	A	G	1-643
319	12-138-141	G	A	1-393; 521-651
320	12-138-42	T	G	1-294; 422-552
321	12-138-67	G	A	1-319; 447-577
322	12-139-380	A	G	94-157; 276-663
323	12-140-134	G	T	1-142; 212-951
324	12-140-329	C	T	1-756
325	12-140-385	G	C	1-700
326	12-141-159	T	C	1-1001
327	12-141-392	C	A	1-1001
328	12-142-315	A	G	1-1001
329	12-142-321	A	G	1-1001
330	12-143-453	A	G	1-1001
331	12-144-169	G	A	97-1001
332	12-144-33	G	A	1-1001
333	12-146-174	T	C	1-529; 765-805
336	12-148-311	T	C	1-251; 684-1001
337	12-149-320	T	C	202-1001
338	12-151-174	G	T	313-1001
339	12-151-196	C	T	291-1001
340	12-151-270	A	G	217-1001
341	12-152-453	C	T	1-239; 526-576; 623-1001
342	12-153-116	C	T	1-819; 866-1001
346	12-157-437	A	C	1-865
347	12-158-213	T	C	1-1001
348	12-158-450	T	G	206-980
350	12-162-21	A	G	1-998
351	10-470-25	A	T	1-339; 413-539; 730-1001
355	10-473-333	C	T	461-744
356	10-494-284	C	T	89-349; 450-513
359	12-639-241	T	G	1-199; 652-667; 742-763
360	12-640-151	G	A	1-806; 943-1001
361	12-640-296	T	G	1-862
362	12-640-325	T	C	1-1001
363	12-640-413	C	G	1-1001
364	12-641-120	G	A	98-1001
365	12-641-122	T	G	100-1001
366	12-641-223	G	A	1-15; 134-1001
367	12-641-267	T	C	1-15; 134-1001
368	12-642-387	A	G	1-224; 292-1001
369	12-642-417	A	G	1-194; 262-1001
372	12-647-145	A	G	1-898
373	12-648-123	A	G	1-751
374	12-648-300	C	T	1-839
375	12-648-402	G	C	1-810; 909-1001
376	12-652-115	C	T	1-30; 191-798

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FIG. 2 (following)

377	12-652-203	A	C	1-30; 191-886
378	12-652-274	G	T	1-30; 191-957
379	12-652-371	C	T	138-1001
380	12-653-423	T	A	1-603
381	12-654-115	T	C	161-1001
382	12-654-207	G	A	1-95; 253-1001
383	12-657-396	A	G	329-1001
384	12-658-120	A	T	1-1001
385	12-659-382	A	G	1-1001
386	12-660-134	A	G	291-608; 886-983
387	12-662-80	G	C	480-1001
391	12-906-451	A	C	447-532; 865-1001
392	12-907-199	G	T	
394	12-909-36	A	G	
397	12-910-76	A	G	1-785; 854-870
398	12-910-295	C	T	1-1001
399	12-911-22	G	C	1-740
400	12-912-65	C	T	1-183; 290-1001
401	12-914-106	C	T	1-1001
402	12-914-252	A	T	1-1001
404	10-453-330	C	T	1-207; 761-1001
406	12-5-158	C	T	672-1001
407	12-9-367	G	A	1-15; 249-283; 400-425; 493-666; 722-1001
409	12-14-264	C	T	1-1001
410	12-17-86	T	A	1-1001
411	12-19-163	A	G	230-388; 525-709; 824-866
414	10-460-232	A	G	1-349; 521-1001
415	10-460-235	C	T	1-346; 518-1001
416	10-460-236	A	G	1-345; 517-1001
417	10-460-285	A	T	1-296; 468-1001
418	12-605-58	G	T	1-1001
419	12-607-207	G	A	1-746; 885-902
420	12-609-119	T	G	1-234; 294-1001
421	12-609-180	T	G	40-295; 355-1001
422	12-609-233	G	A	138-348; 404-1001
423	12-611-294	G	A	1-617; 895-967
424	12-612-41	C	T	1-56; 398-708
425	12-613-302	C	G	1-86; 336-1001
426	12-614-471	T	A	1-1001
427	12-620-192	G	T	318-1001
428	12-621-49	A	G	1-242; 451-815
429	12-622-325	C	T	
430	12-624-82	T	C	1-1001
431	12-624-83	G	A	1-1001
432	12-624-107	T	C	1-989
433	12-624-146	T	C	1-1001

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FIG. 2 (following)

434	12-624-288	T	G	1-1001
435	12-624-293	T	C	1-1001
436	12-421-135	T	-	1-1001
438	12-449-63	AT	-	1-107; 314-656
439	12-454-242	AT	-	1-436; 498-587; 719-740
440	12-463-250	CAT	-	1-30; 102-601; 752-1001
441	12-462-199		deletion	1-1001
442	10-430-287	T	-	1-330; 442-740; 782-1001
443	12-718-432	T	-	1-1001
444	12-269-301	T	-	774-820
450	12-345-410		deletion	1-649
460	12-586-443	C	-	1-42; 120-911
461	12-593-287		deletion	1-17; 455-942
462	12-795-383		insertion	166-500; 540-1001
465	12-659-251	deletion	-	1-929
466	12-912-419	A	-	1-686
467	12-914-28	T	-	1-806
468	12-624-307	T	-	1-1001
469	10-290-326	A	G	1-197; 437-1000
472	12-449-300	T	C	1-542; 908-1000
484	10-290-328	deletion		1-194; 434-1000

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Fig. 3

SEQ ID NO.	BIALLELIC MARKER ID	ORIGINAL ALLELE	ALTERNATIVE ALLELE
10	12-441-343	G	A
18	12-456-380	G	T
32	10-429-84	T	C
45	10-153-329	T	G
46	10-95-342	G	A
47	10-100-277	T	C
57	10-76-217	C	T
59	10-77-316	A	T
60	10-155-78	T	C
61	10-155-104	C	G
62	10-156-52	G	A
63	10-157-39	C	T
64	10-157-131	A	G
65	10-157-166	G	A
66	10-157-246	G	A
67	10-159-161	T	A
68	10-159-162	C	A
69	10-83-169	T	C
70	10-84-152	C	T
71	10-84-243	C	T
74	10-85-43	C	T
76	10-85-320	A	T
81	12-254-180	G	A
83	12-271-118	T	C
87	10-213-292	C	G
90	2-1-216	G	A
91	2-1-397	T	C
92	2-3-232	C	T
93	2-4-51	A	C
94	2-4-126	A	G
95	2-5-202	A	G
96	2-5-275	G	A
97	2-5-346	C	T
98	2-8-171	A	G
99	2-9-188	G	A
100	2-9-223	T	G
103	2-11-284	A	G
106	2-12-223	A	T
107	2-14-239	C	T
108	2-14-370	C	G
109	2-17-104	A	G
110	2-17-396	A	C
111	2-22-43	A	G
112	2-22-138	G	A
113	2-23-82	A	G
114	2-23-166	G	A
115	2-23-244	G	T

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FIG. 3 (following)

116	2-24-115	C	T
117	2-25-36	G	C
118	2-27-185	G	A
119	2-27-378	G	C
120	2-29-142	G	A
124	2-29-314	C	T
125	2-32-68	A	G
126	2-35-357	T	C
127	2-36-256	G	C
128	2-36-354	A	C
129	2-42-236	C	T
130	2-43-139	G	A
131	2-44-215	C	T
132	2-45-38	C	T
133	2-45-183	T	C
134	2-45-335	T	A
135	2-45-394	C	T
136	2-48-39	A	G
137	2-48-72	C	T
138	2-48-156	T	G
139	2-48-285	A	G
140	2-49-167	A	G
151	12-324-219	C	T
171	12-346-204	G	A
172	10-364-55	T	G
173	10-364-108	T	C
174	10-364-267	T	A
175	10-367-20	T	G
176	10-351-389	A	G
177	10-353-102	T	A
178	12-474-346	G	A
179	10-354-320	G	A
180	10-354-360	A	G
181	10-355-87	G	A
182	10-358-60	G	A
183	12-468-63	T	C
184	12-468-388	T	C
185	12-468-491	G	A
186	12-469-132	T	C
187	12-469-245	G	A
188	12-472-435	G	A
189	12-473-311	A	C
190	12-473-483	T	C
191	12-475-85	G	T
193	12-477-100	A	G
194	12-477-331	G	A
195	12-477-332	T	C
196	12-477-44	C	G
197	12-478-223	G	A
198	12-478-320	G	A
199	12-479-289	G	T

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FIG. 3 (following)

200	12-482-237	A	G
201	12-482-285	T	A
202	12-482-482	A	T
203	12-483-322	A	T
204	12-484-46	G	A
205	12-490-312	A	T
206	12-491-295	A	G
207	12-493-417	G	C
208	12-494-373	C	T
209	12-495-166	C	T
210	12-495-272	A	T
211	12-495-424	T	C
212	12-500-220	A	G
213	12-501-155	G	T
214	12-503-52	T	G
215	12-503-62	T	A
216	12-504-54	G	A
217	12-504-96	C	T
218	12-504-428	G	C
219	12-507-53	T	C
220	12-507-92	A	G
221	12-507-159	T	G
222	12-507-177	C	G
223	12-508-29	G	A
224	12-509-42	G	A
225	12-509-126	G	A
226	12-510-59	G	A
227	12-511-74	T	C
229	10-327-120	C	T
230	10-331-179	G	A
233	10-321-226	A	G
234	12-183-98	G	A/T
241	12-192-63	C	G/T
243	12-192-268	G	C
245	12-192-352	G	A
250	10-442-133	G	C
252	10-445-281	C	T
253	12-668-362	T	A
261	12-680-331	C	T
262	10-151-154	G	A
264	10-138-352	T	C
266	12-587-379	A	C
267	12-588-103	G	A
273	12-602-350	C	A
278	12-785-393	G	A
283	12-793-383	T	G
288	12-809-119	C	G
290	10-265-178	G	A
292	10-403-312	C	T
298	10-410-280	C	T
299	10-410-337	A	G

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FIG. 3 (following)

300	12-121-326	G	A
307	12-126-222	C	T
309	12-128-225	G	T
312	12-130-260	C	T
314	12-132-157	T	C
334	12-146-47	A	G
335	12-148-283	G	A
343	12-154-480	C	T
344	12-155-403	C	A
349	12-161-157	G	A
354	10-472-202	T	C
358	12-639-95	G	A
370	12-646-429	T	C
371	12-646-433	T	G
388	12-906-149	G	A
389	12-906-154	A	C
390	12-906-251	A	T
395	12-909-176	C	T
396	12-909-484	G	T
403	10-448-266	A	C
405	10-455-367	T	C
408	12-10-303	C	T
413	10-460-221	C	T
437	12-442-133	C	-
445	2-13-398	G	-
446	2-28-132	-	T
447	2-39-27		deletion
448	2-45-155		deletion
449	2-4-391	G	-
452	10-360-190	-	T
453	10-365-374	-	A
454	10-367-58	-	insertion
455	12-468-424	-	T
457	12-499-86		deletion
458	12-500-217		insertion
459	12-511-101	A	-
463	10-494-332	insertion	
470	10-290-37	C	T
471	10-523-232	C	T
473	10-186-212	G	C
474	10-286-289	C	G
475	10-286-345	A	T
476	10-286-375	A	G
477	10-289-201	T	C
478	10-321-28	G	A
479	10-98-265	A	G
480	12-157-115	T	C
481	12-472-48	T	G
482	12-477-151	A	G
483	12-479-214	G	T

Fig. 4

SEQ ID NO.	BIALLELIC MARKER ID	1 ST ALLELE	2 ND ALLELE
9	12-441-233	G	A
11	12-442-221	T	C
48	10-102-294	C	T
50	10-414-243	A	G
52	10-418-177	A	G
56	10-76-177	A	T
58	10-76-333	G	C
72	10-84-277	A	G
73	10-84-295	A	G
75	10-85-117	G	T
77	10-86-121	A	C
80	12-254-115	A	T
88	10-214-279	C	T
89	10-214-380	A	G
122	2-29-205	C	T
123	2-29-206	A	G
145	12-631-208	A	G
242	12-192-64	T	C
244	12-192-334	G	A
263	10-138-206	C	T
276	12-783-421	C	T
282	12-792-233	G	A
291	10-266-203	C	T
294	10-408-356	C	T
295	10-409-148	G	C
296	10-409-249	G	C
311	12-130-203	C	T
345	12-156-91	A	G
352	10-471-84	A	T
353	10-471-85	A	C
357	12-637-219	G	A
393	12-907-482	A	T
412	10-457-284	G	T
451	10-358-353		deletion
456	12-481-293	T	-

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Fig. 5

SEQ ID NO.	POSITION RANGE OF PREFERRED SEQUENCES
9	940-1001
18	1-425; 920-1001
32	1-175; 713-787
50	683-1001
52	1-450; 606-1001
58	732-832
59	612-725
87	717-742; 881-899; 951-1001
88	1-24; 276-305
103	369-387
129	433-449
145	152-241; 540-933
151	1-176; 395-857
171	1-98; 753-798
212	986-1001
229	1-439; 639-1001
230	254-396; 551-908
233	1-161; 283-406; 583-695; 843-1001
261	1-452
267	552-1001
273	1-86; 282-487; 963-1001
276	1-421; 633-1001
278	158-317; 834-1001
283	1-112
288	1-174; 252-399; 583-987
290	1-342; 790-1001
291	86-460
292	654-1001
298	637-799
299	580-742
300	1-297; 727-803
307	1-433; 869-1001
309	1-17
311	928-953
312	871-896; 972-1001
314	289-755
334	1-402; 638-678; 969-1001
335	1-223; 656-923
343	629-1000
349	98-251; 960-1001
352	1-52; 399-436
353	1-52; 399-436
354	754-1001
357	527-810
358	1-53; 506-521; 596-617
370	1-80; 675-1001
371	1-80; 675-1001

FIG. 5 (following)

388	1-293; 748-833
389	1-288; 743-828
390	1-191; 646-731
403	745-1001
405	984-1001
408	797-897; 931-1001
412	1-207; 979-1001
455	1-22
463	1-299; 400-463
470	1-485; 725-1000
471	1-432; 514-1000
474	1-353; 656-1000
475	1-298; 601-1000
476	1-268; 571-1000
477	1-452; 538-1000
479	385-391
480	910-954
482	443-531; 730-854
483	347-392

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Fig. 6

SEQ ID NO.	POSITION RANGE OF MICROSEQUENCING PRIMERS	COMPLEMENTARY POSITION RANGE OF MICROSEQUENCING PRIMERS
1	481-500	502-521
2	481-500	502-521
3	481-500	502-521
4	481-500	502-521
5	441-460	462-481
6	481-500	502-521
7	482-500*	502-521
8	481-500	502-521
9	482-500*	502-521
10	481-500	502-521
11	481-500	502-521
12	482-500*	502-521
13	481-500	502-520*
14	481-500	502-521
15	481-500	502-520*
16	481-500	502-521
17	481-500	502-521
18	481-500	502-521
19	481-500	502-521
20	481-500	502-521
21	481-500	502-521
22	481-500	502-521
23	481-500	502-521
24	481-500	502-521
25	481-500	502-520*
26	481-500	502-521
27	481-500	502-521
28	481-500	502-521
29	481-500	502-521
30	481-500	502-521
31	481-500	502-521
32	481-500	502-521
33	481-500	502-521
34	481-500	502-521
35	213-231*	233-252
36	266-285	287-306
37	477-499*	501-520
38	461-479*	481-500
40	406-425	427-446
41	481-500	502-520*
42	484-502*	504-523
43	481-500	502-521
44	482-500*	502-521
45	310-329	331-349*
46	322-341	343-361*
47	258-276*	278-297
48	278-296*	298-317

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FIG. 6 (following)

49	482-500*	502-520*
50	481-500	502-521
51	482-500*	502-520*
52	481-500	502-520*
53	482-500*	502-521
54	482-500*	502-521
56	158-177	179-198
57	198-217	219-238
58	315-333*	335-354
59	481-500	502-521
60	58-77	79-98
61	84-103	105-124
62	32-51	53-71*
63	20-38*	40-59
64	111-130	132-150*
65	146-165	167-186
66	226-245	247-266
67	142-160*	162-181
68	142-161	163-182
69	150-168*	170-189
70	132-151	153-172
71	224-242*	244-263
72	257-276	278-297
73	275-294	296-314*
74	24-42*	44-63
75	97-116	118-136*
76	300-319	321-340
77	102-120*	122-141
78	481-500	502-521
79	431-449*	451-470
80	226-245	247-266
81	292-310*	312-331
82	479-498	500-519
83	481-500	502-521
84	482-500*	502-521
85	483-502	504-522*
86	482-500*	502-521
87	484-502*	504-523
88	481-500	502-521
89	481-500	502-520*
90	196-215	217-236
91	377-396	398-417
92	212-231	233-252
93	31-50	52-71
94	106-125	127-146
95	182-201	203-222
96	255-274	276-295
97	326-345	347-366
98	151-170	172-191
99	168-187	189-208
100	203-222	224-243

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FIG. 6 (following)

101	87-106	108-127
102	357-376	378-397
103	264-283	285-304
104	136-155	157-176
105	359-378	380-399
106	203-222	224-243
107	219-238	240-259
108	350-369	371-390
109	84-103	105-124
110	375-394	396-415
111	23-42	44-63
112	118-137	139-158
113	62-81	83-102
114	146-165	167-186
115	224-243	245-264
116	95-114	116-135
117	16-35	37-56
118	165-184	186-205
119	358-377	379-398
120	122-141	143-162
121	146-165	167-186
122	184-203	205-224
123	185-204	206-225
124	293-312	314-333
125	48-67	69-88
126	337-356	358-377
127	236-255	257-276
128	333-352	354-373
129	216-235	237-256
130	119-138	140-159
131	193-212	214-233
132	18-37	39-58
133	163-182	184-203
134	315-334	336-355
135	374-393	395-414
136	19-38	40-59
137	52-71	73-92
138	136-155	157-176
139	265-284	286-305
140	147-166	168-187
141	482-500*	502-521
142	481-500	502-520*
143	482-500*	502-521
144	457-476	481-499*
145	414-432*	434-453
146	481-500	502-521
147	483-502	504-523
148	481-500	502-521
149	481-500	502-521
150	481-500	502-520*
151	337-356	358-377

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FIG. 6 (following)

152	454-472*	474-493
153	481-500	502-521
154	481-500	502-521
155	459-478	480-498*
156	480-499	501-520
157	481-500	502-521
158	481-500	502-521
159	483-502	504-523
160	483-502	504-523
161	481-500	502-521
162	481-500	502-521
163	361-380	382-401
164	442-460*	462-481
165	453-472	474-493
166	471-490	492-511
167	481-500	502-520*
168	481-500	502-521
169	481-500	502-520*
170	481-500	502-521
171	481-500	502-521
172	481-500	502-521
173	481-500	502-521
174	481-500	502-521
175	477-496	498-517
176	481-500	502-521
177	481-500	502-521
178	482-500*	502-521
179	481-500	502-521
180	481-500	502-521
181	481-500	502-521
182	481-500	502-521
183	481-500	502-520*
184	481-500	502-521
185	481-500	502-521
186	481-500	502-521
187	481-500	502-521
188	481-500	502-521
189	481-500	502-521
190	481-500	502-521
191	481-500	502-521
192	465-484	486-505
193	481-500	502-521
194	481-500	502-521
195	481-500	502-521
196	481-500	502-521
197	481-500	502-521
198	481-500	502-521
199	481-500	502-521
200	481-500	502-521
201	481-500	502-521
202	481-500	502-521

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FIG. 6 (following)

203	479-498	500-519
204	481-500	502-521
205	481-500	502-521
206	481-500	502-521
207	481-500	502-521
208	481-500	502-521
209	481-500	502-521
210	481-500	502-521
211	481-500	502-521
212	481-500	502-521
213	481-500	502-521
214	481-500	502-521
215	481-500	502-521
216	479-498	500-519
217	481-500	502-521
218	482-500*	502-521
219	454-473	475-493*
220	481-500	502-521
221	480-499	501-520
222	481-500	502-521
223	481-500	502-521
224	481-500	502-521
225	481-500	502-521
226	481-500	502-521
227	483-500*	502-521
228	481-500	502-521
229	481-500	502-521
230	481-500	502-521
231	481-500	502-521
232	481-500	502-521
233	481-500	502-521
234	481-500	502-521
235	481-500	502-521
236	481-500	502-520*
237	482-500*	502-521
238	482-500*	502-521
239	481-500	502-521
240	481-500	502-520*
241	481-500	502-521
242	482-501	503-522
243	481-500	502-521
244	481-500	502-521
245	481-500	502-521
246	481-500	502-521
247	481-500	502-521
248	481-500	502-521
249	481-500	502-521
250	482-500*	502-521
251	464-483	485-503*
252	482-500*	502-521
253	481-500	502-521

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FIG. 6 (following)

254	481-500	502-521
255	481-500	502-521
256	482-500*	502-521
257	482-500*	502-521
258	233-252	254-273
259	359-378	380-399
260	414-433	435-454
261	483-502	504-523
262	134-153	155-173*
263	186-204*	206-225
264	332-350*	352-371
265	482-500*	502-521
266	479-498	500-519
267	482-500*	502-521
268	481-500	502-521
269	482-500*	502-521
270	481-500	502-520*
271	481-500	502-520*
272	481-500	502-520*
273	481-500	502-521
274	481-500	502-520*
275	481-500	502-521
276	481-500	502-521
277	481-500	502-521
278	481-500	502-521
279	481-500	502-521
280	481-500	502-521
281	481-500	502-521
282	481-500	502-521
283	485-504	506-525
284	481-500	502-521
285	481-500	502-521
286	481-500	502-521
287	481-500	502-521
288	481-500	502-521
289	481-500	502-521
290	481-500	502-521
291	483-502	504-523
292	481-500	502-521
293	481-500	502-521
294	481-500	502-521
295	481-500	502-521
296	481-500	502-521
297	481-500	502-521
298	481-500	502-521
299	481-500	502-521
300	481-500	502-520*
301	481-500	502-521
302	481-500	502-521
303	481-500	502-521
304	482-500*	502-521

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FIG. 6 (following)

305	481-500	502-521
306	481-500	502-521
307	481-500	502-521
308	481-500	502-521
309	481-500	502-520*
310	481-500	502-521
311	481-500	502-521
312	481-500	502-521
313	481-500	502-521
314	235-254	256-275
315	481-500	502-521
316	646-665	667-686
317	481-500	502-521
318	229-248	250-269
319	481-500	502-521
320	481-500	502-521
321	481-500	502-521
322	481-500	502-520*
323	481-500	502-520*
324	481-500	502-521
325	481-500	502-521
326	482-500*	502-521
327	481-500	502-521
328	481-500	502-521
329	481-500	502-520*
330	481-500	502-520*
331	481-500	502-521
332	481-500	502-521
333	481-500	502-521
334	481-500	502-521
335	481-500	502-521
336	481-500	502-520*
337	481-500	502-521
338	481-500	502-521
339	481-500	502-521
340	481-500	502-521
341	481-500	502-521
342	482-500*	502-520*
343	481-500	502-521
344	481-500	502-521
345	482-500*	502-520*
346	481-500	502-521
347	481-500	502-521
348	460-479	481-500
349	481-500	502-521
350	478-497	499-518
351	484-502*	504-523
352	484-502*	504-523
353	483-502	505-523*
354	484-502*	525-543*
355	483-502	504-523

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FIG. 6 (following)

356	483-502	504-523
357	480-498*	500-519
358	480-498*	500-519
359	479-498	500-519
360	479-498	500-519
361	479-498	500-519
362	479-498	500-518*
363	479-498	500-519
364	479-498	500-519
365	479-498	500-519
366	412-431	433-452
367	368-387	389-408
368	483-502	504-523
369	484-502*	504-523
370	414-433	435-454
371	418-437	439-458
372	483-502	504-523
373	231-250	252-271
374	408-427	429-447*
375	481-500	502-521
376	278-297	299-318
377	367-385*	387-406
378	437-456	458-477
379	481-500	502-521
380	479-498	500-519
381	479-498	500-519
382	479-498	500-519
383	483-502	504-523
384	483-502	504-523
385	481-500	502-521
386	286-305	307-326
387	477-496	498-517
388	482-500*	502-521
389	481-500	502-521
390	481-500	502-521
391	481-500	502-521
392	224-243	245-263*
393	481-500	502-521
394	33-52	54-73
395	173-192	194-213
396	481-500	502-521
397	327-346	348-366*
398	483-502	504-523
399	221-239*	241-260
400	481-500	502-521
401	365-383*	385-404
402	483-502	504-523
403	483-502	504-523
404	483-502	504-523
405	483-502	504-523
406	484-502*	504-523

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FIG. 6 (following)

407	479-498	500-518*
408	482-500*	502-521
409	482-500*	502-521
410	479-498	500-518*
411	481-500	502-520*
412	483-502	504-523
413	483-502	504-523
414	483-502	504-523
415	483-502	504-523
416	483-502	504-523
417	483-502	504-523
418	481-500	502-520*
419	481-500	502-521
420	479-498	500-518*
421	479-498	500-519
422	479-498	500-519
423	481-500	502-520*
424	481-500	502-520*
425	479-498	500-519
426	481-500	502-520*
427	483-502	504-522*
428	483-502	504-523
429	344-363	365-384
430	481-500	502-521
431	481-500	502-521
432	469-488	490-509
433	481-500	502-521
434	481-500	502-521
435	481-500	502-521
436	481-500	-
437	-	502-520*
438	481-500	-
439	481-500	-
440	481-500	-
441	481-500	-
442	481-500	-
443	481-500	-
444	482-500	-
445	481-500	-
446	481-500	-
447	481-500	-
448	481-500	-
449	481-500	-
450	481-500	-
451	481-500	-
452	481-500	-
453	481-500	-
454	481-500	-
455	481-500	-
456	481-500	-
457	481-500	-

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FIG. 6 (following)

458	481-500	-
459	481-500	-
460	481-500	-
461	481-500	-
462	481-500	-
463	481-500	-
465	409-428	-
466	481-500	-
467	286-305	-
468	481-500	-
469	481-500	502-521
470	481-500	502-521
471	481-500	502-521
472	481-500	502-521
473	192-211	213-232
474	481-500	502-521
475	481-500	502-521
476	481-500	502-521
477	481-500	502-521
478	481-500	502-521
479	245-264	266-285
480	481-500	502-521
481	481-500	502-521
482	481-500	502-521
483	481-500	502-521
484	481-500	502-521

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Fig. 7

SEQ ID NO.	POSITION RANGE OF AMPLIFICATION PRIMERS	COMPLEMENTARY POSITION RANGE OF AMPLIFICATION PRIMERS
1	362-380	792-812
2	310-327	751-771
3	304-321	745-765
4	82-99	540-557
5	308-325	830-847
6	304-321	803-823
7	131-150	561-580
8	287-304	805-825
9	284-303	716-734
10	394-413	826-844
11	270-289	704-721
12	444-462	874-893
13	73-91	577-596
14	139-158	634-652
15	372-392	808-826
16	429-449	865-883
17	233-252	693-712
18	122-141	582-601
19	298-317	772-792
20	296-315	770-790
21	200-217	679-696
22	442-459	921-938
23	228-245	760-777
24	378-396	911-928
25	203-221	736-753
26	37-55	570-587
27	222-241	655-675
28	436-455	880-900
29	476-493	945-962
30	266-283	735-752
31	278-295	613-632
32	418-436	823-842
33	216-235	646-665
34	91-109	510-528
35	137-153	586-604
36	137-153	586-604
37	206-225	727-746
38	400-419	856-876
40	146-165	588-607
41	62-81	504-523
42	210-230	591-610
43	307-326	797-817
44	277-296	767-787
45	1-20	402-421
46	3-21	404-422
47	1-18	355-372

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FIG. 7 (following)

48	1-18	356-375
49	108-125	539-556
50	259-276	592-609
51	229-246	630-649
52	325-342	659-676
53	357-377	795-815
54	186-205	621-641
56	1-18	416-435
57	1-18	416-435
58	1-18	416-435
59	185-203	593-610
60	1-18	424-442
61	1-18	424-442
62	1-19	401-420
63	1-18	412-431
64	1-18	412-431
65	1-18	412-431
66	1-18	412-431
67	1-19	403-422
68	1-19	403-422
69	1-19	336-353
70	1-18	406-425
71	1-18	406-425
72	1-18	406-425
73	1-18	406-425
74	1-18	405-424
75	1-18	405-424
76	1-18	405-424
77	1-18	334-352
78	228-247	660-678
79	298-318	806-826
80	132-152	586-603
81	132-152	586-603
82	308-328	779-798
83	122-141	598-618
84	390-409	768-788
85	323-339	800-819
86	411-427	761-777
87	212-230	590-608
88	154-174	746-763
89	124-143	647-664
90	1-18	417-437
91	1-18	417-437
92	1-18	406-426
93	3-24	405-429
94	3-24	405-429
95	1-25	400-420
96	1-25	400-420
97	1-25	400-420
98	1-18	405-427
99	1-21	396-420

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FIG. 7 (following)

100	1-21	396-420
101	1-18	423-443
102	1-18	423-443
103	1-18	429-446
104	1-18	429-446
105	1-18	429-446
106	1-25	399-420
107	1-23	398-418
108	1-23	398-418
109	1-18	427-445
110	1-18	427-445
111	1-18	416-436
112	1-18	416-436
113	1-25	396-420
114	1-25	396-420
115	1-25	396-420
116	1-18	416-434
117	1-21	396-420
118	1-19	405-429
119	1-19	405-429
120	1-21	422-439
121	1-21	422-439
122	1-21	422-439
123	1-21	422-439
124	1-21	422-439
125	1-21	413-432
126	1-18	404-423
127	1-21	411-435
128	1-21	411-435
129	1-18	428-449
130	1-18	395-419
131	3-23	398-420
132	1-21	418-442
133	1-21	418-442
134	1-21	418-442
135	1-21	418-442
136	1-24	404-426
137	1-24	404-426
138	1-24	404-426
139	1-24	404-426
140	1-20	396-420
141	459-476	859-878
142	126-143	526-545
143	451-468	853-872
144	388-407	758-775
145	226-245	705-725
146	220-238	636-655
147	478-496	820-837
148	95-112	504-521
149	297-317	742-759
150	416-435	868-886

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FIG. 7 (following)

151	139-157	579-599
152	139-157	579-599
153	122-140	562-582
154	472-491	926-945
155	449-468	982-999
156	86-105	615-633
157	285-305	751-770
158	290-310	756-775
159	184-202	616-634
160	113-131	545-563
161	85-102	534-552
162	313-331	792-812
163	252-272	681-701
164	252-272	681-701
165	252-272	681-701
166	252-272	681-701
167	403-422	927-947
168	81-101	513-532
169	154-173	685-705
170	53-70	558-578
171	248-267	684-704
172	447-464	849-867
173	394-411	796-814
174	235-252	637-655
175	478-495	889-908
176	113-132	518-537
177	400-417	800-819
178	430-447	830-849
179	182-199	582-601
180	142-159	542-561
181	415-434	821-840
182	442-460	870-889
183	439-458	946-966
184	113-132	620-640
185	10-29	517-537
186	370-387	812-832
187	257-274	699-719
188	68-86	533-553
189	192-210	740-758
190	20-38	568-586
191	108-126	566-585
192	453-471	911-930
193	62-82	580-600
194	294-314	812-832
195	295-315	813-833
196	6-26	524-544
197	234-254	704-723
198	331-351	801-820
199	213-230	678-698
200	223-243	720-737
201	271-291	768-785

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FIG. 7 (following)

202	468-488	965-982
203	311-331	802-820
204	86-106	528-546
205	189-209	621-641
206	266-286	777-795
207	90-109	514-534
208	127-144	571-591
209	336-355	784-802
210	230-249	678-696
211	78-97	526-544
212	283-303	711-731
213	168-188	636-655
214	80-100	535-552
215	90-110	545-562
216	446-463	993-1013
217	406-423	953-973
218	75-92	622-642
219	422-441	982-1001
220	410-429	970-990
221	341-360	901-921
222	324-343	884-904
223	473-491	907-925
224	460-479	889-909
225	376-395	805-825
226	107-127	539-559
227	125-145	558-575
228	191-208	596-613
229	382-400	805-824
230	326-345	728-747
231	148-167	550-569
232	240-257	658-675
233	276-293	692-711
234	136-155	581-598
235	424-444	855-875
236	348-368	784-803
237	105-125	541-560
238	437-456	839-859
239	436-455	838-858
240	384-402	832-849
241	75-94	544-563
242	76-95	545-564
243	280-299	749-768
244	346-365	815-834
245	364-383	833-852
246	363-381	878-893
247	171-189	686-707
248	159-177	674-695
249	17-35	532-553
250	369-386	777-794
251	237-253	567-586
252	221-238	624-641

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FIG. 7 (following)

253	390-410	844-861
254	454-474	883-901
255	411-431	840-858
256	345-365	774-792
257	354-372	784-804
258	9-29	439-458
259	9-29	439-458
260	9-29	439-458
261	173-192	645-665
262	1-18	367-384
263	1-18	406-425
264	1-18	406-425
265	88-107	552-572
266	478-498	857-877
267	60-77	585-603
268	190-210	636-654
269	384-402	830-849
270	138-158	658-675
271	378-397	805-825
272	307-325	704-724
273	153-171	550-570
274	240-260	668-688
275	429-446	858-878
276	81-98	510-530
277	302-322	791-811
278	109-129	598-618
279	74-94	583-602
280	423-443	876-896
281	291-311	671-690
282	284-304	712-732
283	365-385	866-884
284	169-189	605-625
285	135-155	596-615
286	450-469	894-914
287	427-446	871-891
288	383-402	888-908
289	126-146	558-577
290	324-341	662-681
291	301-320	701-720
292	190-208	593-611
293	448-465	848-867
294	146-165	546-565
295	354-372	779-798
296	253-271	678-697
297	228-245	645-664
298	222-239	639-658
299	165-182	582-601
300	178-196	637-656
301	162-180	595-612
302	122-140	555-572
303	334-352	830-848

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FIG. 7 (following)

304	309-327	805-823
305	203-221	699-717
306	444-462	940-958
307	267-286	703-722
308	342-361	778-797
309	276-295	706-725
310	326-344	779-797
311	301-319	733-753
312	244-262	676-696
313	104-124	594-612
314	99-117	557-577
315	68-86	526-546
316	250-270	800-818
317	250-270	800-818
318	12-32	442-461
319	186-204	623-641
320	87-105	524-542
321	112-130	549-567
322	122-139	602-620
323	368-386	868-888
324	173-191	673-693
325	117-135	617-637
326	181-200	640-658
327	414-433	873-891
328	187-205	637-657
329	181-199	631-651
330	50-68	533-552
331	148-167	651-669
332	12-31	515-533
333	271-291	655-674
334	144-164	528-547
335	375-395	765-783
336	403-423	793-811
337	368-387	800-820
338	328-345	827-845
339	306-323	805-823
340	232-249	731-749
341	50-68	553-572
342	386-405	867-887
343	23-43	522-540
344	99-116	628-647
345	412-429	844-862
346	67-87	513-533
347	230-247	691-710
348	446-463	907-926
349	345-363	729-749
350	478-497	909-927
351	479-498	880-899
352	420-439	788-807
353	420-439	788-807
354	304-322	714-732

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FIG. 7 (following)

355	171-189	582-600
356	220-238	624-641
357	230-250	698-717
358	144-164	573-593
359	290-310	719-739
360	156-176	629-649
361	296-316	769-789
362	324-344	797-817
363	412-432	885-905
364	127-147	600-618
365	129-149	602-620
366	163-183	636-654
367	163-183	636-654
368	117-135	592-612
369	87-105	562-582
370	6-26	474-494
371	6-26	474-494
372	359-378	788-808
373	129-147	607-627
374	129-147	607-627
375	100-118	578-598
376	184-203	615-635
377	184-203	615-635
378	184-203	615-635
379	131-150	562-582
380	390-410	903-921
381	76-96	595-613
382	168-188	687-705
383	108-128	566-586
384	384-404	863-883
385	120-139	552-572
386	173-193	692-712
387	418-435	979-1000
388	353-372	809-829
389	348-367	804-824
390	251-270	707-727
391	52-71	508-528
392	46-65	533-553
393	20-39	507-527
394	18-38	505-525
395	18-38	505-525
396	18-38	505-525
397	272-292	704-724
398	209-229	641-661
399	219-237	653-673
400	437-457	908-928
401	279-298	773-793
402	252-271	746-766
403	238-257	660-679
404	172-189	578-597
405	135-152	545-564

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FIG. 7 (following)

406	346-366	801-821
407	386-406	847-865
408	335-355	787-807
409	237-257	680-700
410	121-140	565-584
411	339-357	781-801
412	220-238	621-639
413	283-301	686-704
414	272-290	675-693
415	269-287	672-690
416	268-286	671-689
417	219-237	622-640
418	444-464	901-921
419	179-199	689-707
420	114-134	597-615
421	175-195	658-676
422	228-248	711-729
423	251-271	776-795
424	461-481	981-1001
425	343-363	781-799
426	424-442	952-971
427	309-326	777-797
428	455-473	907-927
429	40-59	551-569
430	114-134	562-582
431	115-135	563-583
432	127-147	575-595
433	179-199	627-647
434	321-341	769-789
435	326-346	774-794
436	367-385	797-817
437	184-203	616-633
438	86-106	546-563
439	260-279	755-773
440	255-272	773-790
441	303-322	736-756
442	215-233	617-635
443	479-499	913-932
444	204-222	634-654
445	104-121	506-525
446	370-387	769-793
447	475-495	870-892
448	347-367	764-788
449	111-132	513-537
450	96-113	601-621
451	149-167	577-596
452	312-329	713-731
453	128-145	530-548
454	444-461	855-874
455	76-95	583-603
456	333-353	774-793

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FIG. 7 (following)

457	136-156	567-586
458	286-306	714-734
459	152-172	585-602
460	59-78	523-543
461	251-271	771-788
462	119-136	679-696
463	170-188	574-591
465	179-198	611-631
466	83-103	554-574
467	279-298	773-793
468	340-360	788-808
469	177-196	576-595
470	465-484	864-883
471	270-288	527-545
472	325-345	783-800
473	1-20	413-432
474	213-231	613-631
475	158-176	558-576
476	128-146	528-546
477	307-324	700-719
478	474-491	890-909
479	1-19	404-422
480	387-407	833-853
481	454-472	919-939
482	113-133	631-651
483	288-305	753-773
484	174-193	573-592

Fig. 8

SEQ ID NO.	POSITION RANGE OF PROBES
1	489-513
2	489-513
3	489-513
4	489-513
5	449-473
6	489-513
7	489-513
8	489-513
9	489-513
10	489-513
11	489-513
12	489-513
13	489-513
14	489-513
15	489-513
16	489-513
17	489-513
18	489-513
19	489-513
20	489-513
21	489-513
22	489-513
23	489-513
24	489-513
25	489-513
26	489-513
27	489-513
28	489-513
29	489-513
30	489-513
31	489-513
32	489-513
33	489-513
34	489-513
35	220-244
36	274-298
37	488-512
38	468-492
40	414-438
41	489-513
42	491-515
43	489-513
44	489-513
45	318-342
46	330-354
47	265-289
48	285-309

Fig. 8 (following)

49	489-513
50	489-513
51	489-513
52	489-513
53	489-513
54	489-513
56	166-190
57	206-230
58	322-346
59	489-513
60	66-90
61	92-116
62	40-64
63	27-51
64	119-143
65	154-178
66	234-258
67	149-173
68	150-174
69	157-181
70	140-164
71	231-255
72	265-289
73	283-307
74	31-55
75	105-129
76	308-332
77	109-133
78	489-513
79	438-462
80	234-258
81	299-323
82	487-511
83	489-513
84	489-513
85	491-515
86	489-513
87	491-515
88	489-513
89	489-513
90	204-228
91	385-409
92	220-244
93	39-63
94	114-138
95	190-214
96	263-287
97	334-358
98	159-183
99	176-200
100	211-235

Fig. 8 (following)

101	95-119
102	365-389
103	272-296
104	144-168
105	367-391
106	211-235
107	227-251
108	358-382
109	92-116
110	383-407
111	31-55
112	126-150
113	70-94
114	154-178
115	232-256
116	103-127
117	24-48
118	173-197
119	366-390
120	130-154
121	154-178
122	192-216
123	193-217
124	301-325
125	56-80
126	345-369
127	244-268
128	341-365
129	224-248
130	127-151
131	201-225
132	26-50
133	171-195
134	323-347
135	382-406
136	27-51
137	60-84
138	144-168
139	273-297
140	155-179
141	489-513
142	489-513
143	489-513
144	465-489
145	421-445
146	489-513
147	491-515
148	489-513
149	489-513
150	489-513
151	345-369

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Fig. 8 (following)

152	461-485
153	489-513
154	489-513
155	467-491
156	488-512
157	489-513
158	489-513
159	491-515
160	491-515
161	489-513
162	489-513
163	369-393
164	449-473
165	461-485
166	479-503
167	489-513
168	489-513
169	489-513
170	489-513
171	489-513
172	489-513
173	489-513
174	489-513
175	485-509
176	489-513
177	489-513
178	489-513
179	489-513
180	489-513
181	489-513
182	489-513
183	489-513
184	489-513
185	489-513
186	489-513
187	489-513
188	489-513
189	489-513
190	489-513
191	489-513
192	473-497
193	489-513
194	489-513
195	489-513
196	489-513
197	489-513
198	489-513
199	489-513
200	489-513
201	489-513
202	489-513

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Fig. 8 (following)

203	487-511
204	489-513
205	489-513
206	489-513
207	489-513
208	489-513
209	489-513
210	489-513
211	489-513
212	489-513
213	489-513
214	489-513
215	489-513
216	487-511
217	489-513
218	489-513
219	462-486
220	489-513
221	488-512
222	489-513
223	489-513
224	489-513
225	489-513
226	489-513
227	489-513
228	489-513
229	489-513
230	489-513
231	489-513
232	489-513
233	489-513
234	489-513
235	489-513
236	489-513
237	489-513
238	489-513
239	489-513
240	489-513
241	489-513
242	490-514
243	489-513
244	489-513
245	489-513
246	489-513
247	489-513
248	489-513
249	489-513
250	489-513
251	472-496
252	489-513
253	489-513

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Fig. 8 (following)

254	489-513
255	489-513
256	489-513
257	489-513
258	241-265
259	367-391
260	422-446
261	491-515
262	142-166
263	193-217
264	339-363
265	489-513
266	487-511
267	489-513
268	489-513
269	489-513
270	489-513
271	489-513
272	489-513
273	489-513
274	489-513
275	489-513
276	489-513
277	489-513
278	489-513
279	489-513
280	489-513
281	489-513
282	489-513
283	493-517
284	489-513
285	489-513
286	489-513
287	489-513
288	489-513
289	489-513
290	489-513
291	491-515
292	489-513
293	489-513
294	489-513
295	489-513
296	489-513
297	489-513
298	489-513
299	489-513
300	489-513
301	489-513
302	489-513
303	489-513
304	489-513

Fig. 8 (following)

305	489-513
306	489-513
307	489-513
308	489-513
309	489-513
310	489-513
311	489-513
312	489-513
313	489-513
314	243-267
315	489-513
316	654-678
317	489-513
318	237-261
319	489-513
320	489-513
321	489-513
322	489-513
323	489-513
324	489-513
325	489-513
326	489-513
327	489-513
328	489-513
329	489-513
330	489-513
331	489-513
332	489-513
333	489-513
334	489-513
335	489-513
336	489-513
337	489-513
338	489-513
339	489-513
340	489-513
341	489-513
342	489-513
343	489-513
344	489-513
345	489-513
346	489-513
347	489-513
348	468-492
349	489-513
350	486-510
351	491-515
352	491-515
353	491-515
354	491-515
355	491-515

Fig. 8 (following)

356	491-515
357	487-511
358	487-511
359	487-511
360	487-511
361	487-511
362	487-511
363	487-511
364	487-511
365	487-511
366	420-444
367	376-400
368	491-515
369	491-515
370	422-446
371	426-450
372	491-515
373	239-263
374	416-440
375	489-513
376	286-310
377	374-398
378	445-469
379	489-513
380	487-511
381	487-511
382	487-511
383	491-515
384	491-515
385	489-513
386	294-318
387	485-509
388	489-513
389	489-513
390	489-513
391	489-513
392	232-256
393	489-513
394	41-65
395	181-205
396	489-513
397	335-359
398	491-515
399	228-252
400	489-513
401	372-396
402	491-515
403	491-515
404	491-515
405	491-515
406	491-515

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Fig. 8 (following)

407	487-511
408	489-513
409	489-513
410	487-511
411	489-513
412	491-515
413	491-515
414	491-515
415	491-515
416	491-515
417	491-515
418	489-513
419	489-513
420	487-511
421	487-511
422	487-511
423	489-513
424	489-513
425	487-511
426	489-513
427	491-515
428	491-515
429	352-376
430	489-513
431	489-513
432	477-501
433	489-513
434	489-513
435	489-513
436	489-513
437	489-513
438	489-513
439	489-513
440	489-513
441	489-513
442	489-513
443	489-513
444	489-513
445	489-513
446	489-513
447	489-513
448	489-513
449	489-513
450	489-513
451	489-513
452	489-513
453	489-513
454	489-513
455	489-513
456	489-513
457	489-513

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Fig. 8 (following)

458	489-513
459	489-513
460	489-513
461	489-513
462	489-513
463	489-513
464	489-513
465	417-441
466	489-513
467	294-318
468	489-513
469	489-513
470	489-513
471	489-513
472	489-513
473	200-224
474	489-513
475	489-513
476	489-513
477	489-513
478	489-513
479	253-277
480	489-513
481	489-513
482	489-513
483	489-513
484	489-513

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ALLELE FREQUENCY DATA (FRENCH and US)

Seq. ID No.	Protein	Biallelic Marker ID	caucasian FRENCH					caucasian US				
			size	A	C	G	T	size	A	C	G	T
21	MGST-II	12-458/198	no genotyped for this population					180	80,83			19,17
15	MGST-II	12-455/328						93	58,06		41,94	
5	MGST-II	12-426/154						181	58,01		41,99	
9	MGST-II	12-441/232						182		35,44		64,56
437	MGST-II	12-442/133						94		5,85	94,15	
7	MGST-II	12-430/80						93	5,38		94,62	
1	MGST-II	12-421/140						183	79,51		20,49	
436	MGST-II	12-421/139						185			84,59	15,41
13	MGST-II	12-453/429						183		56,28		43,72
12	MGST-II	12-447/58						93		55,38	44,62	
25	MGST-II	12-461/299						183		40,44		59,56
3	MGST-II	12-424/198						176			61,08	38,92
14	MGST-II	12-454/363						188	18,62		81,38	

Figure 9

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ALLELE FREQUENCY DATA (US)

Seq. ID No.	Protein	Blallelic Marker ID	caucasian US				
			size	A	C	G	T
37	ME1	12-716-295	189		66,14		33,86
31	ME1	10-428-219	189	66,67		33,33	
38	ME1	12-720-80	190		33,95	66,05	
33	ME1	10-420-284	184		1,36		98,64
41	ME1	12-721-440	94	1,6		98,4	
44	ME1	12-724-225	190		73,16		26,84
42	ME1	12-723-293	92		99,46		0,54
35	ME1	12-713-95	190		32,63		67,37

Figure 10

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ALLELE FREQUENCY DATA (FRENCH and US)

Seq. ID No.	Protein	Biallelic Marker ID	Caucasian FRENCH					Caucasian US				
			size	A	C	G	T	size	A	C	G	T
336	UGT1A7	12-148-311	88	47,73		52,27		190	44,47		55,53	
345	UGT1A7	12-156-91	90	50,56		49,44		93	50,54		49,46	
300	UGT1A7	12-121-326	93	30,11		69,89		188	28,99		71,01	
309	UGT1A7	12-128-225	93	50,54	49,46			187	55,35	44,65		
304	UGT1A7	12-124-194	85		19,41		80,59					
326	UGT1A7	12-141-159	92	37,5		62,5						
330	UGT1A7	12-143-453	82	50,61		49,39						
322	UGT1A7	12-139-380	85	17,65		82,35		190	20,79		79,21	
342	UGT1A7	12-153-116	90		62,22		37,78					
323	UGT1A7	12-140-134	89			58,99	41,01	183			56,01	43,99
329	UGT1A7	12-142-321	90	54,44		45,56						

Figure 11

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ALLELE FREQUENCY DATA (FRENCH and US)

Seq. ID No.	Protein	Biallelic Marker ID	Caucasian FRENCH					Caucasian US				
			size	A	C	G	T	size	A	C	G	T
380	UGT2B4	12-653-423	6	25			75	177	73,45			26,55
351	UGT2B4	10-470-25	179	56,15			43,85	90	55,56			44,44
356	UGT2B4	10-494-284	6		16,67		83,33	185		22,97		77,03
352	UGT2B4	10-471-84	178	24,44			75,56	92	27,17			72,83
353	UGT2B4	10-471-85	0					188	26,6	73,4		
354	UGT2B4	10-472-202	182		14,29		85,71	93		9,68		90,32
357	UGT2B4	12-637-219	0					187		33,42		66,58
358	UGT2B4	12-639-95	0					187		35,56		64,44
377	UGT2B4	12-652-203	4	50	50			189	57,67	42,33		
369	UGT2B4	12-642-417	0					186	73,66		26,34	
374	UGT2B4	12-648-300	0					91		62,09		37,91

Figure 12

MARKERS		ESTIMATED FREQUENCIES												
MGST2		markers in bac												
		12-421/136	12-430/80	12-441/233	12-442/133	12-447/58	12-455/226	12-461/299	12-453/429	12-424/198	12-454/303	12-458/196	12-426/154	
		inB												
allelic frequency % (cases/controls)	size (cases / controls)	88 vs 194	88 vs 97	87 vs 198	68 vs 104	89 vs 198	65 vs 102	88 vs 189	64/82 (T)	88 vs 189	80 vs 180	83 vs 194	83 vs 194	85 vs 188
	diff freq. all. (cases - controls)	18/12 (T)	91/91 (G)	39/34 (C)	92/91 (G)	47/44 (G)	56/55 (A)	56/55 (A)	40/38 (T)	41/40 (T)	22/20 (A)	22/16 (T)	22/16 (T)	60/59 (A)
		5.6	0.4	0.4	5.6	1.3	3.1	0.8	1.8	2.7	1.0	2.5	5.5	1.8
		7.9e-02	7.5e-01	1.9e-01	6.6e-01	4.8e-01	7.5e-01	7.5e-01	6.6e-01	5.3e-01	7.5e-01	4.8e-01	1.2e-01	6.6e-01
p-value	Hardy Weinberg	0.00 HW	0.83	0.02 HW	0.85	-0.04 HW	0.01 HW	0.01 HW	-0.01 HW	0.04 HW	-0.00 HW	0.03 HW	-0.00 HW	0.03 HW
	Equilibrium	-0.01 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
Test	Hardy Weinberg	0.00 HW	0.83	0.02 HW	0.85	-0.04 HW	0.01 HW	0.01 HW	-0.01 HW	0.04 HW	-0.00 HW	0.03 HW	-0.00 HW	0.03 HW
	Equilibrium	-0.01 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
p-value	Hardy Weinberg	0.00 HW	0.83	0.02 HW	0.85	-0.04 HW	0.01 HW	0.01 HW	-0.01 HW	0.04 HW	-0.00 HW	0.03 HW	-0.00 HW	0.03 HW
	Equilibrium	-0.01 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
p-value	Hardy Weinberg	0.00 HW	0.83	0.02 HW	0.85	-0.04 HW	0.01 HW	0.01 HW	-0.01 HW	0.04 HW	-0.00 HW	0.03 HW	-0.00 HW	0.03 HW
	Equilibrium	-0.01 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
p-value	Hardy Weinberg	0.00 HW	0.83	0.02 HW	0.85	-0.04 HW	0.01 HW	0.01 HW	-0.01 HW	0.04 HW	-0.00 HW	0.03 HW	-0.00 HW	0.03 HW
	Equilibrium	-0.01 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	-0.00 HW	0.03 HW
		0.00 HW	0.00 HW	0.01 HW										

Fig. 15

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HAPLOTYPE ANALYSIS ; PERMUTATION TEST RESULT

Zyflo secondary effects

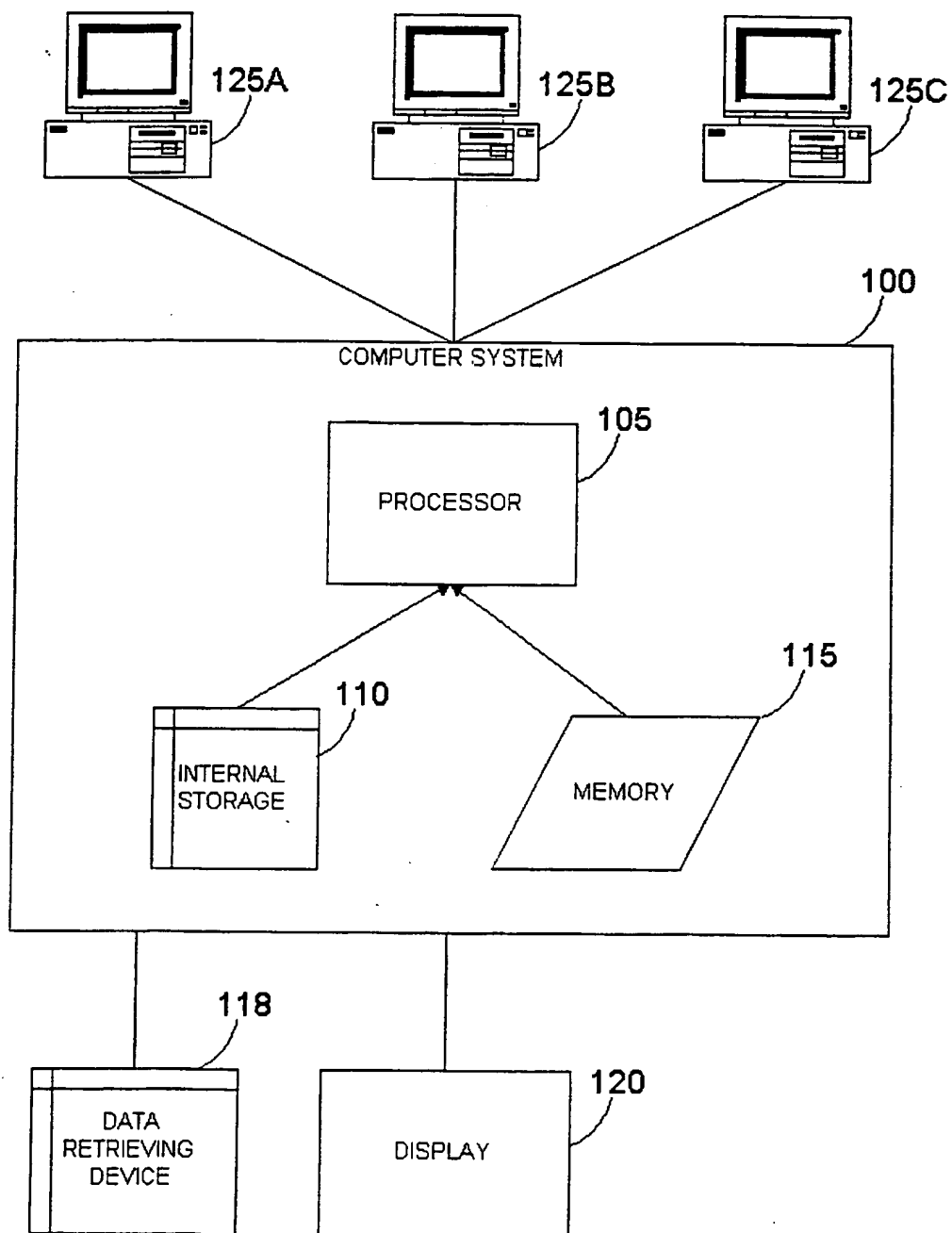
PROTEIN MGST2	12-441/233			12-461/299			12-453/429			12-426/154		
	C			T			T			T		
	markers in bac			T			T			T		
	C			T			T			T		
	A			T			T			T		
	1.92E-01	6.55E-01	5.27E-01	1.92E-01	6.55E-01	5.27E-01	1.92E-01	6.55E-01	5.27E-01	1.92E-01	6.55E-01	5.27E-01
	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)
	7.52E-01	2.73E-01	1.47E-01	7.52E-01	2.73E-01	1.47E-01	7.52E-01	2.73E-01	1.47E-01	7.52E-01	2.73E-01	1.47E-01
	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)
	C			T			T			T		
	1.92E-01	6.55E-01	5.27E-01	1.92E-01	6.55E-01	5.27E-01	1.92E-01	6.55E-01	5.27E-01	1.92E-01	6.55E-01	5.27E-01
	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)
	7.52E-01	2.73E-01	1.47E-01	7.52E-01	2.73E-01	1.47E-01	7.52E-01	2.73E-01	1.47E-01	7.52E-01	2.73E-01	1.47E-01
	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)

HAPLOTYPE CTT	sample sizes cases vs controls	haplotype frequencies		p-excess	odds- ratio	chi-S	P value	PERMUTATIONS	
		cases	controls					Av. Chi-S	Max Chi-S
ALT+ vs ALT-	86 vs 198	0.157	0.049	11.34	3.63	18.68	1.5e-05	1.9	18.9
ALT+ vs ALT- (1)	86 vs 104	0.157	0.088	7.54	1.93	4.26	3.8e-02	1.9	25.4
ALT+ vs ALT- (2)	86 vs 94	0.157	0.042	11.91	4.19	13.36	2.5e-04	1.1	16.5
ALT vs caucasian US	284 vs 176	0.092	0.071	2.2	1.32	1.18	2.7e-01	1.5	15.4
ALT vs caucasian US (2)	284 vs 94	0.092	0.047	4.67	2.04	3.77	5.1e-02	2.1	20.9
ALT vs caucasian US (3)	284 vs 82	0.092	0.116	-2.79	0.77	0.88	3.4e-01	1.9	17.3
								1.8	17.7

HAPLOTYPE CTTA	sample sizes cases vs controls	haplotype frequencies		p-excess	odds- ratio	chi-S	P value	PERMUTATIONS	
		cases	controls					Av. Chi-S	Max Chi-S
ALT+ vs ALT-	83 vs 187	0.141	0.028	11.64	5.75	25.13	5.2e-07	2.6	25.2
ALT+ vs ALT- (1)	83 vs 98	0.141	0.066	8.03	2.33	5.61	1.7e-02	2.5	35
ALT+ vs ALT- (2)	83 vs 89	0.141	0.034	11.03	4.6	12.42	4.1e-04	1.7	17.4
ALT vs caucasian US	270 vs 167	0.082	0.058	2.61	1.46	1.85	1.7e-01	1.7	18.3
ALT vs caucasian US (2)	270 vs 89	0.082	0.023	6.12	3.89	7.61	5.5e-03	2.7	25.9
ALT vs caucasian US (3)	270 vs 78	0.082	0.110	-3.06	0.73	1.11	2.7e-01	2.7	30.3
								2.3	17.8

Figure 16

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**FIG.17**

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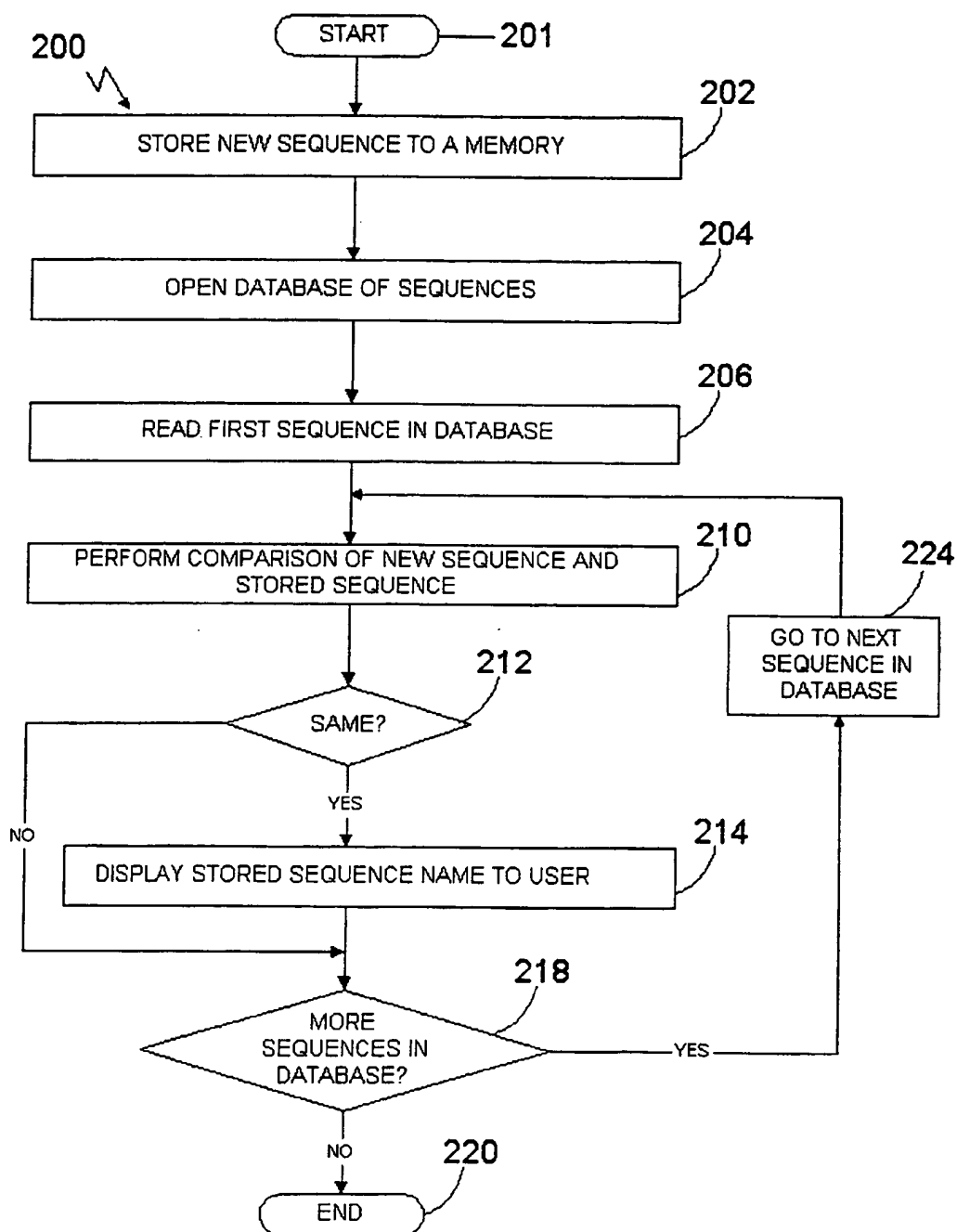


FIG.18

64/65

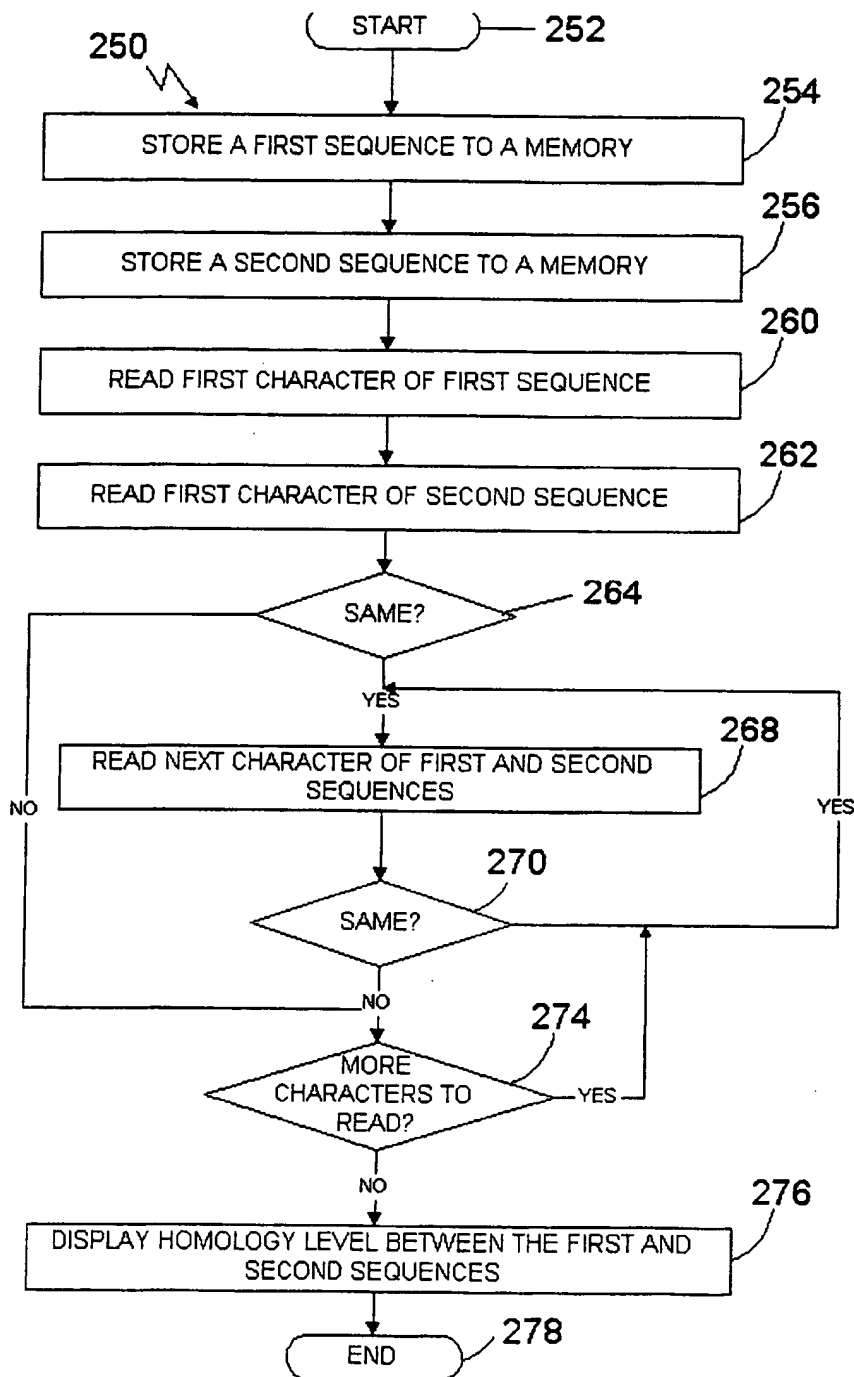


FIG.19

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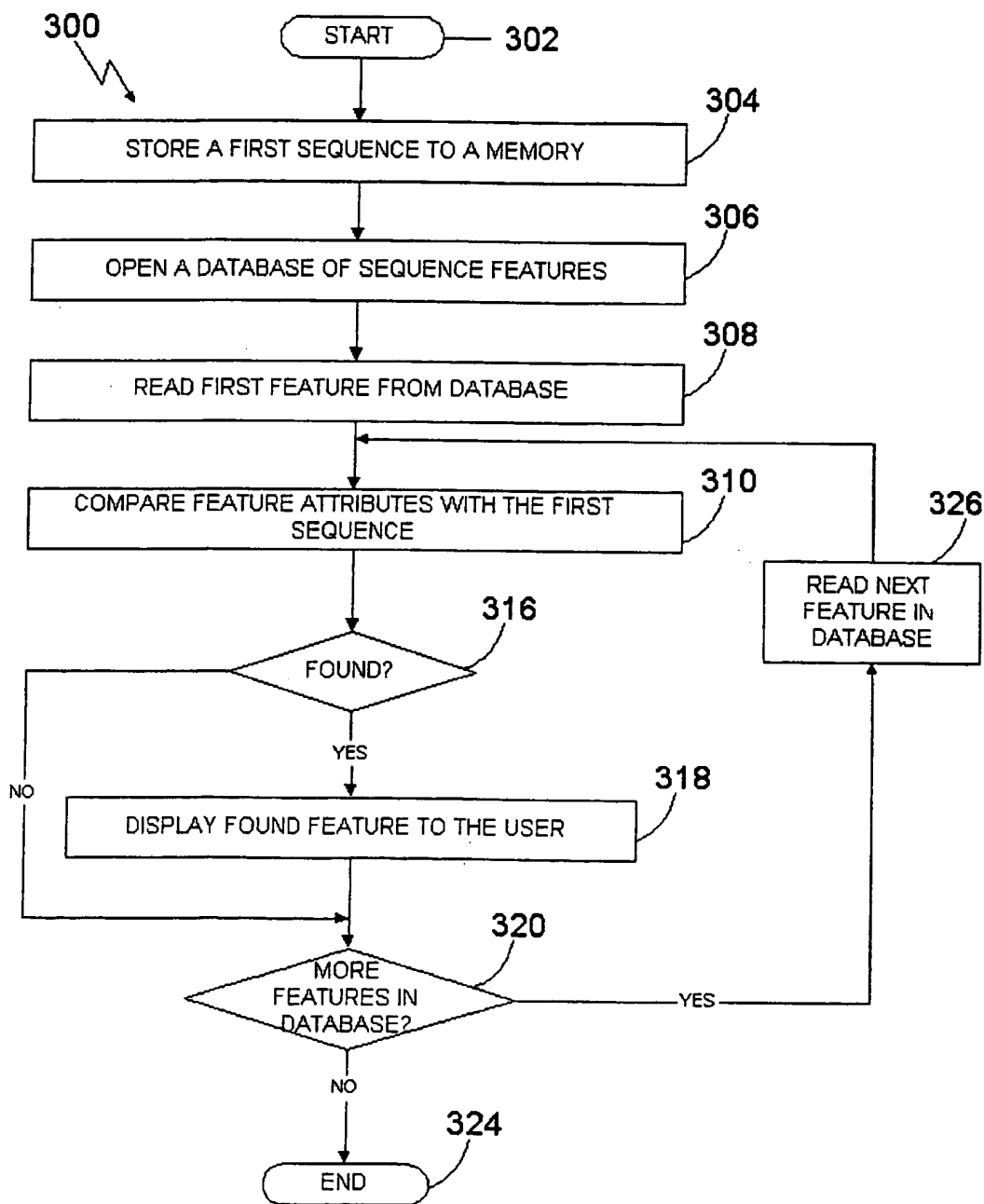


FIG.20

SEQUENCE LISTING

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<120> BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

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<150> US 60/126,269

<151> 1999-03-25

<150> US 60/131,961

<151> 1999-04-30

<160> 493

<170> Patent.pm

<210> 1

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-421-140 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-421-140.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-421-140.mis2, potential complement

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<221> primer_bind

<222> 362..380

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 792..812

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-421-140 potential probe

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ttgccttaaa	ataatctggg	cctaattgtt	ttctgggtgg	aaatttttaa	attatgggat	180
ttgcattctt	taatgattat	tggactaggc	aggctttttg	ttacatcttg	aatcaatttt	240
ggtaggcctt	ggctccttgag	atgataacat	tggtctcttg	attatccact	tgctccaagg	300
agggttttac	agactactcc	ctaggcttga	aagcgtgggg	tgaataccac	cgggagtaca	360
cgagataatt	gtaagaggtg	tgtagacttg	gtttttaaata	acattgaact	acatgatgag	420
aagtcattct	catttcaatt	atctttgaat	ccttatgggt	aagtcaagtg	gaaagtattg	480

2

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tgccccctacc tccccctctcc ctctatccct agagataacc ctttttgatt actactttgg 660
gtattttactt ctgtattttct aaacattata ctttctactgc tattttattga ttcacaaatt 720
ttagacattg tcagttgggt tctttttatg gaagaaataa tttcatgctc ctttacttct 780
tcttttcctt acctcaccct tccagtaaca ttatatcact ctgttaggtt aaatcaatag 840
ccaatgttta taattattgt gattaagaaa ataattgtga aagcagggcc ttatagtata 900
ctgtgggttac atttccttct tgtgcaattt tttttcccta gggtaataa ttgctcttta 960
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<213> Homo Sapiens

<220>

<221> allele

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<220>

<221> misc_binding

<222> 502..521

<223> 12-424-192.mis2, potential complement

<220>

<221> primer_bind

<222> 310..327

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 751..771

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-424-192 potential probe

<220>

<221> misc_feature

<222> 521,541,635

<223> n=a, g, c or t

<400> 2

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gtggggggga tggggaattc ctctcttacc aaccctgcct catttcagtt tttgcttcag 180
aagcttgggc ttctcaccac ttctccatc tggctagctg gtctactcta agccctactg 240
tggggccact catccagggc tcacagaggc ccccatggta aggccaccag ctcttgattc 300
agcttccgca caatgtggga acttaggaca gctcaggaaa cctaactcag ggccttcctt 360
ctccttacca tactacttta ctctgctatg gctgtgtaaa agactgaatg ggacagagat 420
cttgtaccag gagagaaacg cccattagta atttccaagc atgcacacat gttatagggt 480
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gtcacacttg gctctacagt ggtagcaaa tctgnacaca gtcctcatgg atcttacata 660
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3

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tatttggtga	atgaatgaat	aaataaatgc	atgaaagcta	tgagattact	tctgagaggt	900
cagggatgaa	ttcctgaggc	agtgttattt	tggctgatgt	taaagagaaa	aaaaaattct	960
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<223> 12-424-198.mis1, potential

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<221> misc_binding

<222> 502..521

<223> 12-424-198.mis2, potential complement

<220>

<221> primer_bind

<222> 304..321

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 745..765

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-424-198 potential probe

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<222> 515,535,629

<223> n=a, g, c or t

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gggatgggga	attcctctct	taccaaccct	gcctcatttc	agtttttgct	tcagaagctt	180
gggctttctca	ccactttctc	catctggcta	gctgggtctac	tctaagccct	actgtggggc	240
cactcatcca	gggctcacag	agggccccc	ggtaaggcca	ccagctcttg	attcagcttc	300
cgcacaatgt	gggaacttag	gacagctcag	gaaacctaac	tcagggcctt	ccttctccct	360
accatactac	tttactctgc	tatggctgtg	taaaagactg	aatgggacag	agatcttgta	420
ccaggagaga	aacgcccatt	agtaatttcc	aagcatgcac	acatgttata	ggttctgagg	480
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cttggtctta	cagtggtttag	caaactctgna	cacagtcctc	atggatctta	cataagagga	660
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4

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<222> 502..521

<223> 12-425-57.mis2, potential complement

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<221> primer_bind

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<222> 82..99

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<222> 489..513

<223> 12-425-57 potential probe

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cttgaaggaa ctcaagagtt tttatttccg tgcttgaggt ggctagcagg tccctaagag	240
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 <223> 12-426-154.mis2, potential complement

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 <223> downstream amplification primer, complement

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 <223> 12-426-154 potential probe

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 ttcagtgcag gctaaagtgt gagaaactaca gatacaaaagg agggctctgt atctgcaaca 180
 acaactatgt aatgatgact agtccccact cttctgaagc taccatggc aaaattagaa 240
 acataattct tcaaaaacca ctggcactga tttagtgcac agaacacctg tggataactc 300
 aattcccttt gtccctccct gtgtcaaggc caaaggatct aatgtgatat aagcattcca 360
 gaggtggaag ggagtggtag ctactcaaga cccagtattt ttacaggtga tcttcaatgt 420
 gatctgtcag taaatatcaa tggctttcag actgtaaact rcagctcaca gttcatgac 480
 taggatatat acatgtgggt ttaaaacaga aagaaaagt tctgatatgc tctggttaatt 540
 tctgttgat ttcattttaa aaatgttgg tgtgaccac taagttgtt ccaataacct 600
 tgtgtgttgc aatctgagaa gttaaaaatg ctaccttaga tcagaaaatt ttcacctcagt 660
 ctattgataa agttcaggga tacttgtgaa attatataaa agttntgtat atatttacat 720
 attatatgtt tctctgcaag aggcttcata gctttttgca nnacacttaa aggaataggt 780
 aacttttgag aagctaggac acattgatct agatcccaca aaatgggcag aggatgggat 840
 taggatcttct gctgctaggt gacccctgta gcccctgaa aactcctgtg gataagatta 900
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 t 961

<210> 6
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-429-198 : polymorphic base C or T

<220>

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<221> misc_binding
<222> 481..500
<223> 12-429-198.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-429-198.mis2, potential complement

<220>
<221> primer_bind
<222> 304..321
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 803..823
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-429-198 potential probe

<220>
<221> misc_feature
<222> 44,561..562,954
<223> n=a, g, c or t

<400> 6
ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccngtccgt actaaaaata      60
aaaaaattag ctgggcgtgg tggcaggcac ctgtagtctc agctactcag gaggctgagg      120
caggagaatc gcttgaaccc aggaggcgga gggtgcagtg agttgacagt gtaccactgc      180
actccagcat gggcgacaga ccaagattct gtcttaaaaa acaaaacaaa acaaaacaaa      240
aaactgggag gggaaaatat ttttttattt tctaatatgt tagaaccctt tctcaatgtg      300
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catcatgtta gtctatcagg tgttatttag ataattggtg cctttgactt acattcttgt      420
aaacgttgct ttagttcata aactcataat attcccagac ctgaagcctg tcttaaaatt      480
gataatgtaa atcatctagg yctgaatgcc taaagtgatg gggagctcac cacctcttgt      540
ttctggtcat aggtagggtga nngatccctt ctgcagcaag aagtcagggg caggcctgtg      600
acactagctc tgattcctgc aaatgaccaa atgaggggca gggcctggtg gtctccag      660
ccagctgag gtctcccatga cctgcacctc cctgccctcc caactctcag gttctcccaa      720
cagccctccc ccagctaatt tcataaaagg cactaaaaac ttttgatcag tcacaaaatc      780
atgggaagag aaagaaatac aagaagagag aaagaaggga aagtggcgtg aatcattaac      840
aaaggcacca catccctgat actgtactgt tctgggtgct tttttctcaa tgaattctca      900
caaaatcctg ttggtattag tgattcatat ttcttacata tagaaactga gtcngcaaag      960
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<210> 7
<211> 996
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-430-80 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-430-80.mis1, potential complement

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<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-430-80.mis2

<220>
 <221> primer_bind
 <222> 561..580
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 131..150
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-430-80 potential probe

<220>
 <221> misc_feature
 <222> 918,971,978
 <223> n=a, g, c or t

<400> 7
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 acatctaatt ggtaagtgt taggtattcg ttgtattatt atttctactt tcctgggtgt 180
 ttaaaaatgt ttataataaa gagttaaagg atctgaagag aagttaaaac ctaaaatcag 240
 attcttggtg gccctgaaga ttttctgtgt tgagcattgt taagagatcc agtggatttg 300
 atggatccac agtcatccat gctggcctgg cagctgtcct ggggtgtggca cagatgcctg 360
 ggccccacat gtgtgagagc tgcagtaatt acctccacct gttgcatgaa atgaggcagg 420
 tgtctgtgcc agctactcca gaggacacta gtggaggaat ttaatgtcct tagtacttaa 480
 aagagaattg aggacaaaat yggatttaca aaaagaggaa acaaatcaaa aagaaaatta 540
 aaaggtaaaag actggttacc caaagaggta gctctgttcc attttcagat aatttttctt 600
 gttccacttt tcttttaggg gttggagggtg ggtgggggtat ggccaaaaaa gtcattaata 660
 aacaaaatca ggtcatttga gggtccaccct ttttctccag acacaatctt ccttgaaaag 720
 aatggtcaga ggcagaaaca gctcattgaa tgctatggaa tggtccttaa tcaccagtga 780
 aatacgtctt tctcactggg ggcagatgtc tagtgacttt ctagaaaaat gtttattctc 840
 tcctctttct tccccatca ccatacttac tgcactagga ttttataaag gtcagtaaga 900
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<210> 8
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-433-215 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-433-215.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-433-215.mis2, potential complement

<220>
 <221> primer_bind
 <222> 287..304
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 805..825
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-433-215 potential probe

<220>
 <221> misc_feature
 <222> 92,202
 <223> n=a, g, c or t

<400> 8
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 agctgtgggg gcactcccag ccattgtctc ctcagctgag gcctcagaca ttgaagagca 180
 gagacatgcc agtcctaccg tngccctact gaccacata actcattaga gcctaattaa 240
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 caacctcatt gcaaggtaac aactcagctt cccagggttc atcatttggc tccagtata 360
 ccaccccatg ccctgcaagt gtggcacttc agacaggagc cagggacacc aggagtatgg 420
 ctggtggccc ttaggtggca ggattgcaga ggccccaccg gaagtcagct ggccacagca 480
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 gcgctgcact ggacgtgcct gataaagcaa agaggagag aaaagaggag ttaaggattt 600
 ccacatttct ggtttctgaa cagctagata cattaatgat ggggcaattt actgccacag 660
 aatttagacc aaaggagggg gctaggtttg aagtgcctgt gagtccatta gaaatgacaa 720
 gaagtgggag cccaggtcac caaagatggt caaggtcatt gatcttgaga ccacagggcc 780
 ccaagaaggc ttaagggtct gtccctgatt cttgtttcct gtgtgagaaa tattttgcag 840
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 agacagaagc gaccccagga aaaagcgtgg cttccacaag agctgccata tacaacaag 960
 catgcccac aacgctggca ggagagatat catcagattt a 1001

<210> 9
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-441-233 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-441-233.mis1, potential complement

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-441-233.mis2

<220>
 <221> primer_bind
 <222> 716..734

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 284..303

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-441-233 potential probe

<220>

<221> misc_feature

<222> 661,929,990

<223> n=a, g, c or t

<400> 9

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ttttttgtga	gccacatctg	atatttctga	tatccccagg	aaggagtggc	ctggagggtca	180
ctggttcagg	ctccctttgg	gcgaaatcct	gggagtgatg	ctctaaaaat	ccacctttcc	240
catcatccct	actcatcaga	aagacaaata	taaaatccca	gagaggtgga	ggagctaaaa	300
aagcaattgc	tccaccttac	aaatttggat	agaaaggaga	tgtagtttat	ttcatatggg	360
caaagtagtc	ctcttccaaa	gtcctgtaca	attgttctct	gcaattgacg	cacatctgcc	420
ctaagcgaaa	tctgtcagaa	ggaatcaaca	aggctccttg	cctccccctc	caatccccct	480
tttgaggagc	ttgtggcttc	rgtgtcgtcc	taagtgaag	tggcgtgtgc	tttttccctg	540
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cctttgactt	gctctccgcg	tacccggggg	tgtagagctg	ctcaggaagg	ggcaggatgt	780
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aggtggcagc	agggtgacct	tgaactcccc	aaatggggag	tgatgccact	ggggaaactg	900
agtggatcaa	agagatgaaa	ccaaaaaana	agcaaacaaa	caaatgagaa	gacacaaaac	960
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<210> 10

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-441-343 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-441-343.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-441-343.mis2, potential complement

<220>

<221> primer_bind

<222> 826..844

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 394..413
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-441-343 potential probe

<220>
 <221> misc_feature
 <222> 3,771
 <223> n=a, g, c or t

<400> 10
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 gacaatgcct gaaatgcaaa ggcgacactg gagtcttctt tctctaactg tagcggtga 180
 atgaatatct gcctggaacc aagagggctg ctctgatgtt tgggagtcgg ttttttgtga 240
 gccacatctg atatttctga tatccccagg aaggagtgcc ctggaggtca ctggttcagg 300
 ctccctttgg gcgaaatcct gggagtgatg ctctaaaaat ccacctttcc catcatccct 360
 actcatcaga aagacaaata taaaatccca gagaggtgga ggagctaaaa aagcaattgc 420
 tocaccttac aaatttggat agaaaggaga tgtagtttat ttcatatggg caaagtagtc 480
 ctcttccaaa gtcctgtaca rttgttctct gcaattgacg cacatctgcc ctaagcgaaa 540
 tctgtcagaa ggaatcaaca aggtctcctg cctccccctc caatccccct tttggaggac 600
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 cctccgtgtc ctagacgctg gctgccttct gtgcactccc aggcagatca ctacggaaga 720
 gtcggagcct gtgggggttg actggccaca ctacgtctg agaaggcgag ntggccatgg 780
 aaagctgggg gcagaggtgt ttttgagag gaggcggcag gcaaacattg cctttgactt 840
 gctctccgcg taccgggggt tgtagagctg ctacaggaag ggcaggatgt aaggccagag 900
 gtgectgtg ggtgagaagc ccaggcagg gctgggcgcc ctctccgaag aggtggcagc 960
 aggggtgacct tgaactcccc aaatggggag tgatgccact g 1001

<210> 11
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-442-221 : polymorphic base T or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-442-221.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-442-221.mis2, potential complement

<220>
 <221> primer_bind
 <222> 704..721
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 270..289
 <223> downstream amplification primer

<220>

11

<221> misc_binding
 <222> 489..513
 <223> 12-442-221 potential probe

<220>
 <221> misc_feature
 <222> 180,531..532,822
 <223> n=a, g, c or t

<400> 11
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 agaggacata aacactgatt ttttcccccc attcatttaa ctatttgcac acagagacan 180
 gaagccagaa atctgactgg gaagaaattc ctaccctttt gccagcatgc taagcttctg 240
 gggtctcttt ccctgagtgg ccctagtgat ctggcttctg gcacaactgc ctttgggggc 300
 caagccgcat cataaaggaa aagtatttct ttttgttctg gccaaagcaa aatacgcgta 360
 ataaaacata gatattaacc aggtgctta gcatccaata tcaaactggc aaggcttaaa 420
 tttgccctca ggtgggccct gtcattctta atctaacctc cgactaggag tttcaacatg 480
 tgggtctctgg gcaagatggt ygccctgagt aatagaaaag aaagagaaaag nngagagaga 540
 gaaaaacatt gcctgtggca gggcggggaa ggtgaaatga tcagggaggc agagaaagaa 600
 ccaccattg cagcgacact aaaaagtcca ggtggctgct gtcggtggag caaggatctt 660
 ttccagtta cctaccagct ctcaaatttc cttgttagg gaggaagaaag ctcccatgt 720
 cccaggatcc tgtacattcc taattctgtc acccatagcc atcagcaaag tacaagggag 780
 attaatccaa agagaatagc agttaacatc ccatagtgcc gnaacctgtt cttagccgag 840
 agggacttta ccgaagaggg gcctctaacc cgctaaatct tagaagggac tctaactctc 900
 ctaagtcggg cctctaacca gaggtcagtc aagcatcctt gccttttatt aagggggagc 960
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<210> 12
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-447-58 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-447-58.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-447-58.mis2, potential complement

<220>
 <221> primer_bind
 <222> 444..462
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 874..893
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-447-58 potential probe

12

<220>
 <221> misc_feature
 <222> 44,894
 <223> n=a, g, c or t

<400> 12
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 tggagtgcag tggcatgata ttagcttatt gcagctttga tctcccaggg tcaaacgata 180
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 ttttttattt tttgtagaga tagagttttg ccatgttgcc taggctgggt tcaaactcct 300
 ggactcaagt tatctgcccc ccttggcctc ccaaggtgct gggattacaa acgttagcca 360
 ctgccccag ctgtctccat tttttaaatt aaaatacata atgttctagt aaatattctt 420
 gtgggcaatt cattggacct gtcttagatt acatgcccag agtaaattct agaaatgaaa 480
 ttcttggtct tctccgaaga sggaattgag tggggaaaaa aaagaaaatg aaaaaagaaa 540
 taaacacaag atattcttgg tcaaatttg tctgccctt ctctccagt gagctacgat 600
 gaagccacag taatccacat tcccagggga acacaggtgg tctgcctctc catgtgctca 660
 gagtgccaat tcttggttaag gagatataag gactggagtg aaacattgga ataatgactc 720
 atattcatgt tttataaaca aatttaaaat attggatcag gttatttatc tggaaaccct 780
 gaagtttggc tgtttaaagg gctattttta atataggcaa cagaaaacaa aatacaaagt 840
 cttatttctg acactttaaa atgttggtgca agtgtcttcc ttgttagtat ggtnggtgag 900
 tatccccacc tgtcataaaa tggcaaata gctgggtgca gtggctcatg cctgtaatcc 960
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<210> 13
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-453-429 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-453-429.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-453-429.mis2, complement

<220>
 <221> primer_bind
 <222> 73..91
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 577..596
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-453-429 potential probe

<400> 13
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 cagtgtctgc tacaagtgc atcaagtagc atctatcaag tggcattact ttaacaaata 180

13

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ataaggtaaa	cggatgatgt	tgccacacta	gtggtagagg	tttcatagtt	ttacccaaac	300
cagtttttat	ttttagtgct	tggttggggg	cactgaaact	tccaggttgt	cctaacctgt	360
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acaaaaaaca	gggtagaagg	taataacaca	tgcaaaggga	tgtgtagcaa	tcaaagggaa	480
atgttatcct	tcctaggaga	yaggatttat	gggattcctg	gatctttttt	gtgtctgatt	540
gttaagggtct	tgacagcctt	tcaattgagg	aatacggctg	tgtctgttaa	actaatgtta	600
gctgttcact	ccactatata	attttacaac	atttcagctt	caaatagaat	ggcttcaata	660
aacataaagc	agactgacac	atcccagatt	tctgcagttt	attttacacc	aagaaattac	720
atntagagat	ttccagacac	atactataaa	tgaaaattca	acaggaagtt	tctttcattt	780
cctctagatc	tgacctatat	ttcaaaaata	tatgagtggg	ctataaccag	gaacttcttc	840
tcttgctccc	attattcaca	ccgttttctg	aagagttttt	ttctcgccg	cgactctaatt	900
ggccattaag	ggaattgcag	acattggaag	actatacaac	cctaagttaa	atgagtgaat	960
tgataaatgt	tatccacaag	atggccaaat	tgtatggttc	t		1001

<210> 14

<211> 929

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-454-363 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-454-363.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-454-363.mis2, potential complement

<220>

<221> primer_bind

<222> 139..158

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 634..652

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-454-363 potential probe

<220>

<221> misc_feature

<222> 674..679,881..882,892..893

<223> n=a, g, c or t

<400> 14

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aatattggcc	tccctggctg	gggagttgtg	tggttttctt	ttccaggcag	ttgaggtttt	180
ccatggagcc	tactctacag	tgtcagcagg	agtataacat	agaaggcttc	caggtcaggt	240
ggcccagagt	caaatcaaag	ccccatccct	ttttagcaaa	tttctcagcc	ttacttagct	300
gtgccggcct	gcctctttct	aaaatgagga	aaataataat	acccacttca	ctggtttatt	360
gagaggatta	aatgaggaca	tgtgttattt	cacaccatta	ttgcttctgt	tgttattatt	420

14

ttaaaatcta ggttggtgat tgcatacagtt tcttagggct gctctaaaga aagtaccaca	480
agctgagtga cttacatagc rgaaaagtgt tttcttacag gttaagagggc tggaaagtctg	540
aaatcaaggt gtcagcaggg ccatgctccc actgaaaccc atagcgggga atcctttctt	600
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cttcttcttt cttnnnnnnc ttcttcttct tcttcttctt cttcttcttc ttcttcttct	720
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<210> 15

<211> 827

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-455-326 : polymorphic base T or C

<220>

<221> misc_binding

<222> 502..520

<223> 12-455-326.mis1, complement

<220>

<221> misc_binding

<222> 481..500

<223> 12-455-326.mis2, potential

<220>

<221> primer_bind

<222> 808..826

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 372..392

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-455-326 potential probe

<220>

<221> misc_feature

<222> 798..799

<223> n=a, g, c or t

<400> 15

ttcataagcc gtaatatctt tagcttgaag aaaaaataa taattcagag aactctgttt	60
cttagaggaa attgacagga agaggaattg agaagaattc tatagaatgg gtaatgaaca	120
atggatcagg aacaatagca gaataataag gcttgcagaa ctacctggaa acctgaactc	180
tgggtcacac acaggggtgca aacttaagaa aactccccac agctttttaa acagctcagg	240
aaatctgtga gttaaaggaa agcctaacac aaatacagct ttaccttaag catctttgtc	300
caccctcgcc ctataattcc tcagctttga gagaaagcct tccttcgaga ctgctactgt	360
agatttcaat ttgttttgtt tttagagatg ccataacctg acttagcatt atcctagggg	420
aaggcctgag gctgtccaca agagatcccc aggcggcttc tgtgagggtc tgcacagaga	480
atcttgaca gcaggctctt ycttatagga ggtgtgaggt tgtcatataa agctgaaggg	540
ccaacataag tctgcctcac agttatcctt ctagaatatt cctgataggg tcagaatttt	600
atgaattttt tcttaaagaa atagagacgg ggtcgcaacta tgttgaccag gctgggtctg	660
aacttctggc ctcaagcgat cctcccatct cagcctccca aagtgctagg attacagatg	720

15

tgagccacca cgccctgccga gaattttgca aatttactaa gcatccacca ccgtgtatcc 780
tgtgtaggac acggggccnng ggaggtccct attaaccaag atagcag 827

<210> 16
<211> 884
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-455-383 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-455-383.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-455-383.mis2, potential complement

<220>
<221> primer_bind
<222> 865..883
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 429..449
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-455-383 potential probe

<220>
<221> misc_feature
<222> 855..856
<223> n=a, g, c or t

<400> 16
tgatttctgg tacaggggtc tgtgtaatca gcacatggcg gggactgtct cacatgcttc 60
ataagccgta atatttctag cttgaagaaa aaaataataa ttcagagAAC tctgtttctt 120
agaggaaatt gacaggaaga ggaattgaga agaattctat agaattgggt atgaacaatg 180
gatcaggaac aatagcagaa taataaggcc tgcagaacta cctggaaacc tgaactctgg 240
gtcacacaca gggtgcaaac ttaagaaaac tccccacagc ttttaaaaca gctcaggaaa 300
tctgtgagtt aaaggaaagc ctaacacaaa tacagcttta ccttaagcat ctttgtccac 360
cctcgcccta taattcctca gctttgagag aaagccttcc ctgcagactg ctactgtaga 420
tttcaatttg ttttgttttt agagatgccc atacctgact tagcattatc ctagggaaaag 480
gcctgaggct gtccacaaga ratccccagg cggcttctgt gagggctctg acagagaatc 540
ttgcacagca ggctctttct tataggaggt gtgaggtgtg catataaagc tgaaggccca 600
acataagtct gcctcacagt tatccttcta gaatatccct gatagggtca gaattttatg 660
aattttttct taaagaaata gagacggggc cgcactatgt tgaccaggct ggtctcgaac 720
ttctggcctc aagcgatcct cccatctcag cctcccaaag tgctaggatt acagatgtga 780
gccaccacgc cctgccagaa ttttgcaaat ttactaagca tccaccaccg tgtatcctgt 840
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<210> 17
<211> 1001
<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-456-269 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-456-269.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-456-269.mis2, potential complement

<220>

<221> primer_bind

<222> 233..252

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 693..712

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-456-269 potential probe

<220>

<221> misc_feature

<222> 20,447

<223> n=a, g, c or t

<400> 17

catatttcata gcttttttan tttattaaat atcaccattg ggttgactca gtagcatctc	60
atatacctac ctgatgggct gcagcagata ttggcactca gacaagccaa ttttaggcac	120
cagagccctg tagccgtggt aacctcaccc ctgtgctgga cgggaggcag gtcggctaag	180
cagaggtgct ggaagtgtgt gtggtaccag gactgggccg caggagctgc acagcctcac	240
agcacattag ccaatggccc catgccaaac cccttggtcg ggttttctgg aacaggtacc	300
tccttaccat tccaagaaaa agtctcctcc tgccccccaa aagtgggggg caggatgatcc	360
aaaagatcac taagcaaatg cctgtttgtc ctttgaata ctcaaccctg atcagtgggtg	420
aatactcagt caccaactat gtggaangag gcacaacccat ggcagacaac agatatggaa	480
agagcaggaa ttcttctagc rggaattctt atatcaaatg caatgggtggc catgccccca	540
acagctctgc agttggaaaa atgaagcctt caagtaaggc caaagtccta ctgtttgagg	600
gcaattcatc tgggccaaat ccctcaggag cagggccatg cgggggttac aactgttcat	660
gcaacacaac agattgggct taagctggcc agggcagtga cgggcttttc atcttaattg	720
tagttgtctg tgtcccaaga aaatgttate agcttttcag aaaaactttc aagagactcg	780
agcaagtcaa acccaagctg ccctccttgt ctgcatatcc tgctctgttt tcccatttgg	840
gaaatgaaac cagcagcagc tgagagggag aaggttctac actcactggt tttctccact	900
cctaccactc cctccttccc cctcctctct gtcacctga agaaatctcc ttctggaata	960
aggtgtcatt catccttgct acctccagta tagttatgct a	1001

<210> 18

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501
 <223> 12-456-380 : polymorphic base G or T

 <220>
 <221> misc_binding
 <222> 481..500
 <223> 12-456-380.mis1, potential

 <220>
 <221> misc_binding
 <222> 502..521
 <223> 12-456-380.mis2, potential complement

 <220>
 <221> primer_bind
 <222> 122..141
 <223> upstream amplification primer

 <220>
 <221> primer_bind
 <222> 582..601
 <223> downstream amplification primer, complement

 <220>
 <221> misc_binding
 <222> 489..513
 <223> 12-456-380 potential probe

 <220>
 <221> misc_feature
 <222> 336
 <223> n=a, g, c or t

<400> 18
 tttaggcatc agagccctgt agccgtggta acctcacccc tgtgctggac gggaggcagg 60
 tcggctaagc agaggtgctg gaagtgtgtg tggtagcagg actgggcccgc aggagctgca 120
 cagcctcaca gcacattagc caatggcccc atgccaaccc ccttggctgg gttttctgga 180
 acaggtacct ccttaccatt ccaagaaaaa gtctcctcct gcccccaaa agtggggggc 240
 aggtgatcca aaagatcact aagcaaatgc ctgtttgtcc tttggaatac tcaaccctga 300
 tcagtgggtga atactcagtc accaactatg tggaangagg cacaaccatg gcagacaaca 360
 gatattggaaa gagcaggaat tcttctagca ggaattctta tatcaaatgc aatggtggcc 420
 atgcccccaa cagctctgca gttggaaaaa tgaagccttc aagtaaggcc aaagtcctac 480
 tgtttgaggg caattcatct kggccaaatc cctcaggagc agggccatgc ggggggttaca 540
 actgttcatg caacacaaca gattgggctt aagctggcca gggcagtgac gggcttttca 600
 tcttaattgt agttgtctgt gtcccaagaa aatgttatca gcttttcaga aaaactttca 660
 agagactcga gcaagtcaaa cccaagctgc cctccttgct tgcataatcct gctctgtttt 720
 cccatttggg aaatgaaacc agcagcagct gagagggaga aggttctaca ctactgggtt 780
 ttctccactc ctaccactcc ctcttccccc ctctctctg tcaccctgaa gaaatctcct 840
 tctggaataa ggtgtcattc atccttgctc cctccagtat agttatgtca gatgcagtga 900
 ggtgctggat ttagattaca agaagcggga ggattcttgc aaagagagga caacatttgc 960
 ttaactatgc caagggtccc cttgtccccc gaccaagagg g 1001

<210> 19
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-457-204 : polymorphic base A or G

 <220>

18

<221> misc_binding
 <222> 481..500
 <223> 12-457-204.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-457-204.mis2, potential complement

<220>
 <221> primer_bind
 <222> 298..317
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 772..792
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-457-204 potential probe

<400> 19
 ttgagggcaa ttcattctggg ccaaattccct caggagcagg gccatgcggg gggtacaact 60
 gttcatgcaa cacaacagat tgggcttaag ctggccaggg cagtgcaggg cttttcatct 120
 taattgtagt tgtctgtgtc ccaagaaaat gttatcagct tttcagaaaa actttcaaga 180
 gactcgagca agtcaaacc cagctgccct ccttgtctgc atatcctgct ctgttttccc 240
 atttgggaaa tgaaaccagc agcagctgag agggagaagg ttctacactc actgggtttc 300
 tccactccta ccactccctc cttccccctc ctctctgtca ccctgaagaa atctccttct 360
 ggaataagggt gtcattcatc cttgtcacct ccagtatagt tatgtcagat gcagtgaggt 420
 gctggattta gattacaaga agcgggagga ttcttgcaaa gagaggacaa catttgctta 480
 actatgccaa ggggtcccctt rtcccccgac caagagggcc ttcattgctcc ctcagcttga 540
 ctgaacttta ggcaggattc ttctaacct ccctttttt tttagagcat ttcttgctat 600
 tgtacatttt ttctctgccc ctttgagatg tatgtaaatc tcttcaaaaag cctcctgcca 660
 gttttacaat ccaggaatgt ctttctcaag gacctgggag ccctcccttt gaaatgtaat 720
 catcaaagga gatggcaccc ctgtctccca gtcttctgtg agagtttttg tgggagtcta 780
 acttcagcag gacaccttcc tccaagtcac aaaaccatcc cttgtcaaaa gatagaagtt 840
 tattagcaaa cacaaatggc ctacgacctc ttcacaacat cctctggcat gtttcactag 900
 cctttaaaag cctttaaaaa ctttgaccc tctgcatcag cagcattgag ttcacactga 960
 gttctagtcc ctctctctctg ttgcaataac ttcggaataa c 1001

<210> 20
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-457-206 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-457-206.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-457-206.mis2, potential complement

<220>
 <221> primer_bind
 <222> 296..315
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 770..790
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-457-206 potential probe

<400> 20
 gagggcaatt catctggggc aaatccctca ggagcagggc catgcggggg ttacaactgt 60
 tcatgcaaca caacagattg ggcttaagct ggccagggca gtgacgggct tttcatctta 120
 attgtagttg tctgtgtccc aagaaaatgt tatcagcttt tcagaaaaac tttcaagaga 180
 ctcgagcaag tcaaacccaa gctgccctcc ttgtctgcat atcctgctct gttttcccat 240
 ttgggaaatg aaaccagcag cagctgagag ggagaagggt ctacactcac tggttttctc 300
 cactcctacc actccctcct tccccctcct ctctgtcacc ctgaagaaat ctccttcttg 360
 aataagggtg cattcatcct tgtcacctcc agtatagtta tgtcagatgc agtgagggtg 420
 tggattttaga ttacaagaag cgggaggatt cttgcaaaga gaggacaaca tttgcttaac 480
 tatgccaaag gtccccttgt yccccgacca agagggcctt catgctccct cagcttgact 540
 gaacttttagg caggattctt cctaacctcc cttttttttt tagagcattt cttgtcattg 600
 tacatttttt ctctgcccct ttgagatgta tgtaaattct ttcaaaagcc tcctgccagt 660
 tttacaatcc aggaatgtct ttctcaagga cctgggagcc ctccctttga aatgtaatca 720
 tcaaaggaga tggcacccct gtctcccagt ctttgtggag agtttttgtg ggagtctaac 780
 ttcagcagga caccttcttc caagtcataa aaccatccct tgtcaaaaga tagaagttta 840
 ttagcaaaaca caaatggcct acgacctctt cacaacatcc tctggcatgt ttcactagcc 900
 tttaaaagcc tttaaaaact ttgcaccctc tgcatacagc gcattgagtt cacactgagt 960
 tctagtcctt ctctcctgtt gcaataactt cggataaact t 1001

<210> 21
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-458-196 : polymorphic base T or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-458-196.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-458-196.mis2, potential complement

<220>
 <221> primer_bind
 <222> 679..696
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 200..217
 <223> downstream amplification primer

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<220>
<221> misc_binding
<222> 489..513
<223> 12-458-196 potential probe

<220>
<221> misc_feature
<222> 33,792
<223> n=a, g, c or t

<400> 21
ctgctgcaac cactacaaga caggaagaag ggnaagggaa gggaagctga gtgctcaggg      60
catgctgtgg agggaaggcg agggcacttc ccgccgtcat ctccagaacc gccacagcct      120
tgggaggggg gctgagagag atcagtgtctg actgcctgag aagaggcctt ccacaagctg      180
cctttctggt gtcccatgtt tcttccttcc ttccttccag aggccgtgag agggagggcc      240
cgtgtcagcc tgctctgccg gtttcccgac tgctgaacct gtctgtggga agctgggttt      300
gactatgtga tgctgaggct ctgagaggag ggctaccctt tccccaccc tcggccccc      360
ttcctatgag tagaagcctg ccagctgcg gtggtggggt ttgaggaggc taggacttag      420
agcagggaaa aacaagggaag cagaatgaaa aacagaaaca cttagaaatc tgggattggt      480
acttctcctt atgtaaagat wgtggctgac gaccagcttc ttagaggaag caagtctagg      540
agaagggtc atacctggc cgtgagggcc tatgggggat cagggcataa gaccacctga      600
ccctgggcct tgcattccaca agaaccttga gtttagattt ttagacatat tctttgaaca      660
agggtttaca tatatagtca ctgagaaatc ctgagaggat tgaaaaatag catctatttt      720
acagctttaa attgtgccct gagctgagcg tgggtggctca tgcctgtaat ccagcactt      780
tgggaggctg anggtgggag gattgcttga gttcagttca ggaccagcct gggcaacagc      840
aagacctcat ctctactaaa aataaaaaaa ttagctgggc atggtggtgt gcacctgtag      900
tcccaattac tcaggaggct gaggtgggag gattgcttga gcctgggagg ttgaggctgc      960
agtgaactgt gattgtgccca ctgcactcca gcttgggtga c                                     1001

<210> 22
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-458-438 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-458-438.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-458-438.mis2, potential complement

<220>
<221> primer_bind
<222> 921..938
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 442..459
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513

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<223> 12-458-438 potential probe

<220>
<221> misc_feature
<222> 275
<223> n=a, g, c or t

<400> 22
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tcctgagcta ctgtttcccc caaccgagc ctttctctct tattgtaccc accctttctg      120
atgaagtcac caaagcaaag attgcataac tgatgcatag gcctatcttg tgttatactg      180
ggagacaggc caatgtttcc attaatagac aagagcacca ccacgctgcc aaatggagct      240
ctctgctgca accactacaa gacaggaaga agggnaaggg aagggagct gagtgctcag      300
ggcatgctgt ggagggaaag cgagggcact tcccgcctgc atctccagaa ccgccacagc      360
cttgggaggg gggctgagag agatcagctg tgactgcctg agaagaggcc ttccacaagc      420
tgcctttctg gtgtcccat gttcttcctt ccttccttcc agaggccgtg agagggaggg      480
cccggtgcag cctgctctgc yggtttccg actgctgaac ctgtctgtgg gaagctgggt      540
ttgactatgt gatgctgagg ctctgagagg agggctaccc ttttccccc cctcggcccc      600
cattcctatg agtagaagcc tgcccagctg cgggtggtggg gtttgaggag gctaggactt      660
agagcagggg aaaacaagga agcagaatga aaaacagaaa cacttagaaa tctgggattg      720
gtacttctcc ttatgtaaag attgtggctg acgaccagct tcttagagga agcaagtcta      780
ggagaagggc tcatacctgg tccgtgaggg cctatggggg atcagggcat aagaccacct      840
gacctggggc cttgcatcca caagaacctt gagtttagat ttttagacat attctttgaa      900
caagggttta catatatagt cactgagaaa tcctgagagg attgaaaaat agcatctatt      960
ttacagcttt aaattgtgcc ctgagctgag cgtggtggct c                                     1001

<210> 23
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-460-274 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-460-274.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-460-274.mis2, potential complement

<220>
<221> primer_bind
<222> 228..245
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 760..777
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-460-274 potential probe

<220>
<221> misc_feature

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<222> 873

<223> n=a, g, c or t

<400> 23

gacataattg	ccctctgcct	ccttaggaaa	acaccagacc	tctgagaagg	aggtgattaa	60
accgttcagt	cacttgacaa	agataatcta	attaattaat	gaaaggattt	aacacccatg	120
tctggagcat	ttgcaatgtg	ctagacaccc	ttctgcatat	gccgtgacag	ctctgacatg	180
acaaacaagg	cctgtggaga	aacgcagact	aggtaacaga	ataaacaaga	atgtgtaagg	240
tgggtgacaaa	tgctatgatg	aaaattaaca	aaggggaagta	ttaaaccaga	gaagtattca	300
atagaagtgt	ggctgggtag	ctacccttgg	ttgggtggcc	aggggaagaca	tctttgagga	360
agtgactttt	atgctgagac	caaaaaccag	ctaagagaag	ataaggggag	gggaatccca	420
ggtaaggagg	aactgtgaat	gcaaagggtcc	cgaggtagga	cagaacaaaa	tgcaaaggcc	480
ctgaggtagg	atagaacaaa	rcagtctcgg	cctcccaaag	tgctaggatt	acaggcatga	540
gccaccactc	ctggctacac	tggaaggctt	taagcagggc	aaagccttat	gtgatctgac	600
ttgaaaggcc	actctcctac	ccatgaagaa	caggcaagag	tagaggcaga	agcacaaatg	660
aattgatga	cagcagggat	gctgggtggcc	actatgtagt	gtacactcaa	ccgtgtgcct	720
ggagctcctt	aaagcccttt	atctgcatta	tccattaatc	cacacaacct	ctctatagag	780
taatttctag	aatttccata	ttacatatac	agaaaataaa	gtctagaaaa	gtaatgtgcc	840
tccagctggg	aagggttttt	tttttttaac	aancctcttt	ttataactat	ataagtcaat	900
aatagtcatc	ataagaaaca	ttttttaatg	agcaaaaaga	aaaaattaaa	tcacttgaga	960
tcacatcatc	ctgtgataat	tactattaac	attttggtct	a		1001

<210> 24

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-461-124 : polymorphic base A or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-461-124.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-461-124.mis2, potential complement

<220>

<221> primer_bind

<222> 378..396

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 911..928

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-461-124 potential probe

<220>

<221> misc_feature

<222> 850

<223> n=a, g, c or t

<400> 24

23

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aatggaaatt tatttaaatt tctgtgact attaggctct gagggtttta aaatttttact    60
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tatatacatt ttgtgaaatc attattttta aaagtaaaat tttattgaaa atatatctta    180
ataagatagg actagttttt cttccaaata cttcttggtg tgtttttttg tttgtttgct    240
ttttggttaa tatttctaatt tactagaatg agacagggtt ctatatgaat tctattccta    300
cttttatttt ttatagacac aagcaaggaa tattgttgac ataagtagaa atgaatcttg    360
taattgcaat tttacttaatt tttctgaatg cttccaagt tctcaatcaa caatcacagt    420
gatctgacat ccaaaattat ttttaaaatg ttgatactac cagctaaaaa cttgatgaga    480
ttctccttta atacagttga magcagagaa ttgaaaacca cctggcttgc aaaaaggctc    540
gttaccctaaa catttgagtc attgtctatt tcactattaa catcattatt tcaaattctc    600
ctttggttgc tgcactggag gttttgcttt atttggttgc tgggttgggg tttttgttgt    660
tgtgtgtgtt ttctgtcttt ttaactatat aggacagggg ttggcaaact aaggccagtt    720
tgtactgac aaatcttgcc tagcttgctt tcatgcagcc ctcagggtta gaatggtttt    780
catatttttg gtttggtttt ttttttaaaa ggaagtacta cttcttattg atcaaataaa    840
ttctgctttn cttattatca ttattttgta ttgctcaag gaaagctact taaagactaa    900
gtaagaaca gaggttgggag aggtaaagta ccaacttctt gaccacatgt aaggagttct    960
tagactggcc ttcctgtgtg tatacttagg tctcaattca c                               1001

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<210> 25

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-461-299 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-461-299.mis1, potential

<220>

<221> misc_binding

<222> 502..520

<223> 12-461-299.mis2, complement

<220>

<221> primer_bind

<222> 203..221

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 736..753

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-461-299 potential probe

<220>

<221> misc_feature

<222> 675,831,997

<223> n=a, g, c or t

<400> 25

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tcttaataag ataggactag tttttcttcc aaatacttct tgggtgtgtt ttttgtttgt    60
ttgctttttg gttaatatct ctaattacta gaatgagaca gggttctata tgaattctat    120
tctacttttt attttttata gacacaagca aggaatatgt ttgacataag tagaaatgaa    180
tcttgtaatt gcaattttac ttaattttct gaatgccttc caagttctca atcaacaatc    240

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24

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acagtgatct gacatccaaa attattttta aaatgttgat actaccagct aaaaacttga 300
tgagattctc ctttaataca gttgaaagca gagaattaga aaccacctgg cttgcaaaaa 360
ggtctgttac ccaaacatct gagtcattgt ctatttcact attaacatca ttatttcaaa 420
ttctcctttg gttgctgcac tggaggtttt gctttatttg tttgctggtt tgggggtttt 480
gttggtgttg ttgttttctg yctttttaac tatataggac aggggttggc aaactaaggc 540
cagtttgtac tgatcaaata ttgcctagct tgctttcatg cagccctcag gttaagaatg 600
gttttcatat ttttggtttg tttttttttt taaaaggaag tactacttct tattgatcaa 660
ataaattctg ctttncttat tatcattatt ttgtatttgc tcaaggaaag ctacttaaag 720
actaagtaaa gaacagagtt gggagaggta aagtaccaac ttcttgacca catgtaagga 780
gttcttagac tggccttcct gtgtgtatac ttaggtctca attcaccacc natgataagg 840
cctgcttttg catatactct aaactcaggg atgatctcaa aattatatct tctttttttt 900
tttttttgag acggagtcct actctgtcac ccaggctgga gtgcagtggg gtgatctcag 960
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<210> 26

<211> 985

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-461-465 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-461-465.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-461-465.mis2, potential complement

<220>

<221> primer_bind

<222> 37..55

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 570..587

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-461-465 potential probe

<220>

<221> misc_feature

<222> 509,665,831

<223> n=a, g, c or t

<400> 26

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taagtagaaa tgaatcttgt aattgcaatt ttacttaatt ttctgaatgc cttccaagtt 60
ctcaatcaac aatcacagtg atctgacatc caaaattatt tttaaaatgt tgatactacc 120
agctaaaaac ttgatgagat tctcctttta tacagttgaa agcagagaat tagaaaccac 180
ctggcttgca aaaaggctctg ttacccaaac atttgagtca ttgtctatct cactattaac 240
atcattatct caaattctcc tttggttgct gcactggagg ttttgcttta ttgtttgct 300
ggtttggggg ttttgtgtgt gttgtgtgtt tctgtctttt taactatata ggacaggggt 360
tggcaaaacta aggcagttt gtactgatca aatcttgctt agcttgcttt catgcagccc 420
tcaggttaag aatgggtttt atatttttgg tttgtttttt tttttaaaag gaagtactac 480

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25

ttcttattga	tcaaataaat	yctgctttnc	ttattatcat	tattttgtat	ttgctcaagg	540
aaagctactt	aaagactaag	taaagaacag	agttgggaga	ggtaaagtac	caacttcttg	600
accacatgta	aggagtctt	agactggcct	tcctgtgtgt	atacttaggt	ctcaattcac	660
caccnatgat	aaggcctgct	ttggcatata	ctctaaactc	agggatgata	tcaaaattat	720
atcttctttt	tttttttttt	tgagacggag	tctcactctg	tcacccaggc	tggagtgcag	780
tggtgtgata	tcagctcact	gcaagctccc	cctcccgggt	tcatgccatt	ntcctacct	840
cagcctcccg	agtagctggg	actacaggca	cctgccacca	tacctggcta	atttttttgt	900
atttttagta	gagacggggg	ttcactgtgt	tagccaggat	ggtctcgata	tcctgacctc	960
gtgatccgcc	cgctcgggcc	tccca				985

<210> 27

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-462-280 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-462-280.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-462-280.mis2, potential complement

<220>

<221> primer_bind

<222> 222..241

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 655..675

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-462-280 potential probe

<220>

<221> misc_feature

<222> 174

<223> n=a, g, c or t

<400> 27

agggttgctc	aggccagtga	tgtttgcaat	gcaaacccaa	gaattctgaa	aggagcccat	60
ggctgaaagg	agccaattct	tccaggacgg	actactccag	ttgcaactgt	gctgtggagg	120
ctgaggagca	tccatgactg	aggaaggggc	agtcccctat	aatgcccttg	ctanggggag	180
catcagacat	ccctagactt	acaagtccct	cgtgtaataa	ggtgaactat	ggaaaagctat	240
gatttgagga	aagttccctc	tgattgaaag	agttcttcaa	atatgaagaa	tgtaacactt	300
atggggcacc	tactcattgc	aaaacactct	actaggggct	ttcacctgta	tgtttaactc	360
attttgttga	tttttttttt	tttaagccca	aatttctgag	aggttaagga	acttgtctgg	420
tggtggcgct	tctgggattc	tgacttttcc	actgaccata	acatgcatct	ggctctaaatt	480
gagcggacca	cccaggagga	yggtggaata	aaaagaaatg	ggaagggggg	ggggagagga	540
atgggcatag	aataaaaagg	tagaaaccct	tgggatcaaa	ggatgcaact	gaaagagcac	600
caaaatatgc	atcatttttt	ttaatatgtt	gtctgggtacc	caaaattggg	atgcctctgt	660
ggtatcaact	ttgacattta	aagaaagggc	ataagattag	atcattcaac	cataagtggg	720

26

aggaagaaac	aaaataaaat	aaaaccttac	aattcccttt	gaagttgatc	aggtgtcaag	780
gcagtgattt	ggttttcttt	tacaaacttt	ctttttccag	aaaaattttt	actgtgggtt	840
tggagaggtg	tttacaataa	attcatagca	gagctccaaa	agggcccacc	ccatctaata	900
tcctctgtct	cagcagatta	ttgaagaaga	ttggattaaa	aggtttgttt	tgtgatgtgt	960
gatggttggt	tccccaagat	gattgagttt	gaggcagagt	t		1001

<210> 28

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-464-66 : polymorphic. base G or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-464-66.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-464-66.mis2, potential complement

<220>

<221> primer_bind

<222> 436..455

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 880..900

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-464-66 potential probe

<220>

<221> misc_feature

<222> 121,163..164

<223> n=a, g, c or t

<400> 28

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gggccatttc	catagctggt	gaagaaattt	tctttccac	agtcttctc	ctctcttttt	120
ncatactttt	ccctcttttg	ctttctggcc	atatgccttc	ttnttgctt	tcctccctt	180
ccacctctaa	ctcacagcaa	ttctcttccc	tctaccaacc	agcctgttcc	aaaaaaaaa	240
aaaaaaaaaa	aaaagggtccc	cttttattcc	ttagggtagc	acttggtttt	gttttttaac	300
atccaaatcc	ttcttgagc	cccttcgtat	tctctctctg	aggaagacgg	agggggcttc	360
cctcatcctc	cttggttacc	tagcaacttg	tcttcttcc	gacaagtcac	caccctgcca	420
ggatgccagc	tgatgcacac	acaataaagg	gaaagtgagc	agacaccacc	actccagtc	480
actcatagag	gacctctg	kcattagcac	tccgatgagt	ggcttgctat	gggcagggcc	540
cccagacgcc	tctccccag	taagctggcc	acactgctcc	tccagggatc	tcagagagat	600
ggcagcttgt	caagttcctg	agtcgctggg	tatgtactgg	gaatttcaga	tttaatccct	660
aattacatcc	agtcatcac	ctttgtaata	ggagccataa	tcattctttc	attgttgtct	720
ttgagtcact	ggggctgtgt	ggaacactat	atccatattc	atgcattgtt	tttctatttt	780
gctactacat	cctcttcctt	agacttcaaa	atgaaggggg	attttctttt	ctcctgcaaa	840
agcctttatg	aaagaagggtg	tttgcttaac	actttcaagc	ttccccattg	acatcctttg	900
ttctttctct	acacattcat	ggattaacta	ctttgggtcc	agccgtggta	accaacttca	960

27

atttgtcaca gaaaatgtag atgtttttag gtagggctta t

1001

<210> 29

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-465-26 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-465-26.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-465-26.mis2, potential complement

<220>

<221> primer_bind

<222> 476..493

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 945..962

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-465-26 potential probe

<220>

<221> misc_feature

<222> 556,630,796

<223> n=a, g, c or t

<400> 29

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ctttctactt tttaatgtgg ttaccagaaa atttttaatt acatattaat tagtgacttg      60
ctttgtggct tgcgttgat ttctattgaa cagtgcctgg ttagagttaa atgtttacta      120
gttcttttgt tctactaaat taccacaaaa cttcctgctt catttgattt tatgaggtat      180
atgagttgtg gaacgtggac tggtttgaaa gcaatatctt tgcacagaca aattctaggg      240
ttggcttttt gcatactata ataactctag acaaatcatg gaaattgtga cttcccagg      300
aagatgggga ctgggggggag tgaagtatgg aggaagggaa aggaggcttg gagaggaaag      360
gaagaaggcc atatactcca gaggcgatag gatcactgaa aaaaactaaa tgtgtggctt      420
gcaagaagag gaggtggcct ctttctaaga tgtcccttgt cattctgaag aagacttcct      480
cccaaacc aa ctctttccca ytgggcagtc agcttgatct cttgaggttg aggaaggccc      540
tgctattaat tgccntagg agaaagagca tatccactga gctatgagtc aatgatctgt      600
cttaggggtg gattttattt ttctattatn ttgtgtgttt gattttcttg ttagagttct      660
ttccttagga ctggttggtg cttttaacga ggtggtaggg ggtggtagtg tgctgagcag      720
agcagtgcgt atgctgacaa caacaccaca gcaaacagca aacaggacat gcaaagcagg      780
aggcaaacct gtcttnccca accaacattt agctgaggac tagtcagggt gtgtggctat      840
tatgttctag tagctaggag agtcccagca tgtgctctta gaggccattt tggagagggg      900
gaaatagaga aactagaaac attattcatc tcagagactc tctggacctg agagagaaca      960
gtaactgtat tcaggcctaa tccctcagat ggctgccttg g                                1001

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<210> 30

<211> 1001

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<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-465-234 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-465-234.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-465-234.mis2, potential complement

<220>
<221> primer_bind
<222> 266..283
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 735..752
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-465-234 potential probe

<220>
<221> misc_feature
<222> 346,420,586,869..870,876..877
<223> n=a, g, c or t

<400> 30
gcaatatttc tgcacagaca aattctaggg ttggcttttt gcatactata ataactctag      60
acaaatcatg gaaattgtga cttccccagg aagatgggga ctgggggggag tgaagtatgg      120
aggaagggaaggaggccttg gagaggaaag gaagaaggcc atatactcca gaggcgatag      180
gatcactgaa aaaaactaaa tgtgtggcctt gcaagaagag gaggtggcct ctttctaaga      240
tgtcccttgt cattctgaag aagacttcct cccaaaccaa ctctttccca ttgggcagtc      300
agcttgatct cttgagggtg aggaaggccc tgctattaat tgccntagg agaaagagca      360
tatccactga gctatgagtc aatgatctgt cttaggggtg gatttattat ttccattatn      420
ttgtgtgttt gattttcttg ttagagttct ttccttagga ctgtttgttg cttttaacga      480
ggtggatggg ggtggtagtg kgctgagcag agcagtgtct atgctgacaa caacaccaca      540
gcaaacagca aacaggacat gcaaagcagg aggcaaactc gtcttnccca accaacattt      600
agctgaggac tagtcagggt gtgtggctat tatgttctag tagctaggag agtcccagca      660
tgtgtcttta gaggccattt tggagagggt gaaatagaga aactagaaac attattcatc      720
tcagagactc tctggacctg agagagaaca gtaactgtat tcaggcctaa tccctcagat      780
ggctgccttg gcggccactc tctttaccat gaaaattgcc cccagatgg aaacctcttg      840
aacttgga aaacctcttta tttccaaann cagaannaaa aaaaaatcac tatgtatttc      900
ttcttaagaa aaaaaaattg ttattcaact actgtgtccc attttcccaa taaacattaa      960
ttgaactgct agtgggcacc attcatccat ttaacaaata c                                1001

<210> 31
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>

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<221> allele
<222> 501
<223> 10-428-219 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-428-219.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-428-219.mis2, potential complement

<220>
<221> primer_bind
<222> 278..295
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 613..632
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-428-219 potential probe

<220>
<221> misc_feature
<222> 203,238,334,348,369,374..376,645,675
<223> n=a, g, c or t

<400> 31
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cacaataatt tctctaaatt ctttcagcta gtcagtgggt tgttgagcta gaatctgagg      120
aatccagatc ccatcctttc attgattatg tcactaagat aagtcacaga atcttctttt      180
agggaagttt tcaagaatag tangtaagct gctatcttaa aatattgatg tcagtagncc      240
tggaattttt accacgtatg caagcatggg ataagacaac cacaggtttc tcttctgtac      300
cagttaacct gttttatgat tatttcaagt tgtngaataa aagcttgnaa aattggcagg      360
atctgtttng aggnnnttac tcaaggatat ttattacttg tttcaggaac agcatctgtt      420
gcagttgcag gtctccttgc agctcttcga ataaccaaga acaaactgtc tgatcaaaca      480
atactattcc aaggagctgg rgaggatatt gccttggtga atacttatgt tctcctaaac      540
taacatataa ttagtggtta ttgctcatta actcaagatt tgacgtattc tttcaaattt      600
ttagtatatt atgactgtag gctttatgga agattcccaa attanagtac tgagacatat      660
taattattca taggnataat ttagtacaga agtaatgaga tattttttcac agttttaaat      720
ttgtgggtatt atcaaagtgt gccgtaggta ttgtttatgc atatctaagg tgccatacag      780
gaaaactttc caatgtatgt gtatatatgc aagcttttat gtatttaagc tggtttatct      840
gatactggct ttaggtatata tccagtgtta caaaaacaag tttttaaaat ttgactcaca      900
attcagtggt tatgtatgta actacatatg tgtttttaag aaaaaacatt ttgaattagg      960
gatttgtagt atattattac tgttcacatg caaaaatccc                                1000

<210> 32
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-429-84 : polymorphic base C or T

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30

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<220>
<221> misc_binding
<222> 481..500
<223> 10-429-84.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-429-84.mis2, potential complement

<220>
<221> primer_bind
<222> 418..436
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 823..842
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-429-84 potential probe

<220>
<221> misc_feature
<222> 222
<223> n=a, g, c or t

<400> 32
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atttttcatc agtttcattc tgttgccata ttggtcaagt tcccatccaa atgaccaagc      180
ttctttcttc aaattcaatt agagtagctt gaacctaaaca antaaacaat acagttcaat      240
gagcaagggt gaccagttca ttattttgaa ttcagtattt tttcttggag caaatcttgg      300
ttgtattaac aggattaaat aacttgacaa tcaaggatat caccagttta tctgtggcca      360
aatagcaagc cacataatag tggctctggt gtagtaaaaa gggtaaataa ttgttatttg      420
gcttaacctt aatgtgacaa aaatattttg ttcccactaa caactttaaa attttttctt ttcactctg      540
atgtaaccct taataagata ycatgtagaa caactttaaa attttttctt ttcactctg      540
aggctgccct agggattgca cacctgattg tgatggcctt ggaaaaagaa ggtttaccac      600
aagagaaagc catcaaaaag atatggctgg ttgattcaaa aggattaata gttaaggtaa      660
gaatttgtca tttttaacca gaataaagat aactatgccca ttctggatgg ccatctcaaa      720
gacaactctg tttctaccac ctccctttac actatattaa aagagtagcc attaaataca      780
aatgatcatg tcatacagaa tactgatact cttctgaata aagaaaacta tgacttagga      840
acagattcca tctgcaatgt gagtcggctc cttacacccc tttgaattga cagtccattt      900
gaattagttt agttttcttt ctttctttcc ttcctttctt tcctttctct ttctttcttt      960
ctttttcttt ctttctttcc ttccttctct tccttctttt t
                                                                 1001

<210> 33
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-420-284 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-420-284.mis1, potential

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<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-420-284.mis2, potential complement

<220>
 <221> primer_bind
 <222> 216..235
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 646..665
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-420-284 potential probe

<220>
 <221> misc_feature
 <222> 42,308,413
 <223> n=a, g, c or t

<400> 33
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 tgcattgctcc tcctggaagt aaagagtaag acagagaata gtaataatca cccattccag 120
 aactgggtgc acaacatcac aaaagcttgt ccagacttat tagcaagtta ataaaaaact 180
 agacttcttt ctaagtactt ataatttagg ctgtggggta gttctgttat gatacatttg 240
 ttttaaaata ttctgcttct ttttaaagtg agttgtatgt gtctttgttg tagggacgtg 300
 caattttntg ccagtggcag tccttttgat ccagtcactc ttccaaatgg acagacccta 360
 tatectggcc aaggcaacaa ttcttatgtg ttccctggag ttgctcttgg tgnttggtggc 420
 gtgtggattg aggcagatca cagataatat tttcctcact actgctgagg tattgtaaaa 480
 tcctctaagt ttaccaaggg yttaaaatac caagtgtgct cagcctaggt tgtctaattgt 540
 tttatttatc tagcatctca gcttactctc tgaaagaagt aaagtctgaa gaacttccca 600
 gtggagtata aggggtgggt agcatgttca tactgactca caaacgaaag gttcttcttc 660
 agtagtcatt agaaaaattg tgtttttgat ttcttaagag gaacattttt gtgtcttcac 720
 acatcagatc aagttctgtg acagtgtggg gacaattaaa aatattgttt ccagggtctgg 780
 gtgtggtggc tcatgccctt aatcccagca ctttgggagg ctgaggcagg cagatcactt 840
 gagcccagga gttcgaggcc agcttggcca acatggtgaa acttcatctc tactaaaaat 900
 acaaacatta gccgggcatg gtggtgtgtg cctgtgatcc cccctgactc aagaggctga 960
 ggcaggagaa ttgcttgaat ccaggaggca gaggttgcag t 1001

<210> 34
 <211> 821
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-423-411 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-423-411.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521

<223> 10-423-411.mis2, potential complement

<220>

<221> primer_bind

<222> 91..109

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 510..528

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-423-411 potential probe

<220>

<221> misc_feature

<222> 5,804

<223> n=a, g, c or t

<400> 34

cctangattc	tattcccatc	tttttcacca	attatgtgat	ctcaaccacc	accacaccac	60
tctgggctta	tttctttggt	gatagaagtg	gggatgaaat	taggtaatca	tattaatgtc	120
actgggtttt	gtatagacca	ttatatgtaa	ccgttcactt	agttattggc	gtaccacacca	180
cattgtatcg	tgtgaagtat	aaacactttt	tttctttctt	tttttcataa	ggttatagct	240
cagcaagtgt	cagataaaca	cttgggaagag	ggtcggcttt	atcctccttt	gaataccatt	300
agagatgttt	ctctgaaaat	tgcagaaaag	gtaaaaccac	tcttgttcaa	gcttcattat	360
ttttccttcc	ttttcttgct	aaatatgcat	ttttaaatat	taaaaatctg	cttccttgaa	420
atgtatatct	gtatcaactt	actatgtcag	aagtcagaga	aatgaggcac	actgacactg	480
tagagcttag	gagctacatt	ygcttctcag	agaagaatgg	aagtattggg	gccgaataat	540
taatttcctt	ctctatcggt	ctttttttct	cctaaaattt	aaataattca	ttagggtctc	600
ctgtcagcca	gatttctccc	atttcacctt	tttaaagttg	ttcttttcta	tatcacatta	660
gtgataatta	accaaaatat	tacagatatg	ttagagtaac	atttagacct	tgaaccacct	720
tccatatcca	tgtcactatg	atgtgtggca	tcataaatga	cagatcacia	ctgataatac	780
tgggcggaag	gcaaaataaa	gagntcaaag	aacttgaaag	c		821

<210> 35

<211> 732

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 232

<223> 12-713-95 : polymorphic base C or T

<220>

<221> misc_binding

<222> 213..231

<223> 12-713-95.mis1

<220>

<221> misc_binding

<222> 233..252

<223> 12-713-95.mis2, potential complement

<220>

<221> primer_bind

<222> 137..153

<223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 586..604
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 220..244
 <223> 12-713-95 potential probe

<220>
 <221> misc_feature
 <222> 154
 <223> n=a, g, c or t

<400> 35
 ggtctcttct gtgaccccat tattgtcctg tgcatttatt tcaagatcag attcattatt 60
 aaatctatcc agacaattcc tctatcatgt ccttgatcca tttctataac cataaccag 120
 tttctataat cataacccaa cttcaccatt ttantatctt tacaccatct cggtaacttc 180
 tgattttctt taggatcata ttaataagta ttcaggaact tacctttacc cygctattga 240
 ctgttttcac ctacatataa atccctttgt gatctggccc atgcacttca ccttcctgtc 300
 tgccatcctc caccctccg tgtatccttt acaccattgt ataaataaat agtttttagtt 360
 ggctgcacat gtcattgttc tgtcacactt cttctctgta taaactgctc cttcttcccc 420
 cagtgtcttt gcttatttaa ttcattgcta tctttcataa ctcagggtta atatctagac 480
 tggattagag aagttttctg tatagtatcc tagcatggat acaccaaata agcatgtatc 540
 acactgtatt gtaattatat gtatttattt gacttagcat taagtcatca agatattaga 600
 ggtcagggcc tcattctttt ctctcttctt ttataatata tggtgttact gtgatacttc 660
 tttttaataa ctttaatttt aagttcagga gtacatgtgc aggtttgtta cataggtgac 720
 cttgtatgat gg 732

<210> 36
 <211> 786
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 286
 <223> 12-713-149 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 266..285
 <223> 12-713-149.mis1, potential

<220>
 <221> misc_binding
 <222> 287..306
 <223> 12-713-149.mis2, potential complement

<220>
 <221> primer_bind
 <222> 137..153
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 586..604
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 274..298

<223> 12-713-149 potential probe

<220>

<221> misc_feature

<222> 154

<223> n=a, g, c or t

<400> 36

gggtctcttct	gtgaccccat	tattgtcctg	tgcatTTatc	tcaagatcag	attcattatt	60
aaatctatcc	agacaattcc	tctatcatgt	ccttgatcca	tttctataac	cataaccag	120
tttctataat	cataaccac	cttcaccatt	ttantatctt	tacaccatct	cggtaacttc	180
tgatttttctt	taggatcata	ttaataagta	ttcaggaact	tacctttacc	ctgctattga	240
ctgttttcac	ctacatataa	atccctttgt	gatctggccc	atgcasttca	ccttcctgtc	300
tgccatcctc	caccctccg	tgtatccttt	acaccattgt	ataaataaat	agtttttagtt	360
ggctgcacat	gtcattgttc	tgtcacactt	cttctctgta	taaactgctc	cttcttcccc	420
cagtgccttt	gcttatttaa	ttcatgctta	tctttcataa	ctcagggttaa	atatctagac	480
tggattagag	aagttttctg	tatagtatcc	tagcatggat	acacccaaaat	agcatgtatc	540
acactgtatt	gtaattatat	gtatttattt	gacttagcat	taagtcatca	agatattaga	600
ggtcagggcc	tcattctttt	ctctcttctt	ttataatata	tgttgttact	gtgatacttc	660
tttttaataa	ctttaatttt	aagttcagga	gtacatgtgc	aggtttggtta	cataggtgac	720
cttgtatgat	gggggtttgt	tgtacagatt	atttcatcac	ccaggaacta	agcatagtac	780
tcgtta						786

<210> 37

<211> 902

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 500

<223> 12-716-295 : polymorphic base C or T

<220>

<221> misc_binding

<222> 477..499

<223> 12-716-295.mis1

<220>

<221> misc_binding

<222> 501..520

<223> 12-716-295.mis2, potential complement

<220>

<221> primer_bind

<222> 206..225

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 727..746

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 488..512

<223> 12-716-295 potential probe

<220>

<221> misc_feature

<222> 67,139,690,834

<223> n=a, g, c or t

35

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<400> 37
caatgtgtac tacaaaaata aaatgcatgc aatttagagt cactattgca ataattatga      60
actgtgntaa gtcatatatt atgaaaaagc cactcttcta tacattactt aagggtgaaaa      120
tctatgcaaa aaatatggnt agtgtatgta gagaatatat catgacatga ttagaatgat      180
atthtccccca tgcaagatat attcactaga gtcattaaac agatgaaaga gaatttaaac      240
tagaaagaga ggtatagata tccacttact aaataagaag ttattcagaa atagtagctc      300
aagctatctc tctcttgggt tcttttgaag taaactgccc agaagtttgg atctggggaa      360
ctctaagctc ccttccaact ctgagattct atgattttaa gggtttctat aagattttaa      420
cagttgaagc atcaaagttg aagtatcatc agcaatcact gtatttgtat tattattttt      480
atthacatcg aattggacay ttacggtcag atagacagaa aatattctaa aatattcctat      540
ttggtacctt aatttcatat gggttatgcta gatcacttaa aactcaaaat gtgttaagt      600
catacattat atttaaagat atatttcata atatttcctg agaacacaat gaaaacacta      660
atcttccatt tatagaatta attaataaan atcagaaaga tatttttagc actatcaaaa      720
atttaacttg aacatgattc ttgtacatgg cctgggtacta ccttgattta aatttcattg      780
cagagaaggg aatacatgta gaaaattgaa atttcataaa actgtaaatt ttnacaata      840
aattattcca taataagttt tactttaaga tttaaaacta agctttttat aagtcagaca      900
ga                                                                902

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<210> 38
<211> 981
<212> DNA
<213> Homo Sapiens

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```

<220>
<221> allele
<222> 480
<223> 12-720-80 : polymorphic base G or C

```

```

<220>
<221> misc_binding
<222> 461..479
<223> 12-720-80.mis1

```

```

<220>
<221> misc_binding
<222> 481..500
<223> 12-720-80.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 400..419
<223> upstream amplification primer

```

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<220>
<221> primer_bind
<222> 856..876
<223> downstream amplification primer, complement

```

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<220>
<221> misc_binding
<222> 468..492
<223> 12-720-80 potential probe

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```

<220>
<221> misc_feature
<222> 191,218,225,437,480,694,772,775
<223> n=a, g, c or t

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<400> 38
ctgcaggaaa catttggcaa tgtctggaag ctttgagttg tcttaactag ggtagcgggg      60
ttggaagggga gtaaaggag gggctactga catctagcag atagaggcag cggaatgatt      120
ctactaaata tctgtagtg cactggacag cccctgcgac aaggaattat ccagcctaaa      180
atgtcaatag ntgctgaggt tgagaaatac tgcagtanga taagnaccct cctggaagac      240

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36

agggatcacaca	tctcacaaat	ctttatatttc	cttatagcac	ttaatacagt	acttacacaa	300
tgcattgtgca	gtgcaagact	ttaaagtggg	tttagaaaac	tcaaaggaat	ttatgaaact	360
ttattcttta	ttttgtgcat	atataatttt	gattttttacc	ttgtattata	ctccattcct	420
acaagctctt	gtgaaancag	atgacaacgt	tgaaaataat	gatgataact	acaataaaaas	480
gaagtactta	ctccatgaca	ggaactttac	taagtgttta	atattgtttt	tacaaaatat	540
attctgtcaa	taatcttatt	gttttttcatt	tccattatgc	taattgcttt	attcttctgt	600
taaagttact	tcagtgggtg	gtactttact	tttgcagatg	aatcagatgg	ttgtcttaag	660
tgatagcggt	ggtttataaa	acttaattgc	tttngtagcc	tgacaagact	gaaatatact	720
catagaattg	cttataaaga	aagttttacac	attagataca	aatttccaag	tnganttggg	780
aactaactca	atgtactatg	gaagccaaat	attatcttta	gtttttaata	gatatttgta	840
gatttgtagc	cctaaggatt	gtaaggattg	ttggcattaa	caaacttgcc	tctttttgtc	900
actatacttg	aatacaaaata	gtttatatag	cattttgttt	agggtctatt	agaaaatgag	960
ctgatagata	tcattgattt	g				981

<210> 39

<211> 872

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 372

<223> 12-721-227 : polymorphic base C or T

<220>

<221> misc_binding

<222> 352..371

<223> 12-721-227.mis1, potential

<220>

<221> misc_binding

<222> 373..392

<223> 12-721-227.mis2, potential complement

<220>

<221> primer_bind

<222> 146..165

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 588..607

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 360..384

<223> 12-721-227 potential probe

<220>

<221> misc_feature

<222> 756,794,799

<223> n=a, g, c or t

<400> 39

aaattaatga	gttaaatgat	gagtttatta	taaaattatg	gtcaaacacc	tacaattata	60
tggtataata	ttttgtataa	tatgtagagc	aatactaatac	aaacaaatag	ttataactagt	120
aactttacct	ccttctcctt	tccatcttac	ctctgcctaa	atgtccctgg	tcagaagtcc	180
ttagtcaaccg	acgggattta	actccaaact	ccttttttga	cattgataat	gctccagtcc	240
ttatttctgt	accagacccc	tctgctcccc	caggtcagga	cacttggggc	tgctgagtc	300
agctcacaca	caactctgcc	tttggctctga	ctctgttttt	tgtctgaaat	gcctacctac	360
tttctgtttg	tytaactcca	ggctttcctg	taggtttgcc	tttcaagcca	ctgtgcacta	420
taaggccttc	cagaactgct	cttccctctgg	atttcttagc	accacattt	caccattagc	480

37

ctaagccgctc	ttctctttca	gcgttctctt	tttcttcccg	tactctgtta	ccttactaaa	540
ttatacatct	ctcaaggaca	ataacacttt	tcttaagctt	ctccgtagtg	ttatgcttgt	600
tcagtgcata	tatgtttgct	gatggcaaag	aataatat	tggaaataat	ttcatgattt	660
aaaaatctaa	aagatattaa	gatatactga	aaaataagta	tttgattatt	taaaatgtta	720
caaaagagga	aggtttccta	ctccctctct	gcatcncaca	ttttcatgga	acaaaggcct	780
aggataaagc	tgantttang	atttgccccc	atctagaaat	ttaatcaaag	tcttagagct	840
ggagagaaca	tcagggttac	tgagtctccc	tc			872

<210> 40

<211> 926

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 426

<223> 12-721-281 : polymorphic base A or C

<220>

<221> misc_binding

<222> 406..425

<223> 12-721-281.mis1, potential

<220>

<221> misc_binding

<222> 427..446

<223> 12-721-281.mis2, potential complement

<220>

<221> primer_bind

<222> 146..165

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 588..607

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 414..438

<223> 12-721-281 potential probe

<220>

<221> misc_feature

<222> 756,794,799,893

<223> n=a, g, c or t

<400> 40

aaattaatga	gttaaatgat	gagtttatta	taaaattatg	gtcaacaccc	tacaattata	60
tggtataata	ttttgtataa	tatgtagagc	aataactaatc	aaacaaatag	ttatactagt	120
aactttacct	ccttctcctt	tccatcttac	ctctgcctaa	atgtccctgg	tcagaagtcc	180
ttagtccaccg	acgggattta	actccaaact	ccttttttga	cattgataat	gctccagtcc	240
ttatttctgt	accagagacc	tctgtctccc	caggtcagga	cacttgggcc	tgctgagtcc	300
agctcacaca	caactctgcc	tttggctctga	ctctgttttt	tgtctgaaat	gcctacctac	360
tttctgtttg	tctaactcca	ggctttcctg	taggtttgcc	tttcaagcca	ctgtgcacta	420
taaggmcttc	cagaactgct	cttctctctg	atttcttagc	acccacattt	caccattagc	480
ctaagccgctc	ttctctttca	gcgttctctt	tttcttcccg	tactctgtta	ccttactaaa	540
ttatacatct	ctcaaggaca	ataacacttt	tcttaagctt	ctccgtagtg	ttatgcttgt	600
tcagtgcata	tatgtttgct	gatggcaaag	aataatat	tggaaataat	ttcatgattt	660
aaaaatctaa	aagatattaa	gatatactga	aaaataagta	tttgattatt	taaaatgtta	720
caaaaagagga	aggtttccta	ctccctctct	gcatcncaca	ttttcatgga	acaaaggcct	780
aggataaagc	tgantttang	atttgccccc	atctagaaat	ttaatcaaag	tcttagagct	840

38

ggagagaaca tcagggttac tgagtctccc tctctgcctt agggttcaat acnaaaattt 900
 aacactgttt gatttggaac taggga 926

<210> 41
 <211> 1000
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-721-440 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-721-440.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-721-440.mis2, complement

<220>
 <221> primer_bind
 <222> 62..81
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 504..523
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-721-440 potential probe

<220>
 <221> misc_feature
 <222> 672,710,715,809
 <223> n=a, g, c or t

<400> 41
 tagagcaata ctaatcaaac aaatagttat actagtaact ttacctcctt ctcttttcca 60
 tcttacctct gcctaaatgt ccctgggtcag aagtccttag tcaccgacgg gatttaactc 120
 caaactcctt ttttgacatt gataatgctc cagtccttat ttctgtaccc agacctctg 180
 ctccccaggg tcaggacact tgggcctgct gaggccagct cacacacaac tctgcctttg 240
 gtctgactct gttttttgtc tgaaatgcct acctacttct tgtttgtcta actccaggct 300
 ttctgttagg tttgccttct aagccactgt gcactataag gccttcacaga actgctcttc 360
 ctctggattt cttagcacc acatttcacc attagcctaa gccgtcttct ctttcagcgt 420
 tctcttttct tctccgtact ctgttacctt actaaattat acatctctca aggacaataa 480
 cacttttctt aagcttctcc rtagtgttat gcttgttcag tgcataatag tttgctgatg 540
 gcaaagaata atattttgga aataatttca tgatttaaaa atctaaaaga tattaagata 600
 tactgaaaaa taagtatttg attatttaaa atgttacaaa agagggaagg ttctactctc 660
 ctctctgcat cncacatttt catggaacaa aggcctagggt ataagctgan tttangattt 720
 gcccccatct agaaatttaa tcaaagtctt agagctggag agaacatcag gggtactgag 780
 tctccctctc tgccttaggg ttcaatacna aaatttaaca ctgtttgatt tgggaactagg 840
 gaatggtttg gggacagtaa atgttgaggc taattagggt atttagataa tccagagtct 900
 gtgtaaaatt aaaatcctat ttgtagttag actctgaact agctttctca gccttttgct 960
 ctacctctg cacaagaata tgactcagag ctgggagtaa 1000

<210> 42

39

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<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-723-293 : polymorphic base C or T

<220>
<221> misc_binding
<222> 484..502
<223> 12-723-293.mis1

<220>
<221> misc_binding
<222> 504..523
<223> 12-723-293.mis2, potential complement

<220>
<221> primer_bind
<222> 210..230
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 591..610
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-723-293 potential probe

<220>
<221> misc_feature
<222> 312,379
<223> n=a, g, c or t

<400> 42
ctcattagtt ctcagacatt tgaatagtc ttctccagtg catagttact tgggtaaagg      60
gctgtagttc cctgtggata aagattaggg ggattattac cctgtattct tgtcatgggt      120
ttataagggt ctttcttctg ggaactaggc ctcttcttca gtttatgggt tctgggtcta      180
aaaattaact caggttcgga agctgagcaa gagattgtga cttcattggg gcagctacac      240
tcaactttgt ggtcattcat ctttggtttc ttttgatagt aaatattgag tagtagcttt      300
gttagctctc cngttttgcc tctagggatg caagattccg ttaattatct caaaaacatt      360
ttgtgggtta gccacacanc accccacttt tgccactctt atgataattg tgtccatctg      420
gcttctgatt gttaagcatt ctcacctggg cttagcatcc ttattgctat cagtcaggct      480
ggttatatat catccttttc ttytgctact cctgaccttc aggggagaa caccactgaa      540
attttttagta atgttgatgt cttctcattg gcatattcct tatggccttg ggaaatgggt      600
tgttttctgg gccttcctgt ggaatatgtt catcttatgg attttctggc ttttacatgt      660
gtctatatat cagactgccc agttctctga gcctcgcaat cccctcttct gtcatttgcc      720
acagcattcc tggcatttca gtcataatag tatcagccat taatttgctc atgtttctag      780
gaaccatcct agcaatgagt ttgcaccatc ttctgggatt cttgccacat gttaaatcct      840
gtatctcagg agagtgcctg caaatcagta agctctccct tttcctagggt tccagccctt      900
ttaatcaaac accctcagaa ttttaattcta catgtattct cctggctaata acaaatactg      960
gtcttgtggc tcctttgggg taaagtctct ttcttccttt a                                1001

<210> 43
<211> 1001
<212> DNA
<213> Homo Sapiens

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<220>
<221> allele
<222> 501
<223> 12-724-195 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-724-195.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-724-195.mis2, potential complement

<220>
<221> primer_bind
<222> 307..326
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 797..817
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-724-195 potential probe

<220>
<221> misc_feature
<222> 244,249,631,669
<223> n=a, g, c or t

<400> 43
tcacctgagg tcaggagttc gagaccagcc tggccaacat ggtgaaaccc tgtctctact      60
aaaaatacaa aaattagcta ggcgtgggtg caggcgcttg taatcccagc tacttggggag      120
gctgaggcag gagaatcact tgaacccagg tgggtggagg tgcaagtgag cgtgattgca      180
ccaccgcact ccagcctggg caacagagcg agaatccatc tcaaaaaaaaa aaaaaaaaaag      240
aaanaagana aagcatgaag tatgtggagg catacatgaa aagagacaaa tgacatgtta      300
tttttacatt ttaataggca accaagtata acaataatgt gaagcaagac tttctaatta      360
tgtgcacagg ccatctgatg gacggcaaaag gtggaacatg gggagatgag tatgtgaaaag      420
agggaaacatc atggcctctg agctgaaggc agcatgggta cagggtcaaa tcctcagaga      480
agctttggct ctaaaggact yatctgtgct tcaacatacc actgtattct cctatttcta      540
gtttgtacca ttccttatgc ctaaaatgcc ttcatataag ggatgcagaa atttagaaaa      600
tgcttttata aactccatgt gcaaacttac naatagagaa ttaaagggtct cctcaaagca      660
tgttccagnt aaatacctca tctccaacct caatcatgtc atttacttct gtagtttgaa      720
tcactaaatc tgtgactttt tctccattta gcctgaatca aactgtttat ttctaaaagc      780
cagcaacttc tatgaacact aagggtcaca tattcagcag aaaagagaat tgtatattat      840
tttactgaag aatattacag tcataaaatt ttagatctag aaatgtcctc agagatgatt      900
tagcaataac taatgaccag gaagggtaaa aaacacccaa ggttccagaa aaatatatgg      960
tagtgagtgt tgccatctaa gagaaaagcc agagggacta a                                1001

<210> 44
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-724-225 : polymorphic base C or T

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<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-724-225.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-724-225.mis2, potential complement

<220>
 <221> primer_bind
 <222> 277..296
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 767..787
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-724-225 potential probe

<220>
 <221> misc_feature
 <222> 214,219,601,639
 <223> n=a, g, c or t

<400> 44
 tggccaacat ggtgaaaccc tgtctctact aaaaatacaa aaattagcta ggcgtggtgg 60
 caggcgcttg taatcccagc tacttgggag gctgaggcag gagaatcact tgaacccagg 120
 tgggtggagg tgcagtgagc cgtgattgca ccaccgcact ccagcctggg caacagagcg 180
 agaatccatc tcaaaaaaaa aaaaaaaaag aaanaagana aagcatgaag tatgtggagg 240
 catacatgaa aagagacaaa tgacatgtta tttttacatt ttaataggca accaagtata 300
 acaataatgt gaagcaagac tttctaatta tgtgcacagg ccatctgatg gacggcaaag 360
 gtggaacatg gggagatgag tatgtgaaag aggggaacatc atggcctctg agctgaaggc 420
 agcatgggta caggctcaaa tcctcagaga agctttggct cttaaaggact tatctgtgct 480
 tcaacatacc actgtattct yctatttcta gtttgtacca ttccttatgc ctaaaatgcc 540
 ttcatataag ggatgcagaa atttagaaaa tgcttttata aactccatgt gcaaaacttac 600
 naatagagaa ttaaagggtct cctcaaagca tgttccagnt aaatacctca tctccaacct 660
 caatcatgtc atttacttct gtagtttgaa tcaataaatc tgtgactttt tctccattta 720
 gcctgaatca aactgtttat ttctaaaagc cagcaacttc tatgaacact aagggtcaca 780
 tattcagcag aaaagagaat tgtatattat tttactgaag aatattacag tcataaaatt 840
 ttagatctag aaatgtcctc agagatgatt tagcaataac taatgaccag gaagggttaa 900
 aaacacccaa gggtccagaa aaatatatgg tagtgagtgt tgccatctaa gagaaaagcc 960
 agaggggacta agtccaatag ccacgtacgg tagagcagac c 1001

<210> 45
 <211> 421
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 330
 <223> 10-153-329 : polymorphic base G or T

<220>
 <221> misc_binding
 <222> 310..329

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<223> 10-153-329.mis1, potential

<220>
<221> misc_binding
<222> 331..349
<223> 10-153-329.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 402..421
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 318..342
<223> 10-153-329 potential probe

<400> 45
agagtcaccc tbggctcttag gtagtaggtg gagctgaggg ataatggccc aaggccaaga      60
gttgatcctt ccaactttgt tcagtgatcc agctttcata tcaggatgatc aggacaacca      120
ggccaatctg atagggggcg gtgtttataa aaaggccact cacctagagc cagaagctcc      180
acaccagcca ttacaaccct gccaatctca agcacctgcc tctacaggta cctttcttgg      240
gaccaattta caatctcttg gatccccaac tatagaacct ggaagctagt ggggacagaa      300
agacggggag cctgggctag gtgtaggggk cctgagttcc gggctttgct acccagctct      360
tgacttctgt ttcccgatth taaatgagca gtttggaacta agccattttt aaggagagcg      420
a                                                                421

<210> 46
<211> 428
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 342
<223> 10-95-342 : polymorphic base A or G

<220>
<221> misc_binding
<222> 322..341
<223> 10-95-342.mis1, potential

<220>
<221> misc_binding
<222> 343..361
<223> 10-95-342.mis2, complement

<220>
<221> primer_bind
<222> 3..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..422
<223> downstream amplification primer, complement

<220>

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<221> misc_binding
<222> 330..354
<223> 10-95-342 potential probe

<220>
<221> misc_feature
<222> 192,253..254,424..425
<223> n=a, g, c or t

<400> 46
rwtccctcct tttttccctg cagttggtac agatggcatt gtcccagtct gttcccttct      60
cggccacaga gcttctcctg gcctctgcca tcttctgcct ggtattcttg gtgctcaagg      120
gtttgaggcc tcgggtcccc aaaggcctga aaagtccacc agagccatgg ggctggccct      180
tgctcgggca tntgctgacc ctggggaaga acccgcacct ggcactgtca aggatgagcc      240
agcgctacgg ggnngtcctg cagatccgca ttggctccac gcccgctgctg gtgctgagcc      300
gcctggacac catccggcag gccctggtgc ggcagggcga cratttcaag ggccggcctg      360
acctctacac ctccaccctc atcactgatg gccagagctt gaccttcagc acagactctg      420
gagnnata                                     428

<210> 47
<211> 373
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 277
<223> 10-100-277 : polymorphic base C or T

<220>
<221> misc_binding
<222> 258..276
<223> 10-100-277.mis1

<220>
<221> misc_binding
<222> 278..297
<223> 10-100-277.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 355..372
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 265..289
<223> 10-100-277 potential probe

<400> 47
tagggatgga gatggcggtg ggcaggctgt ctggatgggg tggaggtagg agcaacacat      60
gcccagctt tccagccctg agcctcacag tgccctcttc cctcctcagc acaacaagg      120
acacaacgct gaatggcttc tacatcccca agaaatgctg tgtcttcgta aaccagtggc      180
aggtaacca tgaccctgta gtacataccc ctcacgaaaa aatgtgtgca ggttcagcag      240
tcaggaaggc tgtttgctcc tgctaggaac tgtttayata atgaaaggag gggacctcaa      300
ttgctatagt ctgctctaag tgacgatatt tacaaaagtt tcacaaactt tagtgcacag      360
gaatcaacta ggg                                     373

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<210> 48
 <211> 375
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 297
 <223> 10-102-294 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 278..296
 <223> 10-102-294.mis1

<220>
 <221> misc_binding
 <222> 298..317
 <223> 10-102-294.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 356..375
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 285..309
 <223> 10-102-294 potential probe

<220>
 <221> misc_feature
 <222> 30,218
 <223> n=a, g, c or t

<400> 48	
agagwgctgt gggaggaccc ctctgagttt cggcctgagc gggttcctcac cgccgatggc	60
actgccatta acaagccctt gactgagaag atgatgctgt ttggcatggg caagcgccgg	120
tgtatcgggg aagtccctggc caagtgggag atcttcctct tcctggccat cctgctacag	180
caactggagt tcagcgtgcc gccgggcgtg aaagtcgncc tgaccccat ctacgggctg	240
accatgaagc acgcccgtg tgaacatgtc caggcgccgc tgcgcttctc catcaaytga	300
agaagacacc accattctga ggccagggag cgagtggggg ccagccacgg ggactcagcc	360
cttgtttctc ttcct	375

<210> 49
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-413-394 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 482..500
 <223> 10-413-394.mis1

<220>
 <221> misc_binding
 <222> 502..520
 <223> 10-413-394.mis2, complement

<220>
 <221> primer_bind
 <222> 108..125
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 539..556
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-413-394 potential probe

<400> 49
 tgtgatttgt gtaccaattg cctgggtcat tgcgtggcac atcacaggcc atctataagt 60
 ggcagctata acaatcacca tcacatttat gtacaaaatt cagaaatatac gaatctatgt 120
 gtggcaaata tgaacattaa aaaatacaat gaaaatgtca gtctgaatca tacatagtat 180
 ttggagcaaa tagcgactta ttttgctgct atttgcattt cctttcccag ttctcaaaag 240
 tctatggtcc tgtgttcacc gtgtattttg gcatgaatcc catagtgggtg tttcatggat 300
 atgaggcagt gaaggaagcc ctgattgata atggagagga gttttctgga agaggcaatt 360
 cccaatatc tcaaagaatt actaaaggac ttggtaggtg cacatatattc tgtgtcagct 420
 ttggtaactg ggggtgagggg gatggaaaac agagccctaa aaagcttctc agcagagctt 480
 agcctatctg catggctgcc ragtggtgca gcactttctt ccttggtgtg gaattctccc 540
 agtttctgcc ccttttttta ttaggaatca tttccagcaa tggaaagaga tggaggaga 600
 tccggcgttt ctccctcaca accttgcgga attttgggt ggggaagagg agcattgagg 660
 accgtgttca agaggaagct cactgccttg tggaggagt gagaaaaacc aagggtgggt 720
 gactctactc tgcgtcattg accttaacag ttacctgtct tcactagtga cgtccttga 780
 aacatttcag ggggtggccag gtcttcattg cgcctcctgg ttgtcagccc tcagggtgtg 840
 gagggagatt tgaagcacag agacaaggga ggttttgtgt atctgtgctt tgctgtata 900
 aatgtgttgg ttcataagggt gtaggaataa aagggtcattt aatcctattt tctgtcaat 960
 tttgtttcct tgttttcaaa tcagaaatta taaataaggg t 1001

<210> 50
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-414-243 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-414-243.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-414-243.mis2, potential complement

<220>
 <221> primer_bind
 <222> 259..276

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<223> upstream amplification primer

<220>
<221> primer_bind
<222> 592..609
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-414-243 potential probe

<220>
<221> misc_feature
<222> 981
<223> n=a, g, c or t

<400> 50
atgaaaatgt cagtctgaat catacatagt atttggagca aatagcgact tattttgctg      60
ctatttgcac ttcccttccc agttctcaaa agtctatggt cctgtgttca ccgtgtattt      120
tggcatgaat cccatagtgg tgtttcatgg atatgaggca gtgaaggaag ccctgattga      180
taatggagag gagttttctg gaagaggcaa ttccccaata tctcaaagaa ttactaaagg      240
acttggtagg tgcacatatt tctgtgtcag ctttggtaac tggggtgagg gggatggaaa      300
acagagccct aaaaagcttc tcagcagagc ttagcctatc tgcattggctg ccaagtgttg      360
cagcactttc ttccctggct gtgaattctc ccagtttctg cccctttttt tattaggaat      420
catttccagc aatggaaaga gatggaagga gatccggcgt ttctccctca caaccttgcg      480
gaattttggg atggggaaga rgagcattga ggaccgtgtt caagaggaag ctactgcct      540
tgtggaggag ttgagaaaaa ccaagggtgg gtgactctac tctgcgtcat tgaccttaac      600
agttacctgt cttcactagt gacgtccttg gaaacatttc aggggtggcc aggtcttcat      660
tgcgcatcct ggttgtcagc cctcaggtgg tggagggaga tttgaagcac agagacaagg      720
gaggttttgt gtatctgtgc tttgcctgta taaatgtgtt ggttcatagg gtgtaggaat      780
aaaaggcat ttaatcctat tttctgtcga attttggttc cttgttttca aatcagaaat      840
tataaataag ggtcttgagt tcatttttga agagttaaag aaggtttccc ccatagcata      900
aatctgcatt acctccacca gaacatttca ccagagaaca cttggaaagt ggacatggtg      960
aaagtgcact catcacactt natgaaatat gaaccaagtt a                               1001

<210> 51
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-416-273 : polymorphic base A or T

<220>
<221> misc_binding
<222> 482..500
<223> 10-416-273.mis1

<220>
<221> misc_binding
<222> 502..520
<223> 10-416-273.mis2, complement

<220>
<221> primer_bind
<222> 229..246
<223> upstream amplification primer

<220>
<221> primer_bind

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<222> 630..649

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-416-273 potential probe

<220>

<221> misc_feature

<222> 619,997

<223> n=a, g, c or t

<400> 51

aaataatgta ttactttaat ttgtattgtc atatatgcta atttatagaa atgtacttat	60
gcaactgtaat gactagtttg taggagagtg gtatgtatct atattatggg aattcctttt	120
atatggctgg ttgtacttct ggacatgtaa ctcatgtttg taatgttgct gggattttta	180
tatcatgtta atgtggccat gaattgctat gacaaatgtt ccatatatct tcgtttccat	240
cagttcctttc ttgtgtcttg tcagctaaag tccaggaaga gattgatcat gtaattggca	300
gacacaggag cccctgcatg caggatagga gccacatgcc ttacactgat gctgtagtgc	360
acgagatcca gagatacagt gaccttgtcc ccaccggtgt gccccatgca gtgaccactg	420
atactaagtt cagaaactac ctcatcccca aggtaagctt gtttctctta cactatattt	480
ctgtacttct gaaatttcca wagtgtgtg ttggttccaa cctctaaca acacaagatg	540
agagaagtgc aaaactcata catgtggcag cttgatggac tttctgctat tttgtttggg	600
gctataaaga ttataaaang ctaggctctc ttaataggct gctcttaggt gttacacttt	660
caaataattg ttgaaaatat cagtgtgtca atttcccaa acactcttct gagattttta	720
tcaaagtgc attcattgtg tagttcgata tggaaagact taacatgttc atgcattgaa	780
ttttttaatt catgaatatg gttatgctcc caacttattg agctttatcc tattttctca	840
gtaatgtctt attttcagtg cagtggttta caactctttt attaggtttt tctagataa	900
ttaatatattt gttgtgttat aattttttaa tttttttta tttctttgta attggtataa	960
gtaattgtat tcaattatac tattctgatg accttanatc t	1001

<210> 52

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-418-177 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 10-418-177.mis1, potential

<220>

<221> misc_binding

<222> 502..520

<223> 10-418-177.mis2, complement

<220>

<221> primer_bind

<222> 325..342

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 659..676

<223> downstream amplification primer, complement

<220>

<221> misc_binding
 <222> 489..513
 <223> 10-418-177 potential probe

<220>
 <221> misc_feature
 <222> 68,174,203,619,885,890,897,907,918
 <223> n=a, g, c or t

<400> 52
 gggtgtcatc ccagatgaca tcatattaaa atagattaca tgtttattta caaaagttct 60
 atgaacanga tactctggac atttcaagt tcaacagaga cttccatttt aaaccataat 120
 ctacataatc aaaatacaag atgtgtcaaa tttgaagtga tgaaatagag cggncaaatg 180
 aggccagaaa agggcatcca aancttgatg atctggagaa cacattcaga aggttgacac 240
 caagtatcca agatgtaaga cttcaaagt gattggaaag ctctttagca agcttccacc 300
 actggcctta agctcatcca tgtaaattac tgtgtctggc tggacctgag ttctctcatc 360
 tatagatcaa cgttatggcg ctacgtgatg tccactactt ctctcactt ctggacttct 420
 ttataaatca gattatctgt tttgttactt ccagggcaca accataatgg cattactgac 480
 ttccgtgcta catgatgaca ragaatttcc taatccaaat atctttgacc ctggccactt 540
 tctagataag aatggcaact ttaagaaaag tgactacttc atgcctttct cagcaggtaa 600
 tagaaactcg tttccattnt gtatttaaag gaaagagaga actttttgga attagttgga 660
 atttcatgg cactcctct ggggctggtg gaattgctat ttgtccatga tcaagagcac 720
 cactcttaac acccatgtgc tccaccctca caatacacca tcattattgg gccagatagc 780
 ggggcttgca ggagtttaact ctgttggtcc caattgagaa aatgaacatc ttggtttgac 840
 tgaactctgc cactagatac atcactaagg cacccaagag ctccntcctn agaaggntaa 900
 aattcantct gatctttnc ttaacctgcct tgacaaatgt atctaagtcc acaactgcat 960
 tgagtgtcct ctacatggtg tctgtcacct cccaggctga g 1001

<210> 53
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-665-315 : polymorphic base T or C

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-665-315.mis1, potential complement

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-665-315.mis2

<220>
 <221> primer_bind
 <222> 795..815
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 357..377
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-665-315 potential probe

<220>
 <221> misc_feature
 <222> 175,181..182,195,215,227,238,245,652,747
 <223> n=a, g, c or t

<400> 53
 tatcagctaa agtccaggaa gagattgaac gtgtgattgg cagaaaccgg agcccttgca 60
 tgcaagacag gagccacatg ccctacacag atgctgtggg gcacgaggtc cagagataca 120
 ttgaccttct ccccaccagc ctgccccatg cagtgtacgtg tgacattaaa ttcangaaac 180
 nntatctcat tccnaagggt aagtttggtt ctcctacac tgcaacntcc atgttttncg 240
 aagtncccca aattcatagt atcattttta aacctctacc atcacgggtg gagagaagtg 300
 cataactcat atgtatggca gtttaactgg actttctctt gtttccagtt tggggctata 360
 aaggtttgta acaggtccta gtgtctggca gtgtgtgttc tccagattta ttatctttct 420
 tcaagattgg tttggctact cttagggtgt tatatttcca aataattttt aaaggattta 480
 gtttgcatt ttcccaaaac yttgggctgg aatttctggc aggggtgacac taaatttata 540
 ggctagtttg gaaagaactg aatcttgaca cgttgaggct ttccattcct gaataataatt 600
 atgcttccaa tttgtttggg gtttctttta ttaaccagg aatgttgtga antttgttgt 660
 catggctttc gagtctttgg tttccctag ataattaata tttttgttgt agaacataaa 720
 tagtttttat cattctgatg atgttanatc tgtcaacttt gctaaattta ctagtcaacta 780
 ttcgtaattt atttctggat tcattgtaat ttctgtgtat attatactgt atctgagtta 840
 atattgtttt atttcttatt ttccatttct catgggctta atgtctcttt atcgcattca 900
 ttattgcatt agctagaatt tctaggagag cattgaatag aattgggtgac agtggggatc 960
 cttgtttctc atttctaate tgcaggaagc agtgggaagt t 1001

<210> 54
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-666-324 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-666-324.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-666-324.mis2, potential complement

<220>
 <221> primer_bind
 <222> 186..205
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 621..641
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-666-324 potential probe

<400> 54
 gcatactttt ccatttttaa gatccaccat aattttattta caacctccag taaagttttg 60
 tttcaaatct tttatgaata atcataaaat aagcattcat atatatagta attraatatat 120
 accttcagtg atatccatta atactcaaga agtgaaactg tttgaaggat ggaggtgttt 180

50

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atatacattt ctatgaatat cgtcccattg gctttaaaag agagtaaaca aattcacacg 240
ctccttttatg cccacattca ttcattcatt aagtagtcat taatttatct agtatctatt 300
gagccaatat cttctaaaca gtgtttcagg tgtctggaat tcattagtga gccaaataaa 360
gttctctgct catataaaac atgtatttta gggatgaaac ataaacaata aaaataaatg 420
cagagaatta gcaaagttgt tagccacttc tactttccag tcagattgcc cttgttcaac 480
tgttggctct gacacttaaa magctgtgtg accttgaaca agataactaa cagatcatca 540
gtgcaattgt ttggttggtc aaattggtat aataataata tggtaggcta aataatgtct 600
tgacataaag agattaagct ggtgggttcc atgtaatcac aagggtcttt acattagtgt 660
taaatatagt gaaccccaag tttatcttca aagaatcagt atgtcagtat gtgcatctat 720
cttattgttt gattctccat tttaaagttt aacttcttaa ttctctttgc ccccttgctt 780
ccagtttcag taaacaactt tcttaccagt cctaataaat agttcacatc tgttccctg 840
gtcacctgct ttgaccctag tcaccctggt tcacctgctc tatcctgact catcctgagc 900
caccagttct gtaaccgccc ttcccaccaa actacttacc ccaccactct ggctcatact 960
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<210> 55

<211> 436

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 155

<223> 10-72-155 : polymorphic base A or G

<220>

<221> misc_binding

<222> 135..154

<223> 10-72-155.mis1, potential

<220>

<221> misc_binding

<222> 156..175

<223> 10-72-155.mis2, potential complement

<220>

<221> primer_bind

<222> 1..20

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 417..436

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 143..167

<223> 10-72-155 potential probe

<400> 55

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gtggctgaat aaaagcatatc aaatacaatg aaaatatcad kctaaatcag gcttagcaaa 60
tggacaaaat agtaacttcr tttgctgtta wctctrtcta ctttcctagc tctcaaargt 120
ctatggccct gtgttcactc tgtatttttg cctgraaccc atrgtgggtg tgcatggata 180
tgaaghrgtg aaggaagccc tgattgatct tggagaggag tttcttgga gaggcawttt 240
ccactggct gaaagagcta acagaggatt tggtaggtgt gcawgtgcct gtttcagcat 300
ctgtcttggg gatggggagg atggaaaaca gagacttdca gagctcctcg ggcagagctt 360
ggcccatcca catggctgcc cagtgtcagc ttcctcttcc ttgcctgggt ctccctccta 420
gtttcgtttc tcttcc

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436

<210> 56

<211> 678

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 178

<223> 10-76-177 : polymorphic base A or T

<220>

<221> misc_binding

<222> 158..177

<223> 10-76-177.mis1, potential

<220>

<221> misc_binding

<222> 179..198

<223> 10-76-177.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 416..435

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 166..190

<223> 10-76-177 potential probe

<220>

<221> misc_feature

<222> 549,635,642,655,661

<223> n=a, g, c or t

<400> 56	
ttacgcatga ggagtaactg ctctctgtgt ttgctatattt caggaaaacg gatttggtgtg	60
gggagaagcc ctggccggca tggagctgtt tttattcctg acctccattt tacagaactt	120
taacctgaaa tctctggttg acccaaagaa ccttgacacc actccagttg tcaatggwtt	180
tgcctctgtg ccgcccttct accagctgtg cttcattcct gtctgaagaa gagcagatgg	240
cctggctgct gctgtgcagt ccctgcagct ctctttcctc tggggcatta tccatctttc	300
actatctgta atgccttttc tcacctgtca tctcacattt tcccttcctt gaagatctag	360
tgaacattcg acctccatta cggagagttt cctatgtttc actgtgcaaa tatatctgct	420
attctccata ctctgtaaca gttgcattga ctgtcacata atgctcatat ttatctaattg	480
ttgagttatt aatatgttat tattaataag agaaatatga tttgtgtatt ataattcaaa	540
ggcatttctt tttctgcatg ttctaaataa aaagcattat tatttgctga gtcagtttat	600
tagaccttcc ttcttttatg cataatgtag gtcangaaat tnaaagaaaa tagangttcc	660
naggaggcca tgctgggt	678

<210> 57

<211> 718

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 218

<223> 10-76-217 : polymorphic base C or T

<220>

<221> misc_binding

<222> 198..217
 <223> 10-76-217.mis1, potential

<220>
 <221> misc_binding
 <222> 219..238
 <223> 10-76-217.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 416..435
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 206..230
 <223> 10-76-217 potential probe

<220>
 <221> misc_feature
 <222> 549,635,642,655,661,708
 <223> n=a, g, c or t

<400> 57
 ttacgcatga ggagtaactg ctctctgtgt ttgctatattt caggaaaacg gatttggtgtg 60
 gggagaagcc ctggccggca tggagctggt tttattcctg acctccattt tacagaactt 120
 taacctgaaa tctctggttg acccaaagaa ccttgacacc actccagttg tcaatggatt 180
 tgccctctgtg ccgcccttct accagctgtg cttcattyct gtctgaagaa gagcagatgg 240
 cctggctgct gctgtgcagt cctgcagct ctctttcctc tggggcatta tccatctttc 300
 actatctgta atgccttttc tcacctgtca tctcacattt tcccttcctt gaagatctag 360
 tgaacattcg acctccatta cggagagttt cctatgtttc actgtgcaaa tatatctgct 420
 attctccata ctctgtaaca gttgcattga ctgtcacata atgctcatac ttatctaattg 480
 ttgagttatt aatatgttat tattaataag agaaatatga tttgtgtatt ataattcaaa 540
 ggcatttctt tttctgcatg ttctaaataa aaagcattat tatttgctga gtcagtttat 600
 tagaccttcc ttcttttatg cataatgtag gtcangaaat tnaaagaaaa tagangttcc 660
 naggaggcca tgctggttct caaaatgata aggacagaaa ggacaaanga ggaagagg 718

<210> 58
 <211> 834
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 334
 <223> 10-76-333 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 315..333
 <223> 10-76-333.mis1

<220>
 <221> misc_binding
 <222> 335..354
 <223> 10-76-333.mis2, potential complement

<220>

<221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 416..435
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 322..346
 <223> 10-76-333 potential probe

<220>
 <221> misc_feature
 <222> 549,635,642,655,661,708,751
 <223> n=a, g, c or t

<400> 58
 ttacgcatga ggagtaactg ctctctgtgt ttgctatddd caggaaaacg gatttgtgtg 60
 gggagaagcc ctggccggca tggagctgtt tttattcctg acctccattt tacagaactt 120
 taacctgaaa tctctgggtg acccaaagaa ccttgacacc actccagttg tcaatggatt 180
 tgcctctgtg ccgcccttct accagctgtg cttcattcct gtctgaagaa gagcagatgg 240
 cctggctgct gctgtgcagt ccctgcagct ctctttcctc tggggcatta tccatctttc 300
 actatctgta atgccttttc tcacctgtca tctacattt tcccttccct gaagatctag 360
 tgaacattcg acctccatta cggagagttt cctatgtttc actgtgcaaa tatatctgct 420
 attctccata ctctgtaaca gttgcattga ctgtcacata atgtcatac ttatctaattg 480
 ttgagttatt aatatgttat tattaataag agaaatatga tttgtgtatt ataattcaaa 540
 ggcatttctt tttctgcatg ttctaaataa aaagcattat tatttgctga gtcagtttat 600
 tagaccttcc ttcttttatg cataatgtag gtcangaaat tnaaaagaaa tagangttcc 660
 naggaggcca tgctggttct caaatgata aggacagaaa ggacaaanga ggaagagggt 720
 agggaaagcta ttttgggtga gtgttagagt ntacttgagg attggatttg aaagtgagaa 780
 actgtgtcca ggggcagctc taacctctag ggaaatattc agaggatcag tcaa 834

<210> 59
 <211> 995
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-77-316 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-77-316.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-77-316.mis2, potential complement

<220>
 <221> primer_bind
 <222> 185..203
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 593..610

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-77-316 potential probe

<220>

<221> misc_feature

<222> 427,513,520,533,539,586,629,762..765,774..776,813

<223> n=a, g, c or t

<400> 59

acctgaaatc tctgggtgac ccaaagaacc ttgacaccac tccagttgtc aatggatttg	60
cctctgtgcc gcccttctac cagctgtgct tcattcctgt ctgaagaaga gcagatggcc	120
tggctgctgc tgtgcagtcct ctgcagctct ctttcctctg gggcattatc catctttcac	180
tatctgtaat gccttttctc acctgtcatc tcacattttc ctttcctga agatctagt	240
aacattcgac ctccattacg gagagtttcc tatgtttcac tgtgcaaata tatctgctat	300
tctccatact ctgtaacagt tgcattgact gtcacataat gctcatactt atctaagt	360
gagttattaa tatgttatta ttaaataagag aaatatgatt tgtgtattat aattcaaagg	420
catttctnttt tctgcatggt cttaaataaaa agcattatta tttgctgagt cagtttatta	480
gaccttcctt cttttatgca waatgtaggt cangaaattn aaagaaaata gangttccna	540
ggaggccatg ctgggttctca aaatgataag gacagaaagg acaaangagg aagagggtag	600
ggaagctatt ttgggtgagt gttagagtnt acttgaggat tggatttgaa agtgagaaac	660
tgtgtccagg ggcagctcta acctctaggg aaatatcag aggatcagtc aaaggggtgga	720
atggacatta aatgctagaa ttcttatatc cacattgggtg tnnnttcctt tttnnnacia	780
agtcttgctc tgtcacccag gctggagtgc agnggtgtga tctcagctct ctataacctc	840
cgccctccag gttcaagtga ttctcctgcc tcagcctcct gagtagctgg gattacaggt	900
gcatgccacc acacctggct aattttttgt atttttagta cagacgggtt ttcaccgtgt	960
tagccaggat ggtcttaatc tcctgacctt gtgat	995

<210> 60

<211> 442

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 78

<223> 10-155-78 : polymorphic base C or T

<220>

<221> misc_binding

<222> 58..77

<223> 10-155-78.mis1, potential

<220>

<221> misc_binding

<222> 79..98

<223> 10-155-78.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 424..442

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 66..90

<223> 10-155-78 potential probe

<400> 60

accgagctta ttttacccaa aataaggtag tatatttctg ttagagtta gagtttcatg	60
agtcagggac caagttaaytg cttttctttg ccctgtataa aggcttctcc aaggcctttg	120
acttacctaa gtactaaatg ttataaaacc aaactcttct gacctctcaa tctagtcaac	180
tggggctgta attattaatg aaattaatgt ttattttgaa aataatttac tagactgaat	240
tacgaaatcc tgaatcattg tacactatca gtaaatattg gtggacccaa ctgaactgaa	300
tgttttgctt gaaatgaaac ctttgagatg cagggcttat gggttctagt cccagctcta	360
gcactagcag acagcatgtt cttggctaag atactgaatc ttcaaggctc agcttcctca	420
ttccggaaat gggtaattt ta	442

<210> 61

<211> 442

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 104

<223> 10-155-104 : polymorphic base G or C

<220>

<221> misc_binding

<222> 84..103

<223> 10-155-104.mis1, potential

<220>

<221> misc_binding

<222> 105..124

<223> 10-155-104.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 424..442

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 92..116

<223> 10-155-104 potential probe

<400> 61

accgagctta ttttacccaa aataaggtag tatatttctg ttagagtta gagtttcatg	60
agtcagggac caagtattg cttttctttg ccctgtataa aggsttctcc aaggcctttg	120
acttacctaa gtactaaatg ttataaaacc aaactcttct gacctctcaa tctagtcaac	180
tggggctgta attattaatg aaattaatgt ttattttgaa aataatttac tagactgaat	240
tacgaaatcc tgaatcattg tacactatca gtaaatattg gtggacccaa ctgaactgaa	300
tgttttgctt gaaatgaaac ctttgagatg cagggcttat gggttctagt cccagctcta	360
gcactagcag acagcatgtt cttggctaag atactgaatc ttcaaggctc agcttcctca	420
ttccggaaat gggtaattt ta	442

<210> 62

<211> 772

<212> DNA

<213> Homo Sapiens

<220>
 <221> allele
 <222> 52
 <223> 10-156-52 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 32..51
 <223> 10-156-52.mis1, potential

<220>
 <221> misc_binding
 <222> 53..71
 <223> 10-156-52.mis2, complement

<220>
 <221> primer_bind
 <222> 1..19
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 401..420
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 40..64
 <223> 10-156-52 potential probe

<400> 62
 ttcaaggctc agcytcctca ttccggaaat ggggtcaattt tattgtaagc araggtaatt 60
 gagagattca aaagggacat gaggtgtaac aattctctgt aaattgtag aatccctgtt 120
 aaaaatgacc agtaaagctt tgtgcaactg tgtcttgaca taactttatt tttcttaata 180
 aaagaaatgg aaataacctc actagggaat ttagaacaaa tatgatgata tctttaaaga 240
 aaatggcttt gcacaagtat tgacattaat gatctagtaa agtgatatctt tctagttgta 300
 tttagatcct caactcagta tgtcagctcc tgtaagggtc tatacattgt ggtgggtctg 360
 tgctgtgggt ccatttagtg atttccctac ctcccatctt ctattgcac cacaactgtg 420
 gttctgtcca taatttcctt tgctttctgt gcattattac atcatatctg aaaatgagaa 480
 accaaaaaca atagaaaagca gccatgtctg gaggtgactg ggggggtcgag aagccctagt 540
 ttctcaaacc cttagcacca aatttttccc tcagttacac tgagcgtttc acttctgcag 600
 tgatggagaa ggggatccc ttatttcttc tcattgagcat ctctgggtgct gtttccctta 660
 gagacaaata aggggttcta tttaatgtga agcctgtttt atgaacagaa taaatgtggg 720
 gtatattcag aataactaat gtttggaagt ttgttttatt ttgctaaaat tg 772

<210> 63
 <211> 431
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 39
 <223> 10-157-39 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 20..38
 <223> 10-157-39.mis1

<220>
 <221> misc_binding
 <222> 40..59

57

<223> 10-157-39.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 412..431

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 27..51

<223> 10-157-39 potential probe

<400> 63

ctgtgggkcc atttagtgat ttccctacct cccatcttyt attgcatcca caactgtggt	60
tctgtccata atttcctttg ctttctgtgc attattacat catatctgaa aatgagaaac	120
caaaaacaat agaaagcagc catgtctgga ggtgactggg gggtcgagaa gccctagttt	180
ctcaaaccct tagcaccaaa tttttccctc agttacactg agcgtttcac ttctgcagtg	240
atggagaagg gagatccctt atttcttctc atgagcatct ctggtgctgt ttcccttaga	300
gacaaataag gggttctatt taatgtgaag cctgttttat gaacagaata aatgtggtgt	360
atattcagaa taactaatgt ttggaagttt gttttatttt gctwaaaatt gggtctcaag	420
gcagctctgg t	431

<210> 64

<211> 431

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 131

<223> 10-157-131 : polymorphic base A or G

<220>

<221> misc_binding

<222> 111..130

<223> 10-157-131.mis1, potential

<220>

<221> misc_binding

<222> 132..150

<223> 10-157-131.mis2, complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 412..431

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 119..143

<223> 10-157-131 potential probe

<400> 64

58

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ctgtgggkcc atttagtgat ttccctacct cccatcttyt attgcatcca caactgtggt      60
tctgtccata atttcctttg ctttctgtgc attattacat catatctgaa aatgagaaac      120
caaaaacaat rgaaagcagc catgtctgga ggtgactggg gggtcgagaa gccctagttt      180
ctcaaaccct tagcaccaaa tttttccctc agttacactg agcgtttcac ttctgcagtg      240
atggagaagg gagatccctt atttcttctc atgagcatct ctggtgctgt ttcccttaga      300
gacaaataag gggttctatt taatgtgaag cctgttttat gaacagaata aatgtggtgt      360
atattcagaa taactaatgt ttggaagttt gttttatatt gctwaaaatt ggttctcaag      420
gcagctctgg t                                                                431

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<210> 65
 <211> 431
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 166
 <223> 10-157-166 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 146..165
 <223> 10-157-166.mis1, potential

<220>
 <221> misc_binding
 <222> 167..186
 <223> 10-157-166.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 412..431
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 154..178
 <223> 10-157-166 potential probe

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<400> 65
ctgtgggkcc atttagtgat ttccctacct cccatcttyt attgcatcca caactgtggt      60
tctgtccata atttcctttg ctttctgtgc attattacat catatctgaa aatgagaaac      120
caaaaacaat agaaagcagc catgtctgga ggtgactggg gggtcragaa gccctagttt      180
ctcaaaccct tagcaccaaa tttttccctc agttacactg agcgtttcac ttctgcagtg      240
atggagaagg gagatccctt atttcttctc atgagcatct ctggtgctgt ttcccttaga      300
gacaaataag gggttctatt taatgtgaag cctgttttat gaacagaata aatgtggtgt      360
atattcagaa taactaatgt ttggaagttt gttttatatt gctwaaaatt ggttctcaag      420
gcagctctgg t                                                                431

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<210> 66
 <211> 431
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 246
 <223> 10-157-246 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 226..245
 <223> 10-157-246.mis1, potential

<220>
 <221> misc_binding
 <222> 247..266
 <223> 10-157-246.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 412..431
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 234..258
 <223> 10-157-246 potential probe

<400> 66							
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tctgtccata	atttcctttg	ctttctgtgc	attattacat	catatctgaa	aatgagaaac		120
caaaaacaat	agaaagcagc	catgtctgga	ggtgactggg	gggtcgagaa	gccctagttt		180
ctcaaaccct	tagcaccaaa	ttttccctc	agttacactg	agcgtttcac	ttctgcagt		240
atggaraagg	gagatccctt	atctctctc	atgagcatct	ctggtgctgt	ttcccttaga		300
gacaaataag	gggttctatt	taatgtgaag	cctgttttat	gaacagaata	aatgtggtgt		360
atattcagaa	taactaatgt	ttggaagttt	gttttatttt	gctwaaaatt	ggttctcaag		420
gcagctctgg	t						431

<210> 67
 <211> 581
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 161
 <223> 10-159-161 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 142..160
 <223> 10-159-161.mis1

<220>
 <221> misc_binding
 <222> 162..181
 <223> 10-159-161.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..19
 <223> upstream amplification primer

<220>
 <221> primer_bind

60

<222> 403..422
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 149..173
 <223> 10-159-161 potential probe

<400> 67
 aggaattttt tttagggggg ttaatggtaa aggtgtttat atctgctaag gtaatttact 60
 tgatatatgt ttgggttattt aagatatatg agttatgtta gctatttcat gtttaggctg 120
 ctgtattttt agtaggctat attaaatatt tgaaaggatt wcattataaa gaacaaagtc 180
 tcctaattctt tgatatagca ttgacatact ttttaaatac acaaggcata gaatatggcc 240
 atttctgtta aatcatatat tcccaactgg ttattaatct aagaattcag aattttgagt 300
 aattgctttt gcatcagatt atttacttca gtgctctcaa ttatgatggg gcattagaac 360
 catctggggtt aacatttggt ttttattacc aatacctagg ctccaaccaa gtacagtga 420
 actggaatgt acagagtgga caatggaacg aaggagaaca agaccaaagg acattttatt 480
 tttatctgta tcagtgggtc aaagtccttt cagaaggagc atatagtgga cctaggtgat 540
 tggtcrrttt atccatcaaa gaggcacaca ccgaattagc a 581

<210> 68
 <211> 581
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 162
 <223> 10-159-162 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 142..161
 <223> 10-159-162.mis1, potential

<220>
 <221> misc_binding
 <222> 163..182
 <223> 10-159-162.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..19
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 403..422
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 150..174
 <223> 10-159-162 potential probe

<400> 68
 aggaattttt tttagggggg ttaatggtaa aggtgtttat atctgctaag gtaatttact 60
 tgatatatgt ttgggttattt aagatatatg agttatgtta gctatttcat gtttaggctg 120
 ctgtattttt agtaggctat attaaatatt tgaaaggatt tmattataaa gaacaaagtc 180
 tcctaattctt tgatatagca ttgacatact ttttaaatac acaaggcata gaatatggcc 240
 atttctgtta aatcatatat tcccaactgg ttattaatct aagaattcag aattttgagt 300
 aattgctttt gcatcagatt atttacttca gtgctctcaa ttatgatggg gcattagaac 360
 catctggggtt aacatttggt ttttattacc aatacctagg ctccaaccaa gtacagtga 420

61

actggaatgt acagagtgga caatggaacg aaggagaaca agaccaaagg acattttatt	480
tttatctgta tcagtgggtc aaagtccttt cagaaggagc atatagtgga cctaggtgat	540
tggtcrmttt atccatcaaa gaggcacaca ccgaattagc a	581

<210> 69
 <211> 353
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 169
 <223> 10-83-169 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 150..168
 <223> 10-83-169.mis1

<220>
 <221> misc_binding
 <222> 170..189
 <223> 10-83-169.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..19
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 336..353
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 157..181
 <223> 10-83-169 potential probe

<400> 69	
aagtcatact gcttcttact aggtctgtct ggggtgggaat gtaacttctt tggacctcaa	60
ttttcttatac tattgataaa agagattgga ctaggtgatt tccatcactt cttcccactc	120
tttgacttct ttataactta gtttgtctgt tttgctatct tcagggcayg accataataa	180
catccctgac ttctgtgctg cacaatgaca aagaattccc caaccagag atgtttgacc	240
ctggccactt tctggataag agtggcaact ttaagaaaag tgactacttc atgcctttct	300
cagcaggtaa tagatattca tttccatctg tccttcaggg cacatgatac ctt	353

<210> 70
 <211> 425
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 152
 <223> 10-84-152 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 132..151
 <223> 10-84-152.mis1, potential

<220>

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<221> misc_binding
<222> 153..172
<223> 10-84-152.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 140..164
<223> 10-84-152 potential probe

<220>
<221> misc_feature
<222> 413
<223> n=a, g, c or t

<400> 70
gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg      60
cccgcgatgga gctgttttta ttcctgacca ccattttgca gaactttaac ctgaaatctc      120
aggttgaccc aaaggatatt gacatcacc cyattgccaa tgcatttggt cgtgtgccac      180
ccttgtagca gctctgcttc attcctgtct gaagaagggc agatagtttg gctgctcctg      240
tgctgtcacc tgcaattctc ccttatcagg gccattggcc tctcccttct ctctgtgagg      300
gatattttct ctgacttgtc aatccacatc ttcccatgcc ctcaagatcc aatgaacatc      360
caacctccat taaagagagt ttcttgggtc acttcctaaa tatactctgct atnctccata      420
ctctg                                           425

<210> 71
<211> 425
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 243
<223> 10-84-243 : polymorphic base C or T

<220>
<221> misc_binding
<222> 224..242
<223> 10-84-243.mis1

<220>
<221> misc_binding
<222> 244..263
<223> 10-84-243.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

```


<220>
 <221> misc_binding
 <222> 231..255
 <223> 10-84-243 potential probe

<220>
 <221> misc_feature
 <222> 413
 <223> n=a, g, c or t

<400> 71
 gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg 60
 cccgcacgga gctgttttta ttccctgacca ccattttgca gaactttaac ctgaaatctc 120
 aggttgaccc aaaggatatt gacatcaccc ccattgccaa tgcatttggc cgtgtgccac 180
 ccttgtagca gctctgcttc attcctgtct gaagaagggc agatagtgtg gctgctcctg 240
 tgytgtcacc tgcaattctc ccttatcagg gccattggcc tctcccttct ctctgtgagg 300
 gatattttct ctgacttgtc aatccacatc ttcccattcc ctcaagatcc aatgaacatc 360
 caacctccat taaagagagt ttcttgggtc acttcctaaa tatatctgct atnctccata 420
 ctctg 425

<210> 72
 <211> 425
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 277
 <223> 10-84-277 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 257..276
 <223> 10-84-277.mis1, potential

<220>
 <221> misc_binding
 <222> 278..297
 <223> 10-84-277.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 406..425
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 265..289
 <223> 10-84-277 potential probe

<220>
 <221> misc_feature
 <222> 413
 <223> n=a, g, c or t

<400> 72
 gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg 60

64

```

cccgcacgga gctgttttta ttctgacca ccattttgca gaactttaac ctgaaatctc 120
agggtgaccc aaaggatatt gacatcaccc ccattgcca tgcatttggc cgtgtgccac 180
ccttgtagca gctctgcttc attcctgtct gaagaagggc agatagtgtg gctgctcctg 240
tgctgtcacc tgcaattctc ccttatcagg gccattggc tctcccttct ctctgtgagg 300
gatattttct ctgacttgct aatccacatc tcccattcc ctcaagatcc aatgaacatc 360
caacctccat taaagagagt ttcttgggtc acttcctaaa tatatctgct atnctccata 420
ctctg 425

```

<210> 73
 <211> 425
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 295
 <223> 10-84-295 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 275..294
 <223> 10-84-295.mis1, potential

<220>
 <221> misc_binding
 <222> 296..314
 <223> 10-84-295.mis2, complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 406..425
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 283..307
 <223> 10-84-295 potential probe

<220>
 <221> misc_feature
 <222> 413
 <223> n=a, g, c or t

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<400> 73
gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg 60
cccgcacgga gctgttttta ttctgacca ccattttgca gaactttaac ctgaaatctc 120
agggtgaccc aaaggatatt gacatcaccc ccattgcca tgcatttggc cgtgtgccac 180
ccttgtagca gctctgcttc attcctgtct gaagaagggc agatagtgtg gctgctcctg 240
tgctgtcacc tgcaattctc ccttatcagg gccattggc tctcccttct ctctrtgagg 300
gatattttct ctgacttgct aatccacatc tcccattcc ctcaagatcc aatgaacatc 360
caacctccat taaagagagt ttcttgggtc acttcctaaa tatatctgct atnctccata 420
ctctg 425

```

<210> 74
 <211> 424
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 43
 <223> 10-85-43 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 24..42
 <223> 10-85-43.mis1

<220>
 <221> misc_binding
 <222> 44..63
 <223> 10-85-43.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 405..424
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 31..55
 <223> 10-85-43 potential probe

<400> 74
 gtttcttggg tcacttccta aatatatctg ctattctcca taytctgtat cacttgtatt 60
 gaccaccaca tatgctaata cctatctact gctgagttgt cagtatgtta tcactagaaa 120
 acaaagaaaa atgattaata aatgacaatt cagagccatt tattctctgc atgctctaga 180
 taaaaatgat tattattttac tgggtcagtt cttagatttc tttcttttga gtaaaatgaa 240
 agtaagaaat gaaagaaaat agaatgtgaa gaggtgtgac tggccctcat agtggttaagc 300
 acaaaaaggg agaaaggtaa gagggtagga aagctgtttt agctaaatgc cacctagagt 360
 tattggaggt ctgaatttgg aaaaaaaaaac tatgtccagg agcagctgta acvtgtaggg 420
 aaat 424

<210> 75
 <211> 424
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 117
 <223> 10-85-117 : polymorphic base G or T

<220>
 <221> misc_binding
 <222> 97..116
 <223> 10-85-117.mis1, potential

<220>
 <221> misc_binding
 <222> 118..136
 <223> 10-85-117.mis2, complement

<220>
 <221> primer_bind
 <222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 405..424

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 105..129

<223> 10-85-117 potential probe

<400> 75

gtttcttggg	tcacttccta	aatatatctg	ctattctcca	tactctgtat	cacttgtatt	60
gaccaccaca	tatgctaata	cctatctact	gctgagttgt	cagtatgta	tcactakaaa	120
acaaagaaaa	atgattaata	aatgacaatt	cagagccatt	tattctctgc	atgctctaga	180
taaaaatgat	tattatttac	tgggtcagtt	cttagatttc	tttcttttga	gtaaaatgaa	240
agtaagaaat	gaaagaaaat	agaatgtgaa	gaggctgtgc	tggccctcat	agtgttaagc	300
acaaaaaggg	agaaaggtaa	gagggtagga	aagctgtttt	agctaaatgc	cacctagagt	360
tattggaggt	ctgaatttgg	aaaaaaaaac	tatgtccagg	agcagctgta	acvtgtaggg	420
aaat						424

<210> 76

<211> 424

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 320

<223> 10-85-320 : polymorphic base A or T

<220>

<221> misc_binding

<222> 300..319

<223> 10-85-320.mis1, potential

<220>

<221> misc_binding

<222> 321..340

<223> 10-85-320.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 405..424

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 308..332

<223> 10-85-320 potential probe

<400> 76

gtttcttggg	tcacttccta	aatatatctg	ctattctcca	tactctgtat	cacttgtatt	60
gaccaccaca	tatgctaata	cctatctact	gctgagttgt	cagtatgta	tcactagaaa	120
acaaagaaaa	atgattaata	aatgacaatt	cagagccatt	tattctctgc	atgctctaga	180
taaaaatgat	tattatttac	tgggtcagtt	cttagatttc	tttcttttga	gtaaaatgaa	240
agtaagaaat	gaaagaaaat	agaatgtgaa	gaggctgtgc	tggccctcat	agtgttaagc	300

67

acaaaaaggg agaaaggtaw gagggtagga aagctgtttt agctaaatgc cacctagagt	360
tattggaggt ctgaatttgg aaaaaaaaaac tatgtccagg agcagctgta acvtgtaggg	420
aaat	424

<210> 77
 <211> 352
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 121
 <223> 10-86-121 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 102..120
 <223> 10-86-121.mis1

<220>
 <221> misc_binding
 <222> 122..141
 <223> 10-86-121.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 334..352
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 109..133
 <223> 10-86-121 potential probe

<400> 77	
aaggagaaa ggthagaggg taggaaagct gttttagcta aatgccacct agagttattg	60
gaggtctgaa tttggaaaaa aaaactatgt ccaggagcag ctgtaacctg tagggaaata	120
mtggaacaat catccataag agggatgaac attaatgtt tgaattcatg ctctgctttt	180
gtgttactgt aaacacaaga tcaagatttg gataatcttt ttcctttgtg tttccaaactt	240
agatcatgtc taaatatatg ctttcatatg gctaatacatg tgtaaatgac tgttattttt	300
ctcttccaaa caagagcaaa atctccagaa atcctcacca ggctttattt tt	352

<210> 78
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-244-275 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-244-275.mis1, potential

<220>

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<221> misc_binding
<222> 502..521
<223> 12-244-275.mis2, potential complement

<220>
<221> primer_bind
<222> 228..247
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 660..678
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-244-275 potential probe

<400> 78
atcacgttct gtccagtgtc tgcctattcc cttcttcttt ttttcttccc ttgatgccct   60
tttatcacat gcattgtctc agacccttcg aatatgtgct cataaatgca tggcatcatc   120
tccttcccac atcgattcac tttcaattaa aagccaaaac tctttcattt caactttgga   180
tttaacatgc ttttgaaaga aggggtgaga aatatagaga aacagattgg gaaaccatgc   240
tctgctgttt ctttttttta aactttctat gtaagtgtgg aatttttcat tctgttttat   300
tattaacttt aagccaagac tttttaatag aaggatataa aaatacatct ttgtctatac   360
atttctgctg aatttgaaga aatgctgaat attcttaaac cattgtgttc cctggtgggc   420
tgatggactg tgattttata aggtggcctc agccaactgc agcagctgtt ccctgtcaga   480
ggggctagag gtttggcaag rgcggtggaa gaggtgcagt ggtgtgttcg ttcactagaa   540
gcatcaggga gaagggtttg cctgtttgta tttcatcttc tctcatcaag tcctcagaaa   600
ccacagtgtc gtctgcaggg tgctgtggat ctggcatggc ccatacaggc aacatgactg   660
agtagaaagg acacacagct ctggatgtcc ttgggcccc aagcaactgc ccttgaaca   720
tttagtcctt gtgagcattt gatgatttac ttgccttcaa tttccatgg acctaatact   780
ctttataaag ggaaatattt taaacctatg aaacattgtg gagaatggca tgggaaatac   840
ccatgtatgc accaccagc ttaacaaatg ctctcctgtc atttctaacc acaatctctt   900
tgaagagctc ttttgtcttt caatctctct tccctgtttg gccacatta cccttcatcg   960
tatgaagact tggatggctc ctgtgtcaga ctcttgtgtg g                                     1001

<210> 79
<211> 950
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 450
<223> 12-251-153 : polymorphic base A or C

<220>
<221> misc_binding
<222> 431..449
<223> 12-251-153.mis1

<220>
<221> misc_binding
<222> 451..470
<223> 12-251-153.mis2, potential complement

<220>
<221> primer_bind
<222> 298..318
<223> upstream amplification primer

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<220>
 <221> primer_bind
 <222> 806..826
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 438..462
 <223> 12-251-153 potential probe

<220>
 <221> misc_feature
 <222> 52,54,100
 <223> n=a, g, c or t

<400> 79
 taggaagctg agagaaaagg atcttctccc ctgtgcacag gagccaggaa tnanttatct 60
 gttacattgt ccccttgat attccaaaag aataatacan tgtgtagaaa gaaaaataa 120
 aaacctgatt gtactaaagt tttgagcata gacgttatgg agtggaggga ggggaagggtg 180
 tttgatagct gttggctggc agtgactggg gcaggaaagt tacaatgagg aagttggaat 240
 aacttcaatc ccttcattat tttgctgagg ataccaccaa aatatgaaat attaaacctt 300
 cccaccactt ctaatttctt ttctccaatc ttaaatttta aaagactctg taaaggctat 360
 aggtagggca atgctattgt ttgttgtctg aactggaatg taatttgaat tatgctggaa 420
 caacatgtgt aagctgagcc tgcctgggm agactgggga catgtggtca ctcagctatg 480
 ggatgccccg atcaactttg gagtgatcta tttgtttaat caatatcact gttagtctt 540
 acttttacaa aaataatctg ccctcagagc aacctcagat cccaggagtt ggggaaaagc 600
 aggtgtttca ggaggcttat caggagtgagc agcggagaca tgacgttcac agcaagtctg 660
 aacaggggtg ggctgttcta taaagtgtg aagagacatc agctctgggc gtagactgtg 720
 gggctctggca atgtcaaatt tattgattgg ccgagaaaga gttaattatt ttattcttgt 780
 cctgcagaag cacagtgttg acacaccttt taccatccac actcaacaca aactactgta 840
 attgtctgat tattgggtct gtgtctccct atgactgagg tccttgagct cagaggtggg 900
 tctaactcac cttagtgtct ccatcactcc cagcacaggg ccagctgcat 950

<210> 80
 <211> 746
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 246
 <223> 12-254-115 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 226..245
 <223> 12-254-115.mis1, potential

<220>
 <221> misc_binding
 <222> 247..266
 <223> 12-254-115.mis2, potential complement

<220>
 <221> primer_bind
 <222> 132..152
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 586..603
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 234..258
 <223> 12-254-115 potential probe

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<400> 80
ctgccacaat ctcttgagtc cagacaatct agagcagaag ggtagactga ggaaaatata      60
cacagtataa aaaagtaaca aaatcaaaac ctgaaacaaa gatcaacatc caataaatgc      120
ttctgaataa agggagagta gataagaact ggattttaat cccaacactg ccattttacca      180
gctggccaat actgagctag ttactctaaa gagttcagtt ttctcatttg taaaaatagg      240
atttgwcttt ccattctcact gagttgtgat gagagtcata tgcaacagca tatgaagagg      300
ctagcaaaaag gtattttaaca agcgttcaac attctcatga tgacatgaat aacactgtac      360
atacaacata ccaacttgat aaatacacag cacagttaat agctgagggc agagtttatgg      420
ttgggaagag agagagtgcg acataggcag agtgaggggg gattcccaca atttttctaag      480
acagaaaagt gggggaatca gtagttactg gaaagaatag gcaatgcctg actggataga      540
aaaagattct atgcctttgt caaatttcac aaaagtgact taagcctata ctgcgggatg      600
ttcacactac gtcccttttag tgcagttacg gtacttcagg ctgcaagtaa ccaaatacaa      660
ctaaaattgt cttatacaat aagggcgtaa ttatctcata taacaagaag cttggcatga      720
aggaaatttc aacaatttca caacgg                                     746
```

<210> 81
 <211> 811
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 311
 <223> 12-254-180 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 292..310
 <223> 12-254-180.mis1

<220>
 <221> misc_binding
 <222> 312..331
 <223> 12-254-180.mis2, potential complement

<220>
 <221> primer_bind
 <222> 132..152
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 586..603
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 299..323
 <223> 12-254-180 potential probe

```
<400> 81
ctgccacaat ctcttgagtc cagacaatct agagcagaag ggtagactga ggaaaatata      60
cacagtataa aaaagtaaca aaatcaaaac ctgaaacaaa gatcaacatc caataaatgc      120
ttctgaataa agggagagta gataagaact ggattttaat cccaacactg ccattttacca      180
gctggccaat actgagctag ttactctaaa gagttcagtt ttctcatttg taaaaatagg      240
atttgctttt ccattctcact gagttgtgat gagagtcata tgcaacagca tatgaagagg      300
ctagcaaaaag rtattttaaca agcgttcaac attctcatga tgacatgaat aacactgtac      360
atacaacata ccaacttgat aaatacacag cacagttaat agctgagggc agagtttatgg      420
```


71

ttgggaagag agagagtgca acatagggcag agtgaggggg gattcccaca attttctaag	480
acagaaaaagt gggggaatca gtagttactg gaaagaatag gcaatgcctg actggataga	540
aaaagattct atgcctttgt caaatttcac aaaagtgact taagcctata ctgcgggatg	600
ttcacactac gtcccttttag tgcagttacg gtacttcagg ctgcaagtaa ccaaatacaa	660
ctaaaaattgt cttatacaat aagggcgtaa ttatctcata taacaagaag cttggcatga	720
aggaaaatttc aacaatttca caacggcaac aaaaactctg tttcttctac ctttccacca	780
ttcctgtggt ctcagttcca atatggctgc t	811

<210> 82

<211> 999

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-265-300 : polymorphic base T or C

<220>

<221> misc_binding

<222> 479..498

<223> 12-265-300.mis1, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-265-300.mis2, potential complement

<220>

<221> primer_bind

<222> 779..798

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 308..328

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-265-300 potential probe

<220>

<221> misc_feature

<222> 427,494,669..670,679,772,874,944

<223> n=a, g, c or t

<400> 82

taataatgtg ttttggggta agcctactca tattctcaac ctgtctgcag tagtcgttag	60
aatctgaact tcctgaagtt catgtgcaaa gttgagttaa ttgtttaata ttcaacaagg	120
attatgccag taagatggta ggaaaatatt agatatgtgt catcactgct ggtattattt	180
aaactgcaac atatttttagc tggctgctga tctcagccac catgcctgca ttttatctct	240
gtctcgtggt ctgcaacctt ggaagctttg aacttagctc atagaatcct gggcatcaag	300
aacatgtggt tctaattggct agatagggaa tgagagtaaa aggattttgc ccacggtcac	360
gtgagtaaac aacagatttg gaggggtctg gactactgtg atgacttcat tctgacaata	420
tgttccnagt tgtcctttca tttcctccta atcacatgtc tggctctgatc tggctgtttc	480
ccaccttcca attncctgyc ttctccaatg ctcccttccg taggtcactc tgtggctcag	540
agaccctgct tagcaagcgc ccaacctttc aattattttgt tcagtaaaac ttgaactcat	600
gtctcccttt cttgataaaa agaaaatacgt ttatgtaatg tcgggttact ctataactct	660
tgtctcgtgnn ctctcggcna actactgaac taactgtttt catattgagc aaacgtttat	720
ggaaggactg ccaagagtca ggtactaggc ttggtaatat tccccgttct cntctagtca	780
aagccaacac cagccagact tgcagatcta ggtcccaagc ccactgcaga tcacaggcca	840

72

```

gggtctggtc tcctctgagc tcctttggga gggnaaagac agaattatta acacccattt 900
tgtagattag gcaactgagg ctgaggaagt ttaaataact cagnacaggg cctgcacgtc 960
agtcataattc caaggatccc tactcactgt cttctctct 999

```

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<210> 83
<211> 1001
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 501
<223> 12-271-118 : polymorphic base T or C

```

```

<220>
<221> misc_binding
<222> 481..500
<223> 12-271-118.mis1, potential

```

```

<220>
<221> misc_binding
<222> 502..521
<223> 12-271-118.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 598..618
<223> upstream amplification primer, complement

```

```

<220>
<221> primer_bind
<222> 122..141
<223> downstream amplification primer

```

```

<220>
<221> misc_binding
<222> 489..513
<223> 12-271-118 potential probe

```

```

<220>
<221> misc_feature
<222> 205,525,542,571,657
<223> n=a, g, c or t

```

```

<400> 83
gactgagtcc gaaaaggagt ctgcaaaggg agataggggt gggtcagttt tataggactg 60
gggtaagcag tggaaagttg cagttaaagg aagttatcta ttgtcagcag aggaggggggt 120
cacaagggtg atggtagggg gatcataaga ctcattgtcc agaagaagaa tgtcacgagg 180
tcgatcaatc gatcagttgg ggcangggca gtaacaagtc ataatggaac gttgtaagggt 240
tggccaatca gtttaagacag gagctggctg tttcacctat ttgtagtttt tggttgcctc 300
aggccatctg gatgtaccca tgcaggcttg ggctaagagg cctgaaaccc accactttcc 360
catgtcaaat ctttagtaga tgtaccccca agatacacat tcctcggacc ttcttttcca 420
tagttaaaac ttcacccttg aaatgtagaa acaggaagggt ttttttttta agtttcagtg 480
caaactcgga gcaagtgtca yaattttctg tctccgatgt gtagnagggtg acattttctc 540
angaactttc acggttaagct ggaaaactgg naaagcgagt ccactttgtc attctgtcac 600
tcaactcatt tctcactcaa caaacatgcc tcacacttat ctaaatctgc tagactnaaa 660
agagggtccct ggtgtctgta acttttcta tctgctagaa ttctagagtg agctcatgaa 720
ataaatgaaa aggatgaaga acaaagagaa aaaagactgc acgttccctt ctggcgctca 780
ctcacattcc ctcagcctca gttttctccac atgcccctag aggtgatcat tcaaggattt 840
atgagatttt agagacaaca catgaaaaag caaagagaca tcagaaagac aaggagttac 900
ttagtattta tacacaagga taagacattc agtatcgaca acacttaaag aaaattcaag 960
agtgatttta aatttcccat ttcaaatacc tcctctattt t 1001

```

73

<210> 84
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-272-112 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-272-112.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-272-112.mis2, potential complement

<220>
 <221> primer_bind
 <222> 390..409
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 768..788
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-272-112 potential probe

<400> 84
 aagagggggcc caacttgtaa tcataggagc ttatgctatt ttaatgccat ccatcagact 60
 acaatcaatt accactcatc tagctttttg tccatctctc attcttgtag atcctgagat 120
 agtcaattct gagaactgta gcctagatct atcacctgat gcctctcaaa gatataatcc 180
 gtgcttctca agctaggcta tgcacacaaa tcaactgcac ttgtgaaagt tcagattttg 240
 aatcagtagt tcaaggggtg ggtttgagat ttgcatctc taatgagctc tcagatgctt 300
 ctgacccatg gaccacactt tgaataccaa gaagtggctc gtagaccaat attggtccct 360
 taagtccctc caaacatata ttcgggaaac gtctttgat tttccctaca tttaaccatt 420
 agtggtgcaa attctctcaa agtttgtaa gatataattg agctaaaata aattacattt 480
 ttcttggggg agagtactac mtcataattaa cttacaataa agtactttta ggatcattca 540
 aggaacacac ccataacact gagtatgtta tgcggaaatg ctctctctgg aaattacaca 600
 gctgtgcagg tggcgggggt ggcattgagga ggagtggatg gccacattc tcgaagacct 660
 tgggggaaaac tggattaaaa tgatttgctt tattctgggt ctgtaagata cacatcagaa 720
 tgaaaccacc ccagtgtag ctctgaattg cttttctatt cttttccctt agggatttga 780
 gggcttcaat tagatttctc ttcattctaa ctgtgatgcc ctacattgat ctgatttacc 840
 taaaatgtct ttcctctcct ttcagctctg tccgatctgg agctcgtggc ccaatcaatt 900
 atctttatct ttgctggcta tgaaaccacg agcagtggtc tctccttcat tatgtatgaa 960
 ctggccactc accctgatgt ccagcagaaa ctgcaggagg a 1001

<210> 85
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 10-216-182 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 483..502
 <223> 10-216-182.mis1, potential

<220>
 <221> misc_binding
 <222> 504..522
 <223> 10-216-182.mis2, complement

<220>
 <221> primer_bind
 <222> 323..339
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 800..819
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 491..515
 <223> 10-216-182 potential probe

<220>
 <221> misc_feature
 <222> 76,80,96,319,399,556,578,667,676,731,752,759,914,933
 <223> n=a, g, c or t

<400> 85
 tgctatcctt cccccctctc cccacccac aacaggcccc agtgtgtgat gttccccttc 60
 ctgtgtccat gtgttnctcn attgtatatt tttttnaaat ctaccacatc aaggcacctc 120
 tttttcatgt tgcccattgt ttaggtgaac ataaagacag agctcgtctg aggcaacata 180
 cagtccaaca aagccacctg cctctctgtc tccactctct ctctacactg cacgcgtgct 240
 aggtgttgat cctgtctatt ccagtgggaag aacagggtcc gtaccatgtg gagaatttgc 300
 atgtaaaagg agactgggna tatacaggct ggagaccaca tcaggtggct gggcatgtgg 360
 gataaatcct attgagcatc tgtcataggg cctgtcacnt tagtagacag tcactaaata 420
 tttgttaaat acatgatgcc tgtttaacac attttctaca accatggaga cctccacaac 480
 tgatgtagga caaaatcttt ctrctttgaa ctctagcctt tcgggccagt gggatttatg 540
 aaaaatgcc a tctctnatag ctgaggatga agaattggnaa gagaatacga tcattgctgt 600
 ctccaacatt caccagcgga aaactcaagg aggtatgaaa ataacttggg ttttaattag 660
 aaacttnaaa gaatgnaatc aggtggggac aggtagaaa taagatcaga gttcctttcc 720
 gaggagtagt nctgctgaat ttgagcttcc tnaaaaatna gtctttttat gtacagaaaa 780
 cacatcataa aattcattac acaatgtcac ttattgttcc atgccaggca aagtcattgtc 840
 cttctgggac ttatgtctgc acatttaact atgggtgggtg ttgtgttttg tgcttagatg 900
 gtccctatca ttgncccagt atggagatgt gtntgggtgag aaatctgagg cgggaagcag 960
 agacaggcaa gcctgtcacc ttgaaacagt aagtaggagc a 1001

<210> 86
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-217-91 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 482..500

<223> 10-217-91.mis1

<220>

<221> misc_binding

<222> 502..521

<223> 10-217-91.mis2, potential complement

<220>

<221> primer_bind

<222> 411..427

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 761..777

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-217-91 potential probe

<220>

<221> misc_feature

<222> 20,100,257,279,368,377,432,453,460,615,634,921,946,986

<223> n=a, g, c or t

<400> 86

catgtaaaag gagactgggn atatacaggc tggagaccac atcaggtggc_tgggcatgtg	60
ggataaatcc tattgagcat ctgtcatagg gcctgtcacn ttagtagaca gtcactaaat	120
atttggtaaa tacatgatgc ctgtttaaca cattttctac aaccatggag acctccacaa	180
ctgatgtagg acaaaatctt tctgctttga actctagcct ttcggggccag tgggatttat	240
gaaaaatgcc atctctnata gctgaggatg aagaatggna agagaatacg atcattgctg	300
tctccaacat tcaccagcgg aaaactcaag gaggtatgaa aataacttgg gttttaatta	360
gaaacttnaa agaatgnaat caggtgggga caggtagaaa gtaagatcag agttcctttc	420
cgaggagtag tnctgctgaa tttgagcttc ctnaaaaatn agtcttttta tgtacagaaa	480
acacatcata aaattcatta yacaatgtca cttattgttc catgccaggc aaagtcatgt	540
ccttctggga cttatgtctg cacatttaac tatgggtggg gttgtgtttt gtgcttagat	600
ggtccctatc attgncccag tatggagatg tgtntgggtg gaaatctgag gcggaagca	660
gagacaggca agcctgtcac cttgaaacag taagtaggag cacagccatg gggttctgag	720
ctgtcatgag cccctccagc tgcctgctat ggagctgata ctcccgtgtg tgggttattc	780
cagtgaccag acaaaaggag ggctgtggta atgcaacttc aatgggtctc ccaagatggg	840
gcagctccga tgaggagggtg gggcagctgg aggaaaagga tcttctcccc tgtgcacaga	900
ggtcagggtt tacatatctg nttaaattgt caccttggat attctnngag gactaaatac	960
atcctttagg gggaaaagtg tgattngtat caaagtttta a	1001

<210> 87

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-213-292 : polymorphic base G or C

<220>

<221> misc_binding

<222> 484..502

<223> 10-213-292.mis1

<220>

<221> misc_binding

```

<222> 504..523
<223> 10-213-292.mis2, potential complement

<220>
<221> primer_bind
<222> 212..230
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 590..608
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-213-292 potential probe

<220>
<221> misc_feature
<222> 86,281,718,743,788,878,885,890,1000
<223> n=a, g, c or t

<400> 87
attagtcatg tttgcttcca tgagaaagaa aaaccactac atgggttatgc taaggatttc      60
agtcattggg gttagagcct tcccgnaatg tctcctgctt tcataactcc tccacacatc      120
ttagtggggc attgagcaca tcaaagggca tgacagttat taaaatactt tatgaatgct      180
acaatccttt gccagtatga gttgttctct ggaacttcta acagttcaac agtactacat      240
ggactgagtt aaaagttaat tcaaaaatct caatttatcc naaatctggt tctttctttt      300
caggcaccac ccacctatga tactgtgcta cagttggagt atcttgacat ggtggggaat      360
gaaacactca gattattccc agttgctatg agacttgaga gggctctgca aaaagatggt      420
gaaatcaatg ggatgtttat tcccaaaggg gtgggtggga tgattccaag ctatgttctt      480
catcatgacc caaagtactg gasagagcct gagaagttcc tccctgaaag gtaggaggcc      540
cctgggaagg gagccctccc tgaaccagcc tgggttcaagc atattctgcc tctctacagg      600
acagtctggg cttgtacaat catttgcttg tctttttatg tttaaaaggt tttttcaaat      660
catgaaattg atcattgtca cactttacaa accacagact agataaaaaga aaactatnag      720
ccagtcacag tcccagcaac ttnaagatga aggtcctcaa ttatgtcctt atgggtcata      780
agtgtccnaa aatgtaagga ctctttttaa aacacatgat cacaatgcta ttattatgtc      840
ccacaaatga atattttttc ctgaatataa tcaaatcntt caggnaatcn aaatttgaat      900
aaaaaacatg cgtctaattc tcaaagaatt tatagggttag tgcaacagat agacaaagaa      960
agcagtgatg acactgcttt ccatcaatac agtagcatcn a                               1001

<210> 88
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-214-279 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-214-279.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-214-279.mis2, potential complement

<220>

```

```

<221> primer_bind
<222> 154..174
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 746..763
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-214-279 potential probe

<400> 88
ctcatccatt ttacttaaaa tttaaatacaaaa aaaagaacac aggtttccat gaatttgctct 60
caggcctggc acagaatagt actccataaa tattttgtta aatgatagat gatgaatgct 120
ctcactgtcc aatcttcaca catcttatag actaagtata aagaatccaa gattttatagt 180
gctgaaagta gtttttatat gtttacaaag cattattgtc attactgcat ttttttgcc 240
cattactcca tagagatcag aatatcactc tggtgtgtcc cctcaacact gaaggagtgt 300
ctcactcact ttgatgctat actttctact tttgtttatt taatgcttct caatatgctt 360
gtttaactgt tgcagatccc cctgaaaatta agcttaggag gacttcttca accagaaaaa 420
cccgttgctc taaagggtga gtcaagggat ggcaccgtaa gtggagcctg aattttccta 480
aggacttctg ctttgctctt yaagaaatct gtgcctgaga acaccagaga cctcaaatta 540
ctttgtgaat agaactctga aatgaagatg ggcttcatcc aatggactgc ataaataacc 600
ggggattctg tacatgcatt gagctctctc attgtctgtg tagagtgtta tacttgggaa 660
tataaaggag gtgaccaaat cagtgtgagg aggtagattt ggctcctctg cttctcacgg 720
gactatttcc accaccccca gttagcacca ttaactcctc ctgagctctg ataagagaat 780
caacatttct caataatttc ctccacaaat tattaatgaa aataagaatt attttgatgg 840
ctctaacaat gacatttata tcacatgttt tctctggagt attctataag ttttatgtta 900
aatcaataaa gaccacttta caaaagtatt atcagatgct ttcctgcaca ttaaggagaa 960
atctatagaa ctgaatgaga accaacaagt aaatatTTTTT g 1001

<210> 89
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-214-380 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-214-380.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 10-214-380.mis2, complement

<220>
<221> primer_bind
<222> 124..143
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 647..664
<223> downstream amplification primer, complement

```

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-214-380 potential probe

<220>
 <221> misc_feature
 <222> 398,723,730,789
 <223> n=a, g, c or t

<400> 89
 gaacacgggt tcccatgaat ttgtctcagg tcaaacctca cacagaatag gtgctccatg 60
 aatattttgt taaatgatag atgatgaatg ttctcactat ccaatcttca cacatcttat 120
 agagtaagta taacgaatcc aagatttata gtgctgaaag tagtttttat atgtttacaa 180
 agcattattg tcagtaatgt ttttttactt tgatgctata ctttctactt ttgctttatt 240
 taatgcttct caatatgctc gtttaactgt tgcagatccc cctgaaatta cgctttggag 300
 gacttcttct aacagaaaaa cccattgttc taaaggctga gtcaagggat gagaccgtaa 360
 gtggagcctg atttccctaa ggacttctgg tttgctcntt taagaaagct gtgccccaga 420
 acaccagaga cctcaaatta ctttacaat agaacctga aatgaagacg ggcttcaccc 480
 aatgtgctgc ataaataatc rgggattctg tacgtgcatt gtgctctctc atggtctgta 540
 tagagtgtta tacttggtta tatagaggag atgaccaa atcagtgctggg gaagtagatt 600
 tggcttctct gcttctcata ggactatctc caccacccc agttagcacc attaaactct 660
 cctgagctct gataacataa ttaacatttc tcaataattt caaccacaat cattaataaa 720
 aantaggaan ttattttgat ggctctaaca gtgacattta tatcatgtgt tatatctgta 780
 gtattctant agtaagcttt atattaagca aatcaataaa aacctcttta caaaagtatt 840
 attggatgtt tcctgcacat taaggagaaa tctatagaac tgaatgactg agaaccaaca 900
 actaaatatt ttgatcattg taatcactgt tgggtgtggga actggagtgc agtggtgcaa 960
 tcttggctca ctgcgagctc tgctcccg gttcacgcca t 1001

<210> 90
 <211> 437
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 216
 <223> 2-1-216 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 196..215
 <223> 2-1-216.mis1, potential

<220>
 <221> misc_binding
 <222> 217..236
 <223> 2-1-216.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 417..437
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 204..228
 <223> 2-1-216 potential probe


```

<400> 90
gcccaaagaa gtgtgttggtg tttgcttatt tcttacagag taatgctgaa atctgtgttg      60
cttttcccca ccagggtcatt atcagtagca gaagtgttc ctgggtcatg agtcgggtct      120
gggatgatgg ctatccttgg gatatgatgt atgttaccg ctttgcaccc tttctccgga      180
atgtccttcc ttcattcatc tctgactggt tataatrtcca gaagatgaac acgtgggttta      240
agcatgagaa ctatggcctg atgcctttaa atgggtactt aaaaatggaa atttttttta      300
ttcaaaaaag gggggcactc atttaataaa tttattctct ctagaactta cttttgttgt      360
ctcattgagc ctagaacat taaactcaag gtttcatagg tgacggaata tgcccagaga      420
ccacgtatgg cttggaa                                     437

```

```

<210> 91
<211> 437
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 397
<223> 2-1-397 : polymorphic base C or T

```

```

<220>
<221> misc_binding
<222> 377..396
<223> 2-1-397.mis1, potential

```

```

<220>
<221> misc_binding
<222> 398..417
<223> 2-1-397.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 417..437
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 385..409
<223> 2-1-397 potential probe

```

```

<400> 91
gcccaaagaa gtgtgttggtg tttgcttatt tcttacagag taatgctgaa atctgtgttg      60
cttttcccca ccagggtcatt atcagtagca gaagtgttc ctgggtcatg agtcgggtct      120
gggatgatgg ctatccttgg gatatgatgt atgttaccg ctttgcaccc tttctccgga      180
atgtccttcc ttcattcatc tctgactggt tataatrtcca gaagatgaac acgtgggttta      240
agcatgagaa ctatggcctg atgcctttaa atgggtactt aaaaatggaa atttttttta      300
ttcaaaaaag gggggcactc atttaataaa tttattctct ctagaactta cttttgttgt      360
ctcattgagc ctagaacat taaactcaag gtttcayagg tgacggaata tgcccagaga      420
ccacgtatgg cttggaa                                     437

```

```

<210> 92
<211> 426
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele

```

80

<222> 232
 <223> 2-3-232 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 212..231
 <223> 2-3-232.mis1, potential

<220>
 <221> misc_binding
 <222> 233..252
 <223> 2-3-232.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 406..426
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 220..244
 <223> 2-3-232 potential probe

<220>
 <221> misc_feature
 <222> 419
 <223> n=a, g, c or t

<400> 92	
gagtvgcaga cttttcagtg cttttccatt catgacactt cttgaatctc tggcagaacc	60
agccagccgt gttcacagtg tcaaataaag ggatgtcttt gattgcttcc aggtgttcc	120
cagcaccacc ggagggggat gggatgatcag ccgaatcttt gactcgggct acccatggga	180
catgggtgttc atgacacgct ttcagaacat gttgagaaat tccctcccaa cyccaattgt	240
gacttggttg atggagcgaa agataaaciaa ctggctcaat catgcaaatt acggctta	300
accagaagac aggtaaatat aatgtgactg ccaagggctt ttaggaagaa ggagcctctg	360
cctgtccagc agcctataca agccaggcag taccacagca acatggctga atgtgtggna	420
acactt	426

<210> 93
 <211> 429
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 51
 <223> 2-4-51 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 31..50
 <223> 2-4-51.mis1, potential

<220>
 <221> misc_binding
 <222> 52..71
 <223> 2-4-51.mis2, potential complement

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<220>
<221> primer_bind
<222> 3..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..429
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 39..63
<223> 2-4-51 potential probe

<400> 93
gygctgttac tgtaaagaca ttgcattact actgttgacc tcagagcacg mgcctcttgc      60
ctaattctag gactcctaac taagtctttg gagtttcagc tggaagaatg ctggaggaat      120
acggaactcc tcccatttct cacagccacc tccaactctt aaaaacgctt ccaactgcct      180
cccagcacac aaccaaggga gaaaactatt ctgtcaaaga gacggtgcca aaaggcaaaa      240
acaaaggtaa ggatgatcgc tggggaaaga agctgaaaag gaaaagctca gaactctagc      300
tggaattttg gctcacatcc ctagtatgtt actgcatagt ctggctttgt tcaatgggtc      360
gctttttaat attaaagcta gatgtaagca aggtttgcaa caaagtccat aagaaactca      420
gcttttctc                                     429

<210> 94
<211> 429
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 126
<223> 2-4-126 : polymorphic base A or G

<220>
<221> misc_binding
<222> 106..125
<223> 2-4-126.mis1, potential

<220>
<221> misc_binding
<222> 127..146
<223> 2-4-126.mis2, potential complement

<220>
<221> primer_bind
<222> 3..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..429
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 114..138
<223> 2-4-126 potential probe

<400> 94
gygctgttac tgtaaagaca ttgcattact actgttgacc tcagagcacg agcctcttgc      60
ctaattctag gactcctaac taagtctttg gagtttcagc tggaagaatg ctggaggaat      120

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82

acggarctcc	tcccatttct	cacagccacc	tccaactctt	aaaaacgctt	ccaactgcct	180
cccagcacac	aaccaagggg	gaaaactatt	ctgtcaaaga	gacggtgcc	aaaggcaaaa	240
acaaaggtaa	ggatgatcgc	tggggaaaga	agctgaaaag	gaaaagctca	gaactctagc	300
tggaaatttg	gctcacatcc	ctagtatggt	actgcatagt	ctggctttgt	tcaatgggtc	360
gcttttaaat	attaaagcta	gatgtaagca	aggtttgcaa	caaagtccat	aagaaactca	420
gcttttctc						429

<210> 95

<211> 420

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 202

<223> 2-5-202 : polymorphic base A or G

<220>

<221> misc_binding

<222> 182..201

<223> 2-5-202.mis1, potential

<220>

<221> misc_binding

<222> 203..222

<223> 2-5-202.mis2, potential complement

<220>

<221> primer_bind

<222> 1..25

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 400..420

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 190..214

<223> 2-5-202 potential probe

<400> 95

tgtttaaagc	caatthcctg	agcacatcat	aaggattctc	ttaccgggtg	tcccagttaa	60
gtaatgttga	ttgatcaact	ccttgacagg	agctgatggc	aaagaaggta	gctgtgattg	120
gagctggggt	cagtggccta	atttctctga	agtgtctgtg	ggatgaggga	cttgagccca	180
cttgctttga	gagaactgaa	grtattggag	gagtgtggag	gttcaaagta	agtgagattt	240
tcttgggtct	tgaacagggt	gtgttggtat	ttcagggtga	atcacagtta	ctgatgggtc	300
atattgagaa	atttattaaa	caactctgat	cagattttat	ttctacttat	tgatgtggcc	360
ataatggaac	tgaagtcata	ggctggcatc	tctccccag	tcaataactaa	cccaaccag	420

<210> 96

<211> 420

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 275

<223> 2-5-275 : polymorphic base A or G

<220>

<221> misc_binding

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<222> 255..274
<223> 2-5-275.mis1, potential

<220>
<221> misc_binding
<222> 276..295
<223> 2-5-275.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 400..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 263..287
<223> 2-5-275 potential probe

<400> 96
tgtttaaaagc caatthcctg agcacatcat aaggattctc ttaccggttg tcccagttaa      60
gtaatgttga ttgatcaact ccttgacagg agctgatggc aaagaaggta gctgtgattg      120
gagctggggg cagtggccta atttctctga agtgctgtgt ggatgaggga cttgagccca      180
cttgctttga gagaactgaa gatattggag gagtgtggag gttcaaagta agtgagattt      240
tcttgggtct tgaacagggt gtgttggtat ttcarggtga atcacagtta ctgatgggtc      300
atattgagaa atttattaaa caactctgat cagattttat ttctacttat tgatgtggcc      360
ataatggaac tgaagtcata ggctggcatc tctcccccag tcaataactaa cccaaccagg      420

<210> 97
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 346
<223> 2-5-346 : polymorphic base C or T

<220>
<221> misc_binding
<222> 326..345
<223> 2-5-346.mis1, potential

<220>
<221> misc_binding
<222> 347..366
<223> 2-5-346.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 400..420
<223> downstream amplification primer, complement

<220>

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<221> misc_binding

<222> 334..358

<223> 2-5-346 potential probe

<400> 97

tgttttaaagc caatthcctg agcacatcat aaggattctc ttaccgggtg tcccagttaa	60
gtaatgttga ttgatcaact ccttgacagg agctgatggc aaagaaggta gctgtgattg	120
gagctgggggt cagtggccta atttctctga agtgctgtgt ggatgaggga cttgagccca	180
cttgctttga gagaactgaa gatattggag gagtgtggag gttcaaagta agtgagattt	240
tcttgggtct tgaacagggt gtgttggtat ttcagggtga atcacagtta ctgatgggtc	300
atattgagaa atttattaaa caactctgat cagattttat ttctayttat tgatgtggcc	360
ataatggaac tgaagtcata ggctggcatc tctccccag tcaataactaa cccaaccag	420

<210> 98

<211> 430

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 171

<223> 2-8-171 : polymorphic base A or G

<220>

<221> misc_binding

<222> 151..170

<223> 2-8-171.mis1, potential

<220>

<221> misc_binding

<222> 172..191

<223> 2-8-171.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 405..427

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 159..183

<223> 2-8-171 potential probe

<400> 98

ggttcaagat ycctcagcaa atgaccttc agaatgtttt tcttctgtat gtctcagata	60
cattatgaag gaacctgtac taaatgatga tgtcccaagt cgtctactct gtggagccat	120
caaggtgaaa tctacagtga aagagctcac agaaacttct gccatctttg rggatggaac	180
agtggaggag aacattgatg tcatcatttt tgcaacagga tatagtttct cttttccctt	240
ccttgaagat tcaactgcta aagtagagaa taatatgggt tcaactgtata aatacatatt	300
ccccgctcac ctggacaagt caaccctcgc gtgcattggc ctcattccagc ccctagggtc	360
cattttccca actgctgaac ttcaagctcg ttgggtgaca agagtttcaa aggtaagtgt	420
gtaggcaggt	430

<210> 99

<211> 428

<212> DNA

<213> Homo Sapiens

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<220>
<221> allele
<222> 188
<223> 2-9-188 : polymorphic base A or G

<220>
<221> misc_binding
<222> 168..187
<223> 2-9-188.mis1, potential

<220>
<221> misc_binding
<222> 189..208
<223> 2-9-188.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 176..200
<223> 2-9-188 potential probe

<400> 99
tcacatwgag tgctatgggg gtggcacccc ctgaagtcca acagcacgga agccctgact      60
ggtatgacat ggttcaatgt ccagagtcca attttaagaa tcaacaacta gacaaagtaa      120
tgatattgac tcaaaacttac tattcaaacc aaccttttat tccttaggct tgtgtagcct      180
gccctcarag agaactatga tgatggacat tatcaaaagg aatgaaaaaa gaattgacct      240
gtaagaatct tttttaattc tttacatgaa gcagtgtttc tcaaagtaca gtgatctaac      300
tacttacaag aaccacctag ctgcctgata aaatgcaaat ttctgggcta tagcccagat      360
gattgaatca gaaactccgt gtgtgaggct aaaaagttgc atttttatct tcttcctaag      420
ggtcatag                                     428

<210> 100
<211> 428
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 223
<223> 2-9-223 : polymorphic base G or T

<220>
<221> misc_binding
<222> 203..222
<223> 2-9-223.mis1, potential

<220>
<221> misc_binding
<222> 224..243
<223> 2-9-223.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21

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<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 211..235
<223> 2-9-223 potential probe

<400> 100
tcacatwgag tgctatgggg gtggcacccc ctgaagttca acagcacgga agccctgact      60
ggatgacat gggtcaatgt ccagagttta attttaagaa tcaacaacta gacaaagtaa      120
tgatattgac tcaaacttac tattcaaac aaccttttat tccttaggct tgtgtagcct      180
gccctcagag agaactatga tgatggacat tatcaaaagg aakgaaaaaa gaattgacct      240
gtaagaattt tttttaattc ttacatgaa gcagtgttc tcaaagtaca gtgatctaac      300
tacttacaag aaccacctag ctgctgata aaatgcaaat ttctgggcta tagcccagat      360
gattgaatca gaaactccgt gtgtgaggct aaaaagttgc atttttatct tcttcctaag      420
ggcatag                                           428

<210> 101
<211> 450
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 107
<223> 2-10-107 : polymorphic base C or T

<220>
<221> misc_binding
<222> 87..106
<223> 2-10-107.mis1, potential

<220>
<221> misc_binding
<222> 108..127
<223> 2-10-107.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 423..443
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 95..119
<223> 2-10-107 potential probe

<400> 101
caaaactgagc aaatcgcccta atcttccaaa ttctttttcc tggcttggtta gagcagccaa      60
gggtgggggtg gagcttggtga ataaaaagcc tgcttcatct tcctcaygca ggagaacatg      120
gccaagcgag ttgccattgt gggagctggg gtcagcggcc tggcctccat caagtgtgtg      180
ctggaagaag gactggagcc cacctgcttt gagaggagcg atgaccttgg ggggctgtgg      240
agattcaccg taagtgggggt ttcaacaact ttatctgtct atggagaatg gcttggcagc      300

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87

tgggaaatta tatctgtgct tctttcaca	gggttggtgg ccttgaggaa ggtagaaat	360
gtctgctgaa caggggacca tgaggagcca	ctgaaattgt aaaagaaaca ggacatgggt	420
gagctagggt ggaagtcaga acaggtcata		450

<210> 102
 <211> 450
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 377
 <223> 2-10-378 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 357..376
 <223> 2-10-378.mis1, potential

<220>
 <221> misc_binding
 <222> 378..397
 <223> 2-10-378.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 423..443
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 365..389
 <223> 2-10-378 potential probe

<400> 102		
caaaactgagc aaatcgcccta atcttccaaa	ttctttttcc tggcttggtta gagcagccaa	60
gggtgggggtg gagcttggtga ataaaaagcc	tgcttcattct tcctcatgca ggagaacatg	120
gccaagcgag ttgccattgt gggagctggg	gtcagcggcc tggcctccat caagtgtgt	180
ctggaagaag gactggagcc cacctgcttt	gagaggagcg atgaccttgg ggggctgtgg	240
agattcaccg taagtgggggt ttcaacaact	ttatctgtct atggagaatg gcttggcagc	300
tgggaaatta tatctgtgct tctttcaca	gggttggtgg ccttgaggaa ggtagaaat	360
gtctgctgaa caggggrcca tgaggagcca	ctgaaattgt aaaagaaaca ggacatgggt	420
gagctagggt ggaagtcaga acaggtcata		450

<210> 103
 <211> 446
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 284
 <223> 2-11-284 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 264..283
 <223> 2-11-284.mis1, potential

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<220>
<221> misc_binding
<222> 285..304
<223> 2-11-284.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 429..446
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 272..296
<223> 2-11-284 potential probe

<400> 103
tcagctagtc agactcacat ttattcggta agattaatta acagaagctt gagtcaacac      60
cgtttagaggg taattgatat tatggacttc ccaagtaaaa agcacttaag cacctgccgt      120
acatcaaaagg ttagtthttta gatcacatga gtaaacaacac taggtaggta aactactctg      180
ccttcctttg ttactacttt aatttggtta actaaaggta aagatcaggt tgccttcaac      240
catatctatt actgaagtta tgcaaacttc tcggccttcc aagragattt gtgtctatct      300
ccataactat ctttaatat tttcccacca gcctgattga accccagcat agatatttaa      360
taaaaatttg gccattccgt tgttggaagt tttaagataa atttattatt attattttta      420
tgagaaaaagc ctcaagtaaag ctgact                                     446

<210> 104
<211> 446
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 156
<223> 2-11-156 : polymorphic base A or C

<220>
<221> misc_binding
<222> 136..155
<223> 2-11-156.mis1, potential

<220>
<221> misc_binding
<222> 157..176
<223> 2-11-156.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 429..446
<223> downstream amplification primer, complement

<220>
<221> misc_binding

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<222> 144..168

<223> 2-11-156 potential probe

<400> 104

tcagctagtc agactcacat ttattcggta agattaatta acagaagctt gagtcaacac	60
cgtagaggg taattgatat tatggacttc ccaagtaaaa agcacttaag cacctgccgt	120
acatcaaagg ttagttttaa gatcacatga gtaaaaaaac taggtaggta aactactctg	180
ccttcctttg ttactacttt aatttgttta actaaaggta aagatcaggt tgccttcaac	240
catatctatt actgaagtta tgcaaaacttc tcggccttcc aagaagattt gtgtctatct	300
ccataactat ctttaatat tttcccacca gcctgattga accccagcat agatatttaa	360
taaaaatttg gccattccgt tgttggaagt tttaagataa atttattatt attattttaa	420
tgagaaaagc ctcagtaaag ctgact	446

<210> 105

<211> 446

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 379

<223> 2-11-379 : polymorphic base A or G

<220>

<221> misc_binding

<222> 359..378

<223> 2-11-379.mis1, potential

<220>

<221> misc_binding

<222> 380..399

<223> 2-11-379.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 429..446

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 367..391

<223> 2-11-379 potential probe

<400> 105

tcagctagtc agactcacat ttattcggta agattaatta acagaagctt gagtcaacac	60
cgtagaggg taattgatat tatggacttc ccaagtaaaa agcacttaag cacctgccgt	120
acatcaaagg ttagttttaa gatcacatga gtaaaaaaac taggtaggta aactactctg	180
ccttcctttg ttactacttt aatttgttta actaaaggta aagatcaggt tgccttcaac	240
catatctatt actgaagtta tgcaaaacttc tcggccttcc aagaagattt gtgtctatct	300
ccataactat ctttaatat tttcccacca gcctgattga accccagcat agatatttaa	360
taaaaatttg gccattccrt tgttggaagt tttaagataa atttattatt attattttaa	420
tgagaaaagc ctcagtaaag ctgact	446

<210> 106

<211> 423

<212> DNA

<213> Homo Sapiens

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<220>
<221> allele
<222> 223
<223> 2-12-223 : polymorphic base A or T

<220>
<221> misc_binding
<222> 203..222
<223> 2-12-223.mis1, potential

<220>
<221> misc_binding
<222> 224..243
<223> 2-12-223.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 399..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 211..235
<223> 2-12-223 potential probe

<400> 106
ctgttcgagg tatttcttgg aaatgagcta ttacagcaa ggggtgtttgc ctctcattgc      60
tgtagttccc tgagaaaaga gcctgtgttc aatgatgagc tcccatcccg catcctgtgt      120
ggcactctgt ccatcaagcc cagtgtgaag gaggtcacgg aaacctcagc tgtgtttgag      180
gatgggacca tgtttgaggc tatcgactct gtcattcttg cawcaggcta tgattattcc      240
tacccttccc ttgatgagac catcatgaaa agcagaaaca atgagggtac cttgtttaa      300
ggcatcttcc cccactaat ggagaagcca accttggtg tgattggctt gggttcagtc      360
cttggagctg ccatccccc agcagacctg caagcctggt gggctgctaa agtatttgca      420
ggt                                                                423

<210> 107
<211> 418
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 239
<223> 2-14-239 : polymorphic base C or T

<220>
<221> misc_binding
<222> 219..238
<223> 2-14-239.mis1, potential

<220>
<221> misc_binding
<222> 240..259
<223> 2-14-239.mis2, potential complement

<220>
<221> primer_bind
<222> 1..23

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<223> upstream amplification primer

<220>
<221> primer_bind
<222> 398..418
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 227..251
<223> 2-14-239 potential probe

<400> 107
gttcactgaa rggvacacaa ttcttggtt tctctttaag ctttcttatt ctccctagga      60
ccacacagaa gaaggcagag ccagcattta ccagtctgta ttcacaaact cttccaaaga      120
aatgatgtgc tttccagact tcccttatcc ggatgattac ccaaactata tacaccacag      180
caagctccag gaatatataa agacatatgc tcaaaagaag gatcttttaa gatacataya      240
gtttgaggta ggggtctcat aacttggtact gttgaaatta agatatgtgt ggggttagaga      300
aaaaggaggc agcaaactat tataaaaatt agagccaaat gtttgggcac ctccagtaatc      360
aaatgttggc tctgattata aagcattcat gcattgattt tttctcctag acttacta      418

<210> 108
<211> 418
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 370
<223> 2-14-370 : polymorphic base G or C

<220>
<221> misc_binding
<222> 350..369
<223> 2-14-370.mis1, potential

<220>
<221> misc_binding
<222> 371..390
<223> 2-14-370.mis2, potential complement

<220>
<221> primer_bind
<222> 1..23
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 398..418
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 358..382
<223> 2-14-370 potential probe

<400> 108
gttcactgaa rggvacacaa ttcttggtt tctctttaag ctttcttatt ctccctagga      60
ccacacagaa gaaggcagag ccagcattta ccagtctgta ttcacaaact cttccaaaga      120
aatgatgtgc tttccagact tcccttatcc ggatgattac ccaaactata tacaccacag      180
caagctccag gaatatataa agacatatgc tcaaaagaag gatcttttaa gatacataya      240
gtttgaggta ggggtctcat aacttggtact gttgaaatta agatatgtgt ggggttagaga      300
aaaaggaggc agcaaactat tataaaaatt agagccaaat gtttgggcac ctccagtaatc      360

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aaatgttggs tctgattata aagcattcat gcattgattt tttctcctag acttacta 418

<210> 109

<211> 445

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 104

<223> 2-17-104 : polymorphic base A or G

<220>

<221> misc_binding

<222> 84..103

<223> 2-17-104.mis1, potential

<220>

<221> misc_binding

<222> 105..124

<223> 2-17-104.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 427..445

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 92..116

<223> 2-17-104 potential probe

<400> 109

cggtgatgga aaattcccct ctgctctctg aagatttgct aaaaatctac tgacaaaagg	60
catattgata gaagaaaatg tacacaaatt tattaacttc cacrggagtt ggggtaaaaa	120
tcacatgatt atcccagcat gcaatggggg acggatgctt atatatccct tccttaggtg	180
acagggagat gagaaagtgt ggattgattt tagggtgact atgaaatgat ctctagggga	240
cccaacgggc ttgaagaaca tacaatggcc tggaataaag tatgttgggc ccgcagcgca	300
aacaatggct tatgacaagt ctgtctaggt gtgttgacag aattctttct tcctgcagta	360
tgagttcagt taatgaaaac tcaggggaagg taccaaagggt aattgatttc ttctttggca	420
agtctagact ttaggcaaat aaggg	445

<210> 110

<211> 445

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 395

<223> 2-17-396 : polymorphic base A or C

<220>

<221> misc_binding

<222> 375..394

<223> 2-17-396.mis1, potential

<220>

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<221> misc_binding
<222> 396..415
<223> 2-17-396.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 427..445
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 383..407
<223> 2-17-396 potential probe

<400> 110
cgttgatgga aaattcccct ctgctctctg aagatttgct aaaaatctac tgacaaaagg      60
catattgata gaagaaaatg tacacaaatt tattaacttc cacaggagtt ggggtaaaaa      120
tcacatgatt atcccagcat gcaatggggt acggatgctt atatatccct tccttaggtg      180
acagggagat gagaaagtgt ggattgattt tagggtgact atgaaatgat ctctagggga      240
cccaacgggc ttgaagaaca tacaatggcc tggaataaag tatgttgggc ccgcagcgca      300
aacaatggct tatgacaagt ctgtctaggt gtgttgacag aattctttct tcctgcagta      360
tgagttcagt taatgaaaac tcaggggaagg taccmaaggt aattgatttc ttctttggca      420
agtctagact ttaggcaaat aagggg                                     445

<210> 111
<211> 436
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 43
<223> 2-22-43 : polymorphic base A or G

<220>
<221> misc_binding
<222> 23..42
<223> 2-22-43.mis1, potential

<220>
<221> misc_binding
<222> 44..63
<223> 2-22-43.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..436
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 31..55
<223> 2-22-43 potential probe

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<400> 111
aaggagttca cggaaacctc agctgtgttt gaggatggga ccrtgtttga ggctatcgac      60
tctgtcatct ttgcaacagg ctatgattat tcctaccctt tccttgatga gaccatcatg      120
aaaagcagaa acaatgaggt taccttggtt aaaggcatct tccccccact aatggagaag      180
ccaaccttgg ctgtgattgg cttggttcag tcccttggag ctgccatccc cacagcagac      240
ctgcaagcct ggtgggctgc taaagtattt gcaagtaggt gggccattct gtctttcatt      300
cattttatca atgaacattt actgaacacc tgctatatgc aaagcactgt gctagggata      360
caatgagaac aagacaaaca tgttccttga cctctcaagg cttaaaatgg ggtgtggggg      420
atgcataata ggggaa                                     436

```

```

<210> 112
<211> 436
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 138
<223> 2-22-138 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 118..137
<223> 2-22-138.mis1, potential

```

```

<220>
<221> misc_binding
<222> 139..158
<223> 2-22-138.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 416..436
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 126..150
<223> 2-22-138 potential probe

```

```

<400> 112
aaggagttca cggaaacctc agctgtgttt gaggatggga ccattgttga ggctatcgac      60
tctgtcatct ttgcaacagg ctatgattat tcctaccctt tccttgatga gaccatcatg      120
aaaagcagaa acaatgargt taccttggtt aaaggcatct tccccccact aatggagaag      180
ccaaccttgg ctgtgattgg cttggttcag tcccttggag ctgccatccc cacagcagac      240
ctgcaagcct ggtgggctgc taaagtattt gcaagtaggt gggccattct gtctttcatt      300
cattttatca atgaacattt actgaacacc tgctatatgc aaagcactgt gctagggata      360
caatgagaac aagacaaaca tgttccttga cctctcaagg cttaaaatgg ggtgtggggg      420
atgcataata ggggaa                                     436

```

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<210> 113
<211> 420
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele

```



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<222> 82
<223> 2-23-82 : polymorphic base A or G

<220>
<221> misc_binding
<222> 62..81
<223> 2-23-82.mis1, potential

<220>
<221> misc_binding
<222> 83..102
<223> 2-23-82.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 70..94
<223> 2-23-82 potential probe

<400> 113
caattatttc ctccacagaa acaaggcaag aaggaaaaaa actttcacat gtagaattat      60
aaatggaaaa ataaattttc trgttttctt aaagaccctg gtttccggtg taaagaaatg      120
tcccagcttc ttagtcacgg gccaatgggt tgttgttact gaaaaggatg ggaaacagga      180
atctactatt tttgatgctg taatgatttg ttcaggacat cacgtatacc ccaatctgcc      240
aacggattcc tttcctggta agtttggaat atatataata atctagggac ttatatgcaa      300
acatcaagag ttagaaacat atctttctat aggtattaca taatgattat tcttagattt      360
caaaagaaaa aaattaagtt taatgatagg atatagtaat aaatagccyc ataagtcctt      420

<210> 114
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 166
<223> 2-23-166 : polymorphic base A or G

<220>
<221> misc_binding
<222> 146..165
<223> 2-23-166.mis1, potential

<220>
<221> misc_binding
<222> 167..186
<223> 2-23-166.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>

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96

```

<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 154..178
<223> 2-23-166 potential probe

<400> 114
caattatttc ctccacagaa acaaggcaag aaggaaaaaa actttcacat gtagaattat    60
aaatggaaaa ataaattttc tagttttctt aaagaccctg gtttccggtg taaagaaatg    120
tcccagcttc ttagtcacgg gccaatgggt tggtgttact gaaaargatg ggaaacagga    180
atctactatt tttgatgctg taatgatttg ttcaggacat cacgtatacc ccaatctgcc    240
aacggattcc tttcctggta agtttggaat atatataata atctagggac ttatatgcaa    300
acatcaagag ttagaaacat atctttctat aggtattaca taatgattat tcttagattt    360
caaaagaaaa aaattaagtt taatgatagg atatagtaat aaatagccyc ataagtcctt    420

<210> 115
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 244
<223> 2-23-244 : polymorphic base G or T

<220>
<221> misc_binding
<222> 224..243
<223> 2-23-244.mis1, potential

<220>
<221> misc_binding
<222> 245..264
<223> 2-23-244.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 232..256
<223> 2-23-244 potential probe

<400> 115
caattatttc ctccacagaa acaaggcaag aaggaaaaaa actttcacat gtagaattat    60
aaatggaaaa ataaattttc tagttttctt aaagaccctg gtttccggtg taaagaaatg    120
tcccagcttc ttagtcacgg gccaatgggt tggtgttact gaaaaggatg ggaaacagga    180
atctactatt tttgatgctg taatgatttg ttcaggacat cacgtatacc ccaatctgcc    240
aackgattcc tttcctggta agtttggaat atatataata atctagggac ttatatgcaa    300
acatcaagag ttagaaacat atctttctat aggtattaca taatgattat tcttagattt    360
caaaagaaaa aaattaagtt taatgatagg atatagtaat aaatagccyc ataagtcctt    420

<210> 116

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<211> 434
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 115
<223> 2-24-115 : polymorphic base C or T

<220>
<221> misc_binding
<222> 95..114
<223> 2-24-115.mis1, potential

<220>
<221> misc_binding
<222> 116..135
<223> 2-24-115.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..434
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 103..127
<223> 2-24-115 potential probe

<400> 116
aatgcacttc aactagggaa ttttttaatt acaactgata ataggtttaa aaagacacaa      60
agaaaacatc ttcataatct ctgaaaatca gttcaaacaa cttgccatgt tccayttagg      120
cctggaccag ttctgaggca actacctcca tagccgggat tataagaatc cagaagcctt      180
caaggggaag agggctcctcg tgattggtct ggggaattcg ggatctgaca ttgctgttga      240
gctcagccgt ctggctacac aggtacatga cgtaaagggt ttgggaaata aacctaagggt      300
agggctgtgc tactaaatca gtagccaagg cacagaggat ggtacttcta tgtcacacca      360
caagagatcc acctcttcta tgtggccctt caaatcaagg aggacttgag acatcctcca      420
tgtgaagcca ggta                                         434

<210> 117
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 36
<223> 2-25-36 : polymorphic base G or C

<220>
<221> misc_binding
<222> 16..35
<223> 2-25-36.mis1, potential

<220>
<221> misc_binding
<222> 37..56
<223> 2-25-36.mis2, potential complement

```

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<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 24..48
<223> 2-25-36 potential probe

<400> 117
aggaaaatgc acggaagtgc ccaaagaagt gtgttstggt tgcttatttc ttacagagta      60
atgctgaaat ctgtgttgct tttccccacc aggtcattat cagtaccaga agtgcttcct      120
gggtcatgag tcgggtctgg gatgatggct atccttggga tatgatgtat gttaccgcgt      180
ttgcatcctt tctccggaat gtccttcctt cattcatctc tgactgggta tatgtccaga      240
agatgaacac gtggtttaag catgagaact atggcctgat gcctttaaat gggactactaa      300
aaatggaaat tttttttatt caaaaaaggg gggcactcat ttaatgaatt tattctctct      360
agaacttact tttgttgtct cattgagcct agaaacatta aactcaagggt ttcacagggt      420

<210> 118
<211> 429
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 185
<223> 2-27-185 : polymorphic base A or G

<220>
<221> misc_binding
<222> 165..184
<223> 2-27-185.mis1, potential

<220>
<221> misc_binding
<222> 186..205
<223> 2-27-185.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..429
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 173..197
<223> 2-27-185 potential probe

<400> 118
cttattccag tatgttctct tctttcttca tgtttggcca gagccagact ttgcagacag      60
attacatcac atatgtggat gagctgggct ctttcatagg ggccaagcct aacataccat      120

```

99

```

ggctcttctt gacagatccc cgcttggccc tggaggtgta ctttggccct tgcagcccat 180
accarttttcg actgatggga ccaggaaggt gggatggggc cagaaatgcc atcctgaccc 240
agtgggaaccg gacagtgaag ccaaccagga caagagttgt cagtgaagtt cagcgacccc 300
atcccttttta caatttgctt aaaatgcttt cattcccatt actccttctg gctgttacac 360
ttacatttta ttaatgagaa agtctttgag gtctcaaaat tcagcataga agtgtaatca 420
cacaatata 429

```

<210> 119

<211> 429

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 378

<223> 2-27-378 : polymorphic base G or C

<220>

<221> misc_binding

<222> 358..377

<223> 2-27-378.misl, potential

<220>

<221> misc_binding

<222> 379..398

<223> 2-27-378.mis2, potential complement

<220>

<221> primer_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 405..429

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 366..390

<223> 2-27-378 potential probe

<400> 119

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cttattccag tatgttctct tctttcttca tgtttggcca gagccagact ttgcagacag 60
attacatcac atatgtggat gagctgggct ctttcatagg ggccaagcct aacataccat 120
ggctcttctt gacagatccc cgcttggccc tggaggtgta ctttggccct tgcagcccat 180
accagttttcg actgatggga ccaggaaggt gggatggggc cagaaatgcc atcctgaccc 240
agtgggaaccg gacagtgaag ccaaccagga caagagttgt cagtgaagtt cagcgacccc 300
atcccttttta caatttgctt aaaatgcttt cattcccatt actccttctg gctgttacac 360
ttacatttta ttaatgasaa agtctttgag gtctcaaaat tcagcataga agtgtaatca 420
oacaatata 429

```

<210> 120

<211> 440

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 142

<223> 2-29-142 : polymorphic base A or G

<220>

100

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<221> misc_binding
<222> 122..141
<223> 2-29-142.mis1, potential

<220>
<221> misc_binding
<222> 143..162
<223> 2-29-142.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 130..154
<223> 2-29-142 potential probe

<220>
<221> misc_feature
<222> 9,433
<223> n=a, g, c or t

<400> 120
caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca      60
tagttgctct ggagctcaca gacttctctc ttcttcccc tgaaggatg gagaggttca      120
aaggccaata tttccatagc crccaataca agcatccaga tggatttggg gaaaacgcat      180
cctgggtgatt ggaatgggaa acttgggctc agatattgct gttgagctga gtaagaatgc      240
tgctcaggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca      300
tactggagaa ccycagccat ataatcgcgg ctccaatcct cattaactag ttggttggtg      360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg      420
tcactaacca gcnatgaatg                                     440

<210> 121
<211> 440
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 166
<223> 2-29-166 : polymorphic base C or T

<220>
<221> misc_binding
<222> 146..165
<223> 2-29-166.mis1, potential

<220>
<221> misc_binding
<222> 167..186
<223> 2-29-166.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

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<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 154..178
<223> 2-29-166 potential probe

<220>
<221> misc_feature
<222> 9,433
<223> n=a, g, c or t

<400> 121
caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca      60
tagttgctct ggagctcaca gacttctctc ttcttcccc tgaaggatat gagaggttca      120
aaggccaata ttccatagc cgccaataca agcatccaga tggatytggg gaaaacgcat      180
cctggtgatt ggaatgggaa acttgggctc agatattgct gttgagctga gtaagaatgc      240
tgctcagggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca      300
tactggagaa ccycagccat ataatcgcggt ctccaatcct cattaactag ttggttggtgta      360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg      420
tcactaacca gcnatgaatg                                     440

<210> 122
<211> 440
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 204
<223> 2-29-205 : polymorphic base C or T

<220>
<221> misc_binding
<222> 184..203
<223> 2-29-205.mis1, potential

<220>
<221> misc_binding
<222> 205..224
<223> 2-29-205.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 192..216
<223> 2-29-205 potential probe

<220>
<221> misc_feature

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102

<222> 9,433

<223> n=a, g, c or t

<400> 122

caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca	60
tagttgctct ggagctcaca gacttctctc ttcttcccc tgaaggatg gagaggttca	120
aaggccaata ttccatagc cgccaatata agcatccaga tggatttggg gaaaacgcat	180
cctggtgatt ggaatgggaa actygggctc agatattgct gttgagctga gtaagaatgc	240
tgctcagggtg tgatgctctc tgcttaccat gtacctggag gggagggaagt ggggatgcca	300
tactggagaa ccycagccat ataatcgcggt ctccaatcct cattaactag ttggttggtg	360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg	420
tcactaacca gcnatgaatg	440

<210> 123

<211> 440

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 205

<223> 2-29-206 : polymorphic base A or G

<220>

<221> misc_binding

<222> 185..204

<223> 2-29-206.mis1, potential

<220>

<221> misc_binding

<222> 206..225

<223> 2-29-206.mis2, potential complement

<220>

<221> primer_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 422..439

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 193..217

<223> 2-29-206 potential probe

<220>

<221> misc_feature

<222> 9,433

<223> n=a, g, c or t

<400> 123

caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca	60
tagttgctct ggagctcaca gacttctctc ttcttcccc tgaaggatg gagaggttca	120
aaggccaata ttccatagc cgccaatata agcatccaga tggatttggg gaaaacgcat	180
cctggtgatt ggaatgggaa acttrggctc agatattgct gttgagctga gtaagaatgc	240
tgctcagggtg tgatgctctc tgcttaccat gtacctggag gggagggaagt ggggatgcca	300
tactggagaa ccycagccat ataatcgcggt ctccaatcct cattaactag ttggttggtg	360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg	420
tcactaacca gcnatgaatg	440

103

<210> 124
 <211> 440
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 313
 <223> 2-29-314 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 293..312
 <223> 2-29-314.mis1, potential

<220>
 <221> misc_binding
 <222> 314..333
 <223> 2-29-314.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..21
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 422..439
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 301..325
 <223> 2-29-314 potential probe

<220>
 <221> misc_feature
 <222> 9,433
 <223> n=a, g, c or t

<400> 124	
caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca	60
tagttgctct ggagctcaca gacttctctc ttcttcccc tgaaggtagt gagaggttca	120
aaggccaata tttccatagc cgccaataca agcatccaga tggatttggg gaaaacgcat	180
cctgggtgatt ggaatgggaa acttgggctc agatattgct gttgagctga gtaagaatgc	240
tgctcaggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca	300
tactggagaa ccycagccat ataatcgcg ctccaatcct cattaactag ttggttggtg	360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg	420
tcactaacca gcnatgaatg	440

<210> 125
 <211> 432
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 68
 <223> 2-32-68 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 48..67

<223> 2-32-68.mis1, potential

<220>

<221> misc_binding

<222> 69..88

<223> 2-32-68.mis2, potential complement

<220>

<221> primer_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 413..432

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 56..80

<223> 2-32-68 potential probe

<400> 125

cctatgagta	tcgcctgggt	gggcctgggc	aatgggaagg	agccagaaat	gccatcttca	60
cccagaarca	aagaatactg	aagccactca	agactcgggc	cctgaaggat	tcatactaatt	120
tctcagtttc	ttttctgttg	aaaatcctgg	gccttccttg	tggtgttggtg	gccttttttt	180
gccaaacttca	atgggtcctag	tcagcataat	gcttttgggct	ttattatctt	gtcagtcact	240
acctcctaaa	gaaaaaaaaa	aaggctagaa	gaaaaaacat	tacattcatg	ttctaattat	300
agatttttaga	gttaggtagt	acagghaagg	gggaaattgt	aaagaattag	cagaattagg	360
catatgtaca	aaaccaaagt	ttgtcatga	aattttgcct	ttccacgctt	ccctcagttc	420
accaaagtta	cc					432

<210> 126

<211> 424

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 357

<223> 2-35-357 : polymorphic base C or T

<220>

<221> misc_binding

<222> 337..356

<223> 2-35-357.mis1, potential

<220>

<221> misc_binding

<222> 358..377

<223> 2-35-357.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 404..423

<223> downstream amplification primer, complement

<220>

105

<221> misc_binding
 <222> 345..369
 <223> 2-35-357 potential probe

<400> 126
 gaagagccta ttgacatcat tgtctttgcc actggataca catttgcttt ccccttcctt 60
 gatgagtctg tagtgaaagt tgaagatggc caggcctcac tgtacaagta tatcttcctt 120
 gcacatctgc aaaagccaac cctggccatt attggcctca tcaaaccctt gggctccatg 180
 atacctacag gagaaacaca agctcgggtgg gctgttcgag tcctgaaagg taagtataag 240
 aaatagcagg gcatgtgttt ttggtgtgcc atgtgattct ggatactgga aatgttgaga 300
 ctattattcc tcctgcttct atttaaaata acagaatctt taaaagcagg atgcatycta 360
 ttgtttgctg aattatactg tcataatgat ttgttcatt actgcataaa tggatatatca 420
 gggg 424

<210> 127
 <211> 435
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 256
 <223> 2-36-256 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 236..255
 <223> 2-36-256.mis1, potential

<220>
 <221> misc_binding
 <222> 257..276
 <223> 2-36-256.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..21
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 411..435
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 244..268
 <223> 2-36-256 potential probe

<400> 127
 atatcaatgg tacatcaact ggcaagtgct taatggaaca ttgacaactg ctaatcatat 60
 ctgtgattct tttttcagac caaagtctgc agtgtaacaa aatgctcaga ttctgctgtc 120
 tctggccaat gggagggtgg cactatgcat gaagagaagc aagagtcagc catctttgat 180
 gctgtcatgg tctgcactgg ctttcttact aatccttatt tgccactgga ttcctttcca 240
 ggtacagcat tttctstaac taactttaag ttttctcgtg ggagccattc tgatgcttga 300
 ttggtctggg aatgaattcc tatggctgtt ccattaaata gttaaagtgg ggaggttagga 360
 ggaggctttt ttgtttttgt ttgtttttt tctagccagc attttctggc cagtttttgg 420
 ctttcatttg ttcca 435

<210> 128
 <211> 435
 <212> DNA
 <213> Homo Sapiens

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<220>
<221> allele
<222> 353
<223> 2-36-354 : polymorphic base A or C

<220>
<221> misc_binding
<222> 333..352
<223> 2-36-354.mis1, potential

<220>
<221> misc_binding
<222> 354..373
<223> 2-36-354.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 411..435
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 341..365
<223> 2-36-354 potential probe

<400> 128
atatcaatgg tacatcaact ggcaagtgtc taatggaaca ttgacaactg ctaatcatat      60
ctgtgattct tttttcagac caaagtctgc agtgtaacaa aatgctcaga ttctgctgtc      120
tctggccaat gggaggtggt cactatgcat gaagagaagc aagagtcagc catctttgat      180
gctgtcatgg tctgcactgg ctttcttact aatccttatt tgccactgga ttcctttcca      240
ggtacagcat tttctgtaac taactttaag ttttctcgtg ggagccattc tgatgcttga      300
ttggtctggg aatgaattcc tatggctgtt ccattaaata gttaaagttg ggmggtagga      360
ggaggctttt ttgttttgt tttgtttttt tctagccagc attttctggc cagtttttgg      420
ctttcatttg ttcca                                     435

<210> 129
<211> 449
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 236
<223> 2-42-236 : polymorphic base C or T

<220>
<221> misc_binding
<222> 216..235
<223> 2-42-236.mis1, potential

<220>
<221> misc_binding
<222> 237..256
<223> 2-42-236.mis2, potential complement

<220>
<221> primer_bind

```

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 428..449

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 224..248

<223> 2-42-236 potential probe

<400> 129

agtgggtttg	cgtgtttgga	ggcagatttt	ttccccact	cacacttttg	gcaactsacag	60
tttttcagct	gtctcatgga	gtttgcagcg	gcaagccact	tctttcaaag	gtcctgtgaa	120
ttcttttggg	tttcttggt	tggtcatgca	gtacttcttg	gaggaaaatt	tcactgtgtg	180
agtctccaca	tgctgttctg	tctgtctgcg	tggaactgc	aagttagtcc	tgcttyctat	240
ccaccatttt	ccaacaatct	gtcgtaacc	atttcaaagt	atagaattca	gtggcattta	300
gtacattcat	aatgctgtgt	aaccacaacc	tctatccagt	ttcaaaacac	tttcatcaca	360
cccaaaagaa	aactccatac	tcattagcaa	tccttcccca	ttcccttctt	ttcccagccc	420
ctggcagcca	ctcgatcatg	cctatttta				449

<210> 130

<211> 429

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 139

<223> 2-43-139 : polymorphic base A or G

<220>

<221> misc_binding

<222> 119..138

<223> 2-43-139.mis1, potential

<220>

<221> misc_binding

<222> 140..159

<223> 2-43-139.mis2, potential complement

<220>

<221> primer_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 395..419

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 127..151

<223> 2-43-139 potential probe

<400> 130

cattakcaat	ccttccccat	tccttctttt	ccccagcccc	tggcagccac	tcgatcatgc	60
ctattttaaa	ttgaggaaac	taaagctgag	aaaagttata	caatttttcc	aacatgactc	120
tgataatagc	tggtgaacrc	aatactcgaa	cccaggactt	gtgattccca	agatcagact	180
cctcccatat	acctgtcttt	tatttcccaa	gtgcttgggc	aatcagctgc	acttaaaaag	240

108

cctttacaaa	ttgagtttac	taatgtgagt	aatatatgat	tttttaaaaa	taataattgt	300
ccctaaaggt	gaaatggatc	aaagccctta	aaagtgaatc	tgtgggtgtag	taactgttaa	360
cataattgtc	ttatttttatt	ctcatcccct	taaagaataa	aattgatgaa	caagtgaggg	420
gtcatagct						429

<210> 131
 <211> 425
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 213
 <223> 2-44-215 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 193..212
 <223> 2-44-215.mis1, potential

<220>
 <221> misc_binding
 <222> 214..233
 <223> 2-44-215.mis2, potential complement

<220>
 <221> primer_bind
 <222> 3..23
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 398..420
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 201..225
 <223> 2-44-215 potential probe

<400> 131						
rhcctgcttt	tatttcccaa	gtgcttgggc	aatcagctgc	acttaaaaag	cctttacaaa	60
ttgagtttac	taatgtgagt	aatatatgat	tttttaaaaa	taataattgt	ccctaaaggt	120
gaaatggatc	aaagccctta	aaagtgaatc	tgtgggtgtag	taactgttaa	cataattgtc	180
ttatttttatt	ctcatcccct	taaagaataa	aaytgatgaa	caagtgagga	tgctgggtgta	240
actccctaac	ttagttttata	gtctgtaagc	agaagagtga	gtctaaagta	catatcacca	300
gacagtgttt	ctcctagcat	ttcgctgttg	cattaatcaa	caagttaaaa	tataaacaac	360
ggctaaccct	gggtttcaaa	tttaacattc	cttatctctt	agaccagggt	tatccactgt	420
ggtca						425

<210> 132
 <211> 442
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 38
 <223> 2-45-38 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 18..37

109

<223> 2-45-38.mis1, potential

<220>

<221> misc_binding

<222> 39..58

<223> 2-45-38.mis2, potential complement

<220>

<221> primer_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 418..442

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 26..50

<223> 2-45-38 potential probe

<400> 132

gatgtaggaa	gagtaaaaaa	caaaaaattt	ttgaatgygt	aattatcact	aattatttta	60
tttgatcctt	caggagaatg	tggaagatgg	ccgagcaagt	atctatcaat	ctgtcgttac	120
caacaccagc	aaagaaatgt	cctgtttcag	tgactttcca	atgcctgaag	attttccaaa	180
cttcctgcat	aattctaaac	ttctggaata	tttcaggatt	tttgctaaaa	aatttgatct	240
gctaaaaat	attcagttcc	aggatttga	tttttgggga	aatgggtttc	tctgcattag	300
ttcagctcat	atthagatag	aaaagttact	ctgataatga	aagcaattat	gaatgaagta	360
tcccattcta	agtatttgtt	gaaatataac	agcctcatat	aaaacccaaa	aagtagtgtc	420
attacccttg	gtattataga	tt				442

<210> 133

<211> 442

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 183

<223> 2-45-183 : polymorphic base C or T

<220>

<221> misc_binding

<222> 163..182

<223> 2-45-183.mis1, potential

<220>

<221> misc_binding

<222> 184..203

<223> 2-45-183.mis2, potential complement

<220>

<221> primer_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 418..442

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 171..195

<223> 2-45-183 potential probe

<400> 133

gatgtaggaa	gagtaaaaaa	caaaaaat	ttgaatgcgt	aattatcact	aattatttta	60
tttgatcctt	caggagaatg	tggaagatgg	ccgagcaagt	atctatcaat	ctgtcggttac	120
caacaccagc	aaagaaatgt	cctgtttcag	tgactttcca	atgcctgaag	attttccaaa	180
ctycctgcat	aattctaaac	ttctggaata	tttcaggatt	tttgctaaaa	aatttgatct	240
gctaaaatat	attcagttcc	aggtattgta	tttttgggga	aatgggtttc	tctgcattag	300
ttcagctcat	atntagatag	aaaagttact	ctgataatga	aagcaattat	gaatgaagta	360
tcccattcta	agtatttggt	gaaatataac	agcctcatat	aaaacccaaa	aagtagtgtc	420
attacccttg	gtattataga	tt				442

<210> 134

<211> 442

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 335

<223> 2-45-335 : polymorphic base A or T

<220>

<221> misc_binding

<222> 315..334

<223> 2-45-335.mis1, potential

<220>

<221> misc_binding

<222> 336..355

<223> 2-45-335.mis2, potential complement

<220>

<221> primer_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 418..442

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 323..347

<223> 2-45-335 potential probe

<400> 134

gatgtaggaa	gagtaaaaaa	caaaaaat	ttgaatgcgt	aattatcact	aattatttta	60
tttgatcctt	caggagaatg	tggaagatgg	ccgagcaagt	atctatcaat	ctgtcggttac	120
caacaccagc	aaagaaatgt	cctgtttcag	tgactttcca	atgcctgaag	attttccaaa	180
cttcctgcat	aattctaaac	ttctggaata	tttcaggatt	tttgctaaaa	aatttgatct	240
gctaaaatat	attcagttcc	aggtattgta	tttttgggga	aatgggtttc	tctgcattag	300
ttcagctcat	atntagatag	aaaagttact	ctgawaatga	aagcaattat	gaatgaagta	360
tcccattcta	agtatttggt	gaaatataac	agcctcatat	aaaacccaaa	aagtagtgtc	420
attacccttg	gtattataga	tt				442

<210> 135

<211> 442

<212> DNA

<213> Homo Sapiens


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<220>
<221> allele
<222> 394
<223> 2-45-394 : polymorphic base C or T

<220>
<221> misc_binding
<222> 374..393
<223> 2-45-394.mis1, potential

<220>
<221> misc_binding
<222> 395..414
<223> 2-45-394.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 418..442
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 382..406
<223> 2-45-394 potential probe

<400> 135
gatgtaggaa gagtaaaaaa caaaaaatTT ttgaatgcgt aattatcact aattatttta      60
tttgcctcct caggagaatg tggaagatgg ccgagcaagt atctatcaat ctgtcggttac      120
caacaccagc aaagaaatgt cctgtttcag tgactttcca atgcctgaag attttccaaa      180
cttcctgcat aattctaaac ttctggaata tttcaggatt tttgctaaaa aatttgatct      240
gctaaaatat attcagttcc aggtattgta tttttgggga aatggggttc tctgcattag      300
ttcagctcat atttagatag aaaagttact ctgataatga aagcaattat gaatgaagta      360
tcccattcta agtatttggt gaaatataac agcytcatat aaaacccaaa aagtagtgtc      420
attacccttg gtattataga tt                                         442

<210> 136
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 39
<223> 2-48-39 : polymorphic base A or G

<220>
<221> misc_binding
<222> 19..38
<223> 2-48-39.mis1, potential

<220>
<221> misc_binding
<222> 40..59
<223> 2-48-39.mis2, potential complement

<220>
<221> primer_bind

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<222> 1..24
 <223> upstream amplification primer

 <220>
 <221> primer_bind
 <222> 404..426
 <223> downstream amplification primer, complement

 <220>
 <221> misc_binding
 <222> 27..51
 <223> 2-48-39 potential probe

<400> 136	
gttttatttt attgatgggc tgtctggctc cctcaactrc aaagtaaact ccacaaaggc	60
agagagtttt gcctctttta ttcattgctg tacctgcatc acttagaaaag tttctggcac	120
ctaggaagtg ttcagtaaat atttattgaa taagtttatg taaaacgtct cagactcctt	180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta	240
tctaaggtac acgagggctt gctagtctcc taagttagtc tgctaataaa tgtaaccct	300
aataactgaa attattagca gaggaatta tccagttcta tatcaaggca aaaagacagc	360
agtggataga aagatcttag aagtcccact aggttcatcc aagccaccat acacataggc	420
agaaaa	426

<210> 137
 <211> 426
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 72
 <223> 2-48-72 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 52..71
 <223> 2-48-72.mis1, potential

<220>
 <221> misc_binding
 <222> 73..92
 <223> 2-48-72.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..24
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 404..426
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 60..84
 <223> 2-48-72 potential probe

<400> 137	
gttttatttt attgatgggc tgtctggctc cctcaactac aaagtaaact ccacaaaggc	60
agagagtttt gyccttttta ttcattgctg tacctgcatc acttagaaaag tttctggcac	120
ctaggaagtg ttcagtaaat atttattgaa taagtttatg taaaacgtct cagactcctt	180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta	240

113

tctaaggtac acgagggcctt gctagtctcc taagttagtc tgctaataaa tgtaaccct	300
aataactgaa attattagca gaggttaatta tccagttcta tatcaaggca aaaagacagc	360
agtggataga aagatcttag aagtcacct aggttcatcc aagccacccat acacataggc	420
agaaaa	426

<210> 138
 <211> 426
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 156
 <223> 2-48-156 : polymorphic base G or T

<220>
 <221> misc_binding
 <222> 136..155
 <223> 2-48-156.mis1, potential

<220>
 <221> misc_binding
 <222> 157..176
 <223> 2-48-156.mis2, potential complement

<220>
 <221> primer_bind
 <222> 1..24
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 404..426
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 144..168
 <223> 2-48-156 potential probe

<400> 138	
gttttatttt attgatgggc tgtctggctc cctcaactac aaagtaaact ccacaaaggc	60
agagagtttt gcccttttta ttcattgctg tacctgcac accatgaaag tttctggcac	120
ctaggaagtg ttcagtaaat atttattgaa taagtktatg taaaacgtct cagactcctt	180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta	240
tctaaggtac acgagggcctt gctagtctcc taagttagtc tgctaataaa tgtaaccct	300
aataactgaa attattagca gaggttaatta tccagttcta tatcaaggca aaaagacagc	360
agtggataga aagatcttag aagtcacct aggttcatcc aagccacccat acacataggc	420
agaaaa	426

<210> 139
 <211> 426
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 285
 <223> 2-48-285 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 265..284

114

<223> 2-48-285.mis1, potential

<220>

<221> misc_binding

<222> 286..305

<223> 2-48-285.mis2, potential complement

<220>

<221> primer_bind

<222> 1..24

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 404..426

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 273..297

<223> 2-48-285 potential probe

<400> 139

gttttatttt attgatgggc tgtctggctc cctcaactac aaagtaaact ccacaaaggc	60
agagagtttt gcctctttta ttcattgctg tacctgcatc acttagaaag tttctggcac	120
ctaggaagtg ttcagtaaat atttattgaa taagtttatg taaaacgtct cagactcctt	180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta	240
tctaaggtag acgagggtt gctagtctcc taagttagtc tgctrataaa tgtaaccct	300
aataactgaa attattagca gaggtaatta tccagttcta tatcaaggca aaaagacagc	360
agtggataga aagatcttag aagtcctact aggttcatcc aagccaccat acacataggc	420
agaaaa	426

<210> 140

<211> 420

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 167

<223> 2-49-167 : polymorphic base A or G

<220>

<221> misc_binding

<222> 147..166

<223> 2-49-167.mis1, potential

<220>

<221> misc_binding

<222> 168..187

<223> 2-49-167.mis2, potential complement

<220>

<221> primer_bind

<222> 1..20

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 396..420

<223> downstream amplification primer, complement

<220>

115

<221> misc_binding
 <222> 155..179
 <223> 2-49-167 potential probe

<400> 140
 aagtcccact aggttcatcc aagccacccat acacataggc agaaaaatca aaataagata 60
 tgagcctgga cagggtgagc aatctgggaa aagatgaaca cagtatgcta ggaccagaa 120
 atcatcaagt ctatgaaaac taagccagaa cacaaatgtg aattccrtaa gatcaggaac 180
 ataatctgtc ttgttcatcc aggcattggt atctgccaga aatagtgtt aactgcaaga 240
 actgaatatt tgtagataa ttaaaccatc aactaaatga gattcatgca accatgaaaa 300
 atgctgctat aggtacacaa tattgatata ctagaaagtt aaaaaatcaa gttggaaatt 360
 agactattcc atttctgttt gtgtgtatgt atctacaaat aggtggaakg atataccaaa 420

<210> 141
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-436-43 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 482..500
 <223> 10-436-43.mis1
 <220>
 <221> misc_binding
 <222> 502..521
 <223> 10-436-43.mis2, potential complement

<220>
 <221> primer_bind
 <222> 459..476
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 859..878
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-436-43 potential probe

<220>
 <221> misc_feature
 <222> 297,539,629,650,976..1001
 <223> n=a, g, c or t

<400> 141
 tatatttaac acatatatatt aataaaaaaca ttaaatacat atattttaata aaaatataat 60
 ttatatataa tatacatata tttatatata aatatattta tatataatat gcatatgttt 120
 attttacata tataaatata tttatatata aatatacgta tattttatttt atatataat 180
 gtgtgtgtgt atatataat atacacacac acacgtatat acccaggag aggcactaat 240
 tgtgcagttt tgaaaagttt ctagtgatg ctgccgtggc ctactttcaa agcactntgc 300
 ttaggtttac cacttaaaat gttattacat tttccagaa gtacacttta aaatactttg 360
 tttttaagt gaggcattac aatggtgtca tgagctgaca ttcccagcca ctgactggaa 420
 gatttgggtc aaccaggga acaggcttgg tttaaggag ttcaagtgtt ggtggccttt 480
 gggtaaaagt ttatgtctat sttgtatgt gggattcagc agggattttc tttaatgtnt 540

116

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aaaaattcta gtttcctctg tatttgcttt ccttcttccc ctgtcctccc tgagcctcca    600
cacatgtgta acacatttta ttgccaant aggtcaagga ggtaaaaaan gactttgtcg    660
ggcttggaag tcagcatggt tactgcagtt cccggtaggc taccagtcac gaccatgatt    720
ccagatgttg actgcctgct ctgggccatt gggcggtgcc cgaataccaa ggacctgagt    780
ttaaacaaac tggtaagctg gcttggctctg cccgaaacat ttgtgaatct actgggagtc    840
ttatgggtttt attttcccc cagacaccca aaacttgggt ggattccatt ggattctttt    900
ctcttttttc catgtattca gtttgtgatc aaatttcatt gcttcttccct ttgaaattaa    960
aaaaaaaaagt tttctnnnnn nnnnnnnnnn nnnnnnnnnn n              1001

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<210> 142

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-436-376 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 10-436-376.mis1, potential

<220>

<221> misc_binding

<222> 502..520

<223> 10-436-376.mis2, complement

<220>

<221> primer_bind

<222> 126..143

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 526..545

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-436-376 potential probe

<220>

<221> misc_feature

<222> 206,296,317,643..685,853

<223> n=a, g, c or t

<400> 142

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tccagaagta cactttaaaa tactttgttt ttaaagtgag gcattacaat ggtgtcatga    60
gctgacattc ccagccactg actggaagat ttgggtcaac ccaggggaaca ggcttggttt    120
aaggaggttc aagtgttggg ggcctttggg taaaagttaa tgtctatggt tgtatgtggg    180
attcagtagg gattttcttt aatgtntaaa aattctagtt tcctctgtat ttgctttcct    240
tcttcccttg tcctccctga gcctccacac atgtgtaaca cattttattt gccaantagg    300
tcaaggaggt taaaaangac tttgtcgggc ttggaagtca gcatggttac tgcagttccc    360
ggtaggctac cagtcacgac catgattcca gatgttgact gcctgctctg ggccattggg    420
cgggtcccga ataccaagga cctgagttaa aacaaactgg taagctggct tggctctgcc    480
gaaacatttg tgaatctact rggagtctta tgggttttatt tcccccccag acacccaaaa    540
cttgggtgga ttccattgga ttcttttctc tttttcccat gtattcagtt tgtgatcaaa    600
tttcattgct tcttcttttg aaattaaaaa aaaaagtttt ctnnnnnnnn nnnnnnnnnn    660
nnnnnnnnnn nnnnnnnnnn nnnntcttct ttgtttttga gaaaggtctt gctctgtcac    720
ccaggctgga gttcagtggt gtgatcatag ctcaccgcag tcttaacctc ctagggtcaa    780

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117

```

gtgatccacc cacctcagct tctggagtag atggaactat gtgtgtgcca caatgcccag      840
ctaatttttt tantttttatt ttttttagag atgaggtttc accatgttgc ccaggctggt      900
ctcctcggct caagcgattc gcccatctca gcctcccaga gtgctgggac tataggcatg      960
tcccagcatg tcccagaaaa aggccgccac gtctggcctt t                               1001

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<210> 143

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-431-51 : polymorphic base A or C

<220>

<221> misc_binding

<222> 482..500

<223> 10-431-51.mis1

<220>

<221> misc_binding

<222> 502..521

<223> 10-431-51.mis2, potential complement

<220>

<221> primer_bind

<222> 451..468

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 853..872

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-431-51 potential probe

<400> 143

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agcatccctt atctgaaatg cttgggacca gaagtgtttt cagtttcaga ttttgaata      60
tttgcataata tataatgaga tattttgcag atgcgaccca agtcgaaaca cggaattcat      120
ttgttttaca tacaccttat acacatagtt ggaaggtaac tttatacgat attttaaag      180
tgtgcatgag gcatactttt gtctgcggtt ttgactgcaa cccttcacat gaggtcaggt      240
gtggaatttt ctgcttgttg catcatggtg ctccaacatt ttggattttg gattttgaat      300
ttctggatta gggatgctca acctgtaata gaatgtatag gattctcata agccaatcat      360
tttgagttgt tcgctgaggc atgacatata ttcgctgtat taaactatct agatagtgtg      420
atgaacaatg gtgtgaaact gtcagaacta gggcattaag gtagatggat aaatggctag      480
tggaacaatt tagctatggt maaacagaca gtaagataaa cactgatttt aaaatatctc      540
catagttgca atagctgctg gccgaaaact tgcccatcga ctttttgaat ataaggaaga      600
ttccaaatta gattataaca acatcccaac tgtgggtcttc agccaccccc ctattgggac      660
agtgggactc acggaaggta ggtattttaa aactgaagggt catttgtggt ttcttctctc      720
tttccctgac ccccaacttt aaattaggct tctgtcagct gatgaaacct atctcagccc      780
cagattacat tgcttttttg ttactctctt gtcacagttc cagttttctc ccctgctact      840
actttgagtg tacagtatct ttcttccaca ccacctatc tctttgatct ttttttttta      900
gcttttttat ttgaactaat tttaaattta aagaaaagct ctaaaaataa tacaaaggac      960
tcctctctaa ccttaatat tttgcttttt tattttttca c                               1001

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<210> 144

<211> 980

<212> DNA

<213> Homo Sapiens

```

<220>
<221> allele
<222> 477
<223> 10-432-93 : polymorphic base A or G

<220>
<221> misc_binding
<222> 457..476
<223> 10-432-93.mis1, potential

<220>
<221> misc_binding
<222> 481..499
<223> 10-432-93.mis2, complement

<220>
<221> primer_bind
<222> 388..407
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 758..775
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 465..489
<223> 10-432-93 potential probe

<220>
<221> misc_feature
<222> 297,477,629
<223> n=a, g, c or t

<400> 144
acacacacac atgtctatct ttcctaagaa ctggccctta cataaaccga gtatcatttt 60
cttttttttt ttcttttttg gacaagctct ccactgtca ccaggctgg agtgcagtgg 120
cagcatctct gctcactgca acctccgcct ctgggttcaa gcaattcttc tgcctcagcc 180
tcccgaatag ctgggactac caggcctgca ccaccaccat gcctggctaa tttttttag 240
agatgggggt tctactgtgt gccaggctg gtctcaatct cctgggctca agcgatncca 300
cctgcctctg cctctcaaag tgcagggatt acaggcatga gccactgtgc ctggcctttc 360
ttttcatcta gaggcagaat tcctcagccc ttcttttgtc ttatatgaca ctgacattta 420
ttttgtagaa tactttctcat tttggcgtgg tttgatattt cctcgtgggt tgattgragg 480
ttatgtattt ctggtcatct ccctctttga tagttcagtg taattgttta gttttctgat 540
agatgctttt tttaatgtgc attgtagatg aagccattca taaatatgga atagaaaatg 600
tgaagaccta ttcaacgagc ttaccccng atgtatcacg cagttaccaa aaggaaaaca 660
aaatgtgtga tgaaaatggg ctgtgctaac aaggaagaaa aggtaaggaa aaatccagca 720
aactaaatag tgccttgcaa aatggacagg gatggcagta ttttgagggt gtggaaagga 780
gggagaccaa gcagttgagc cttctgattc aactggacag gccactttg atctgtctta 840
cctgcatttt ggggttcttc ataataattc atctagaagg aggttccact ctttttaaaa 900
aataaagacg atgccaggcg tggtaggtca cacctgtaat ccagcacgc tgggaggccg 960
aggcaggcat atcacctgag

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<210> 145
<211> 933
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 433

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119

<223> 12-631-208 : polymorphic base A or G

<220>

<221> misc_binding

<222> 414..432

<223> 12-631-208.mis1

<220>

<221> misc_binding

<222> 434..453

<223> 12-631-208.mis2, potential complement

<220>

<221> primer_bind

<222> 226..245

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 705..725

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 421..445

<223> 12-631-208 potential probe

<220>

<221> misc_feature

<222> 30

<223> n=a, g, c or t

<400> 145

gcaggcctgt	aatcccagca	ctttgagagn	ccgaggcagg	aggatctctt	gaaccagga	60
gttcgagacc	agcctgggca	acatagtgag	accctgtctc	taaaaacaaa	acaaaaaact	120
tctcagccta	aattctcaca	agaccttcat	cttatcaacc	tgtttatttc	cttttcagtg	180
ttcgccagga	tgcgaaagca	ctgtctatga	ttgcccctgt	gctctttgcc	tctaccctct	240
tacacgtaaa	accatcacac	ctggagggaa	aagggttcctc	gaagtgaagt	cagctccgga	300
agtggggggg	caggggcgat	gcagtctggg	agttgtagtc	aaagctgctc	cgaagccacg	360
cagccgaaga	ggcggtcgtt	ctatgcaaca	ttcctgtgaa	aattaccag	ctgtgactgt	420
cgaaggga	aartcacact	tacctatatc	cgggatccca	cgccggagct	ccagacacac	480
aaggggggaca	gcagagagga	agaaaatgcc	aacaacccca	cgtgaagcca	tggtggcgga	540
agcgctgggt	gcaggcggaa	agcccgcgcc	ttccggccgc	gttttccggg	aaggaagtgg	600
aactcttctt	gccgcggggc	ggctggagag	ggtcaataac	gtggtaaata	ctgacggccg	660
tgctgttatt	gagggggagc	taagccccgt	gttttaaagt	tatagtctgt	agccgtgttt	720
cagaagaaag	gcaagtcgtc	ccccaaagtca	catgatgtcc	agaggagcct	gggctctaga	780
gcggtggctc	cctggagggt	agcagggcag	gggctgcccc	ttcggctctt	gcagcgtctg	840
tgagaaagcg	ctttccagag	ggaaatgaag	ccgaagaaaa	agctgatgct	gtgaggaggc	900
agcctggggc	ccccggcctt	gtggccgtat	agg			933

<210> 146

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-260-282 : polymorphic base G or T

<220>

<221> misc_binding

<222> 481..500

120

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<223> 10-260-282.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-260-282.mis2, potential complement

<220>
<221> primer_bind
<222> 220..238
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 636..655
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-260-282 potential probe

<400> 146
tatcttcctc acagggctga atgatgaatc tatgtaaagt atttaaaata gtaccttgca      60
catagtaagt gctcaataac ttgtgggttt ctttttggtta tttgcatttt gcttttttgc      120
ttctctctct tcaatacgtg gagataaact atcacagaat ctggaagctc tctgggttcc      180
actctcccc  ttccactctc ccaaggtaac cactaatcta cagttggtgt gtcctcagta      240
aatataggcc agactttcca tgggattcca tttgcaggaa gacaacccgt tcacagggtgc      300
cctacccctg tcccattctc tcttcttgat cacagggtgt gagctatgcc ccattcacgc      360
tcttccccct actggtcccc agtgccttgc tggagcaagc ctatgctgtg cagatggact      420
tcaacctgct agtggatgct gtcagccaga acgctgcctt cctggagcaa actctttcca      480
ggtaggggac agtgaagcat kgggggggcca ggagctgcca gagccaagga actggaagat      540
tgcagagccg tgaggtgtta ctgtgtcagc tgacttgggt ggatagagga aaggtacctc      600
caaagaacaa aaagtcatag gagtcaggaa agctggcttc taatcctggc tcgaccagtt      660
atztatatgg cctcaagcca ctccctttcc ttctctgggc ctaagggttc ttcactgaa      720
aatgaagag actggcttaa atccaagatc ccttttattg ttgacattct gtaatccgtg      780
acaccctact ttgaagactg atatttccat ttggaattag gggaaagtcag cctgggtttg      840
gagggaaaaca gaggtaggga aggttattgg gttaaagtca gattttctac ttctcctaag      900
cagcgacact ttcttgtcac ctcaggcctc tcactcttgg atgggatggg gtacagactg      960
ggccacactc agggcatgag gaagcaacct ctgaaatggg t                                1001

<210> 147
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-263-26 : polymorphic base A or C

<220>
<221> misc_binding
<222> 483..502
<223> 10-263-26.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-263-26.mis2, potential complement

<220>
<221> primer_bind

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121

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<222> 478..496
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 820..837
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-263-26 potential probe

<400> 147
ggcatacctg tggggtgaca tgctgatggg tgtacagtca ctggctaggc cagggaaactc      60
cagctatgat tgtgctttcc tgggccccgg gtcacatgtt gcccctggcc accccgacag      120
cagtttccac ttgtaatgag atccttggtg tgtcagggag aaaaaggacc tcatagctca      180
tctagtccctg tccctccatt gtacaggcag agggaaacaat atcttgagag ccccagagag      240
aggaatgcag ggacttctgt ctgggggctg ggccctggtag catccatttc tagccagcag      300
tgatgtcca gggtgcaatg attttagatg gtctgcagca ggattccaga cagcacctgg      360
aggcccagag taaggggctc cagctcactg ggacactagg gtaggttggg gtggggacag      420
aggctctcag gtctcctcca ggcatataca ccaggggcca aggttagggc agcccagcat      480
attccaacct gaagtggatc ttmcaggaat gtgatgggag gatgcttttt agtgctcagc      540
tgattctcag agtcatgttg ctgtatatat gaggtcatgg gcagaggggt cttccaggtc      600
catccaatta ctgaacagcc atctctcttc caacagacat gttctcagtg tcctgagtaa      660
gaccaaagaa gctggcaaga tcctctctaa taatcccagc aagggaactg ccctgggaat      720
tgccaaagcc tgggagctct acggctcacc caagtaaggg tgtgaaaagg tagcaggagg      780
atcctgcttt agtttcagca ttcattgggt tagcaacttc tttcttgcc agccatcatt      840
agagaataag gggatttttc taggaataga aacttatacc tttacatgcc aaaattatct      900
taagggttcc ttcttaaata acagatgctg actatgattt aactttttct tattgagtgg      960
aggtcatcat tatgactgtc aacaattgca gcttgctgta a                                1001

<210> 148
<211> 981
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-258-408 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-258-408.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-258-408.mis2, potential complement

<220>
<221> primer_bind
<222> 95..112
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 504..521
<223> downstream amplification primer, complement

<220>

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122

<221> misc_binding

<222> 489..513

<223> 10-258-408 potential probe

<400> 148

tcctgagggg	tatcctccta	aagacctcca	aagtttttat	ggaagggtaa	atactggtac	60
cttccccag	ctttccatct	gaggaccaga	aaagtgtgt	ctcccttaga	tgagatctag	120
acgccccaa	atccttgaga	tgtgggtata	gctcagggta	agctgctctg	aggtaaagg	180
ccatgaaccc	tgccccactc	ctgtcagccc	ctcatcagcc	ttttcagcag	gttccagtgc	240
ctgacttggg	ataggactga	gtggtaggag	gagggggagt	ggaggggcat	agcctttccc	300
taattctgcc	ttaaataaaa	ctgcattgct	gattcagtga	tgattcctta	cttcgtgcat	360
agaggggagg	cgggagctgt	aatctacgtt	agccactta	agatgtatta	gagcagggaa	420
gtgactggtc	tgtaatcagg	gtccccctag	accagtctct	acaggtggaa	ccctgaagtt	480
tcaatcctta	gccaccact	ratgctctta	ctggatcaca	gggaggaatg	agagtccctg	540
gcaggagccc	aggagggaa	gcaaccaaga	tgggacatac	ataacagttg	tgaactggct	600
tcagtcactt	tcctgcttag	ctcaggggct	tgtcaaaggc	cctgtcagtg	aagcctcctt	660
cgctctgccc	aaaccaaaag	ttctagaagg	aagatatttg	ggatagtcct	aggaaatacc	720
cctcccttcc	catctgccac	acaaatcaga	gccactaatg	aataacagc	ctcagggcac	780
agatacctaa	gaaaacaagt	caccacttct	tgagatcaca	ggctttattc	ctacaaccac	840
agggcttgag	cctgactggg	gcaagaaaac	agagtttcat	ctgagaatgt	ctcttatggg	900
ctgggttctg	ttcaggggag	ggtgggaaca	gaggacaagg	aagacaagct	cctctggccc	960
taggaacaaa	acacatttac	t				981

<210> 149

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-317-259 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-317-259.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-317-259.mis2, potential complement

<220>

<221> primer_bind

<222> 742..759

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 297..317

<223> downstream amplification primer.

<220>

<221> misc_binding

<222> 489..513

<223> 12-317-259 potential probe

<220>

<221> misc_feature

<222> 426,432,443,459,841,849..850,898,914

<223> n=a, g, c or t

123

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<400> 149
gtcacaaaaag atggcatatt gcatgagttc attaatatga agtgtcctga acaggcaatt      60
gcatagagat ggaaaatagt ttcattggtg cctagagcta aggagtttgg tgggaaatag      120
gaagtgactg gtagtgagta caaggctgct tttggggggt gatgaagata ttctaaaatt      180
gattgtggta atggctgcac aactctatga atgtcctaaa aatcacgata ccatgggttaa      240
ctaaatgggt gaattgcatg gtatgtgaat tgtacctcaa agctgttaaa aaaaaaaaaa      300
agtgagtgtg catgtccgca gaaaacagtg cagtgcagac agagagtggg gaccgctcca      360
atcgggtgtg tagagctgaa gagactcagg ggagcacagg cctcgtgagc tggttttccc      420
atcctncatc cnttgggact ganccttgtt gctaagctnc tggccattgc tttggagact      480
gtttcttgaa aatatttatc rcagaaagtc ttgtcaggcc tgcgcaagcc aggcacacaaa      540
agttggtggg gacttggaga ggggtcaggc tgccctgtct ctttcttcgc agacgttcat      600
ttctcagtag gacttgtgtg cccacactg tgccactgc ttgcataaac atccttccct      660
gcaggactcc cttagagcacc atgggctggg tgccaggat gccaaagcac caaggtctca      720
cagcagtgca cgacagaggc aggattctgc gtgatagttc ttcaggttca cttcacagat      780
tagctgacac ttaactgttc tggaagctgg gccaaaggag gctaacatgg aaattgagta      840
nactatagnn ttttttgccc aagggtacagg agaataaata tgagtagata gaatctcntt      900
aaattaaaaa ttttctccag taaatttttc ctaagtcttt gcctcctgcc tgtttagttc      960
ccattaaaaa cttggagatg aaaaagaata caaagtaaca a                                     1001

<210> 150
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-323-385 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..520
<223> 12-323-385.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-323-385.mis2, potential

<220>
<221> primer_bind
<222> 868..886
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 416..435
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-323-385 potential probe

<220>
<221> misc_feature
<222> 303,710
<223> n=a, g, c or t

<400> 150
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cgaggtgggc agatcacttg aggtcaggag accagcctgg ccaacagggt gaaaccctgt      120
ctctactaaa aatataaaaa ttagccagc atggtggtgc atgcctgtag tcccagctac      180

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124

ttgggaggct	gggacagaaa	aattgcttga	accaggagg	cagagggtgc	agtgagcaga	240
gattgtgcca	ttgcgctctg	gcctgggcat	cacagtgaga	ctccgcctta	aaaaaaaaaa	300
tcnttaaaat	ttaagacaaa	acaaaaaacc	ataagaagtg	ggctgggggt	ggtgggacct	360
gttttgggaa	ccatatactg	agttagacag	ggctagagga	actggtgagc	tacaagttac	420
agttgccaat	aatagtagta	gcttacatct	gttttgtact	agggaaaagg	aaaagtggaa	480
gcagttgttc	cccaatgccc	yctgcacagc	aaattcctgt	cctccattac	tagaaataga	540
ggcgagtatg	ggattcatga	gagcttctag	gaatcatgca	ctcgttttgg	gcacattcac	600
tgataccctt	gctaccaggt	cctgtgcatt	gagtcctcag	agaaagggtg	ggatatatgc	660
cttcatcaaa	gtatggtcag	attatttggg	aaatagatgc	aggaacagan	ttattaaaag	720
ttcatgtgat	ctgtgcagtg	aaagagaaac	acccaatcca	gtggaagtaa	attagtggga	780
tgaaggatag	caggtgttat	ctgagtagca	cggggatggg	tcaaaatgag	aaaagttgat	840
gtagtacatg	ccatttacag	attttaagga	gtaatgagtg	agaatagaac	caaatagcac	900
aaggcattcc	ataaaattat	cattcttaat	aaaagctagc	aatagaagga	aaacttataa	960
actatatata	gggtatttat	taaaatttaa	cttataggat	a		1001

<210> 151

<211> 857

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 357

<223> 12-324-219 : polymorphic base C or T

<220>

<221> misc_binding

<222> 337..356

<223> 12-324-219.mis1, potential

<220>

<221> misc_binding

<222> 358..377

<223> 12-324-219.mis2, potential complement

<220>

<221> primer_bind

<222> 139..157

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 579..599

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 345..369

<223> 12-324-219 potential probe

<220>

<221> misc_feature

<222> 442

<223> n=a, g, c or t

<400> 151

attaaagtgt	tgaacaaggc	agcaaagcca	attgccctgg	aagccgccac	cttgaggccg	60
gccacgtggg	catctggtgc	agctccctca	gtcattcttg	tctccctgct	ggagacaggg	120
tgtctgatgc	cagcattctt	accctgcatg	acttgccctg	acagcctgcc	tttcatgtac	180
ctttcatatc	cacctggttt	tcaaatacgg	ccagggacag	agtgcacacg	cgcaccagca	240
tggtggagtc	caccagggag	ctgttgatct	gcttcaggaa	tacctggaac	tatacagaaa	300
ccaagctcac	agcaggcagt	gggctgctgg	ccaggtatgg	ccatggcccc	gggggayagt	360
cactacaagg	ggcatcagcg	acctctacca	gccccactgc	ttcagatagg	aagacagagg	420

125

ctcagataag	ctgaggggacc	tnccctcac	cacccaggta	ctaagaggca	ctccccggaa	480
ttcagcacag	atccgacact	ctctccagt	gttttacgct	caaggggtgct	ggattccttt	540
aatttttact	tttaatttta	cttcagctag	cctgagctgg	gtttctgtca	cacacactcg	600
gtgagcctaa	cacaccaggc	ccagtccctc	cctacagcgg	ctccccaccg	ggcaccacc	660
atgctgcgct	acggcaggcg	cacaagccac	ccattcccac	cctcactccc	taccacaag	720
cagccccggg	tttcatccct	gcattcccag	ggctctagcac	aaagccagac	agagcagggt	780
ccaatgaatg	tttgccaaag	actgcccaga	ctcccccgct	gtctctaacg	taaaacctgt	840
gcctaaagcc	tggcaga					857

<210> 152

<211> 973

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 473

<223> 12-324-335 : polymorphic base G or C

<220>

<221> misc_binding

<222> 454..472

<223> 12-324-335.mis1

<220>

<221> misc_binding

<222> 474..493

<223> 12-324-335.mis2, potential complement

<220>

<221> primer_bind

<222> 139..157

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 579..599

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 461..485

<223> 12-324-335 potential probe

<220>

<221> misc_feature

<222> 442

<223> n=a, g, c or t

<400> 152

attaaagtgt	tgaacaaggc	agcaaagcca	attgcctctg	aagccgccac	cttgaggccg	60
gccacgtggg	catctgggtg	agctccctca	gtcattcttg	tctccctgct	ggagacaggg	120
tgtctgatgc	cagcattctt	accctgcatg	acttgccctg	acagcctgcc	tttcatgtac	180
ctttcataatc	cacctgggtt	tcaaatacgg	ccagggacag	agtgcacacg	cgcaccagca	240
tgctggagtc	caccaggag	ctgctgatct	gcttcaggaa	tacctggaac	tatacagaaa	300
ccaagctcac	agcaggcagt	gggctgctgg	ccaggtatgg	ccatggcccc	gggggatagt	360
cactacaagg	ggcatcagcg	acctctacca	gccccactgc	ttcagatagg	aagacagagg	420
ctcagataag	ctgaggggacc	tnccctcac	cacccaggta	ctaagaggca	ctccccggaa	480
ttcagcacag	atccgacact	ctctccagt	gttttacgct	caaggggtgct	ggattccttt	540
aatttttact	tttaatttta	cttcagctag	cctgagctgg	gtttctgtca	cacacactcg	600
gtgagcctaa	cacaccaggc	ccagtccctc	cctacagcgg	ctccccaccg	ggcaccacc	660
atgctgcgct	acggcaggcg	cacaagccac	ccattcccac	cctcactccc	taccacaag	720
cagccccggg	tttcatccct	gcattcccag	ggctctagcac	aaagccagac	agagcagggt	780

126

ccaatgaatg tttgccaaag actgcccaga ctcccccgtc gtctctaacg taaaacctgt	840
gcctaaagcc tggcagacca ggactccagg tgaacttctg gacaaccag cacactccac	900
agagccctgg gttaacttta cctttgcatc ggtgttgata tatttattga atctcttgaa	960
tgcatacaacg ttg	973

<210> 153

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-324-380 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-324-380.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-324-380.mis2, potential complement

<220>

<221> primer_bind

<222> 122..140

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 562..582

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-324-380 potential probe

<220>

<221> misc_feature

<222> 425

<223> n=a, g, c or t

<400> 153

ggcagcaaag ccaattgccc tggaagccgc caccttgagg ccggccacgt gggcatctgg	60
tgcagctccc tcagtcattc ttgtctccct gctggagaca ggggtgtctga tgccagcatt	120
cttaccctgc atgacttgcc ttgacagcct gcctttcatg tacctttcat atccacctgg	180
ttttcaaatc ggtccaggga cagagtgaaca cagcgacca gcatgttgga gtccaccagg	240
gagctgttga tctgcttcag gaataacctgg aactatacag aaaccaagct cacagcaggc	300
agtgggctgc tggccaggta tggccatggc ccggggggat agtcactaca aggggcatca	360
gcgacctcta ccagccccac tgcttcagat aggaagacag aggtcagat aagctgaggg	420
acctncccc caccacccag gtactaagag gcactccccg gaattcagca cagatccgac	480
actctctcca gtgggtttac rctcaagggt gctggattcc tttaattttt acttttaatt	540
ttacttcagc tagcctgagc tgggtttctg tcacacacac tcggtgagcc taacacacca	600
ggcccagtc ctccctacag cggctcccac cgtggcacc accatgctgc gtcacggcag	660
gcgcacaagc caccattcc caccctcaact ccctacccac aagcagcccc gggtttcatc	720
cctgcattcc cagggtctag cacaaagcca gacagagcag gttccaatga atgtttgcc	780
aagactgccc agactcccc gtcgtctcta acgtaaaacc tgtgcctaaa gcctggcaga	840
ccaggactcc aggtgaactt ctggacaacc cagcacactc cacagagccc tgggttaact	900
ttacctttgc atcgggtgtg atatatttat tgaatctctt gaatgcatca acgttgaact	960
tcatcagctc ccccaggagg tcaaagtaac tctggagcac a	1001

<210> 154
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-325-30 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-325-30.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-325-30.mis2, potential complement

<220>
<221> primer_bind
<222> 472..491
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 926..945
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-325-30 potential probe

<400> 154
ctttgggagg tggaggcgtg tggatcacaa ggtcagaaga tcaagatcat cctgggctaac 60
acggtgaaac cccgtctcta ctaaaataca aaaaattagc caggcgtggt ggtgtgtgcc 120
tgtaatccca gctactcagg gaggctgagg cgggagaatt acttgaaccc aggaggcgga 180
ggttgacgtg agccaagatc gagccactga actccagcct aggcgactga gtgagactcc 240
atatcaaaaa aaaaaaata caaagcctca acccctcctt cccatcaggc ctcttgcac 300
agagtctctg ggatggggcc caggaatctg tattctttcc cagctcccca gaatgttcag 360
ccaggtttgg aaactgatct atccgattct tcttgtttca cagttaggga atctgtagct 420
ctgggaaggg aaggaacttg cccagtcac atctgatatt agtgcttctt tctccaatga 480
agagccttta ggctgggagt ycagagacat gggttcaagt ccaggctata ccagtcacatca 540
cctcgggcaa gtcatttcac ctctccaage ctctgcttcc ttactgtgag aataatgcca 600
ttgtgttggg aatcaaaaaga gagagtggca atggaaatgc tttgtcaagc tttctatttt 660
gtgcacatgg aagttgttaa gagctagaac cagccagtgt tcaactcctgt ataccacgct 720
gttcccttcc aacagaggtc agggctcctgc tgtgttgggg gtggccgcca gccagtttcg 780
gtggttgctg ggcttcaggc catctgttac caactctctt ctctccatct tttgcagggtg 840
ttgggatggc caccaactgg gggagcctct tgcaggataa acagcagcta gaggagctgg 900
cacggcaggc cgtggaccgg gccctggctg agggagtatt gctgaggacc tcacaggagc 960
ccacttctc ggaggtaagc ccctagctcc tccccacagc a 1001

<210> 155
<211> 999
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 479

128

<223> 12-327-31 : polymorphic base G or T

<220>

<221> misc_binding

<222> 459..478

<223> 12-327-31.mis1, potential

<220>

<221> misc_binding

<222> 480..498

<223> 12-327-31.mis2, complement

<220>

<221> primer_bind

<222> 449..468

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 982..999

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 467..491

<223> 12-327-31 potential probe

<220>

<221> misc_feature

<222> 758

<223> n=a, g, c or t

<400> 155

tgtctttaaaa	gctagttttt	caatgttaac	aggctggaaa	tattgttaat	acaaaaacct	60
atcactgtgt	accttatggg	acaccaaata	aacaaggtaa	aattatacaa	atgtatcatt	120
aaaaagcagc	agtagaaaac	catgaccatg	cagaggtagc	cctaatacatg	ctctgaaaac	180
agttctttgt	ttctaaagtc	cagttgtgtg	cattccccag	gctggctctg	cagagttatc	240
aagtgtctta	gagcagcctc	ctctcctgag	gctgaatatg	aacctgccat	tcactctgtt	300
attgtctagt	tttagttagg	aacatgaggt	gatacataact	atactttgta	ggttattagg	360
gaatataatt	ttacatgttg	tagtcatatg	taaaggtaga	agtttgtgga	ctccaacccc	420
agttttattct	ctctctagat	ttgcttttcc	tcctgtgtca	ctagatacaa	ggctcttckt	480
ggctctgtgta	cggtttttct	cccactcctt	tatgatatttg	ggggagttct	catttttagga	540
aatttacatt	tttaaaaaat	atgtgacttt	ccaacatggc	acatatatac	atatgtaaca	600
aacctgcacg	ttgtgcacat	gtaccctaga	acttaaagta	taattttaaa	aaaagtgact	660
ttcattataa	ctaaattata	cctcagagct	ggtgtacaca	cctccatata	cattgacaaa	720
aggtagtatt	tgctaagctc	ctggatatgtg	gcaaacgnct	gggtaactgc	tttacctaga	780
agtgatttta	tttaatcctt	caagtgcctt	gtggaataga	gattagtatc	cccattgcac	840
atgtgaggaa	actgagggct	agaaagggtc	tgtattggat	gcctgtgtat	gccgaggcac	900
taagtaactt	tcattctttta	gtttcccatt	taaggaatct	attctggcag	atgattttga	960
tcctgttagt	attgattgct	tgcttcagat	gcctatttg			999

<210> 156

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 500

<223> 12-327-415 : polymorphic base A or G

<220>

<221> misc_binding

129

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<222> 480..499
<223> 12-327-415.mis1, potential

<220>
<221> misc_binding
<222> 501..520
<223> 12-327-415.mis2, potential complement

<220>
<221> primer_bind
<222> 86..105
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 615..633
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 488..512
<223> 12-327-415 potential probe

<220>
<221> misc_feature
<222> 395,958,975
<223> n=a, g, c or t

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<400> 156
tataatttta catgttgtag tcatatgtaa aggtagaagt ttgtggactc caaccccagt      60
ttattctctc tctagatttg cttttcctcc tgtgtcacta gatacaaggt cttccttggt      120
ctgtgtacgg ttttcttccc actcctttat gattttgggg gagttctcat tttaggaaat      180
ttacattttt aaaaaatatg tgactttcca acatggcaca tatatacata tgtaacaaac      240
ctgcacgttg tgcacatgta ccctagaact taaagtataa ttttaaaaaa agtgactttc      300
attataacta aattatacct cagagctggt gtacacacct ccatatacat tgacaaaagg      360
tagtatttgc taagctcctg gtatgtggca aacgnctggg taactgcttt acctagaagt      420
gattttatatt aatccttcaa gtgccctgtg gaatagagat tagtatcccc attgcacatg      480
tgaggaaaact gagggctagr aagggtctgt attggatgcc tgtgtatgcc gaggcactaa      540
gtaactttca tcttttagtt tcccatttaa ggaatctatt ctggcagatg attttgatcc      600
tgttagtatt gattgctttc agatgcctat ttgtaaaactg acttaagtaa aaccagcatt      660
accattatt cttgaggaat gaactgttct ggtcagctgg gcttttttga ttaactgaga      720
acggaaagcc cagtttttgt ttttgttttt ttatttgga gttttttctt aaagtctcta      780
taaaataatc tagattcact ttcatactcg tgtgactagc ctagtagaca gtctatgtgt      840
gattctgctt gtagcttttg ggataaagcc taaaagttgt agttccacac atgaggttgt      900
gcaggatctg acccttccca accctgacca taattcctac tccattccct taccgcgnac      960
gattttctcc attcnaaatg ccctgggaag gccaaagctgg      1000

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<210> 157
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-331-270 : polymorphic base G or A

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<220>
<221> misc_binding
<222> 481..500
<223> 12-331-270.mis1, potential

<220>

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130

<221> misc_binding
 <222> 502..521
 <223> 12-331-270.mis2, potential complement

<220>
 <221> primer_bind
 <222> 751..770
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 285..305
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-331-270 potential probe

<400> 157
 aactacggct tgggaggtgt actaagccaa gggccagaac acaaaatcag gtcctaacac 60
 taagtgccat cctcttttgt ttctaccaga ttgcttttctt tattcaccat tcttcctggc 120
 tcagtgggtca acctagtaga gtccgtgctca atatatgggc ggggcttctg gttctcattt 180
 tgtttttctaa caaggaaaat gaagaaatag gcataatgga gttaaaatga gtcttaaagg 240
 tcacagtctg ccaacacttg tcaccttttg acaagtgtcc agtttctact tggacagctc 300
 taaggccaaa ggagtttact acctgctgca gcagtcctgg ctcttaacaa ctgctacaaa 360
 attctgcctc cccgtaattt ctaccagtta gtctgtgatt tcaggcacac ataaaataag 420
 cccgattccc ccaactgtctg aaagcagctc ttatgtctgc cattctactc gaattattccc 480
 atcttaaaca ttgcagacct rgtaggggag ataaacagag cccagtggtc aggggtactt 540
 acacagacac aggtattata caggatactc aagcagtcct tggacatttc atcacttact 600
 gaaagtgaag gggtaatgac tgggtatttt tctcaatgaa aagatagtag aacagttacc 660
 acattttttt cagcataaga actgttataa tccccccaa gatgattatt ttccctttta 720
 tatacttctt ccagcccctg tctaccaaag gttttcatag tgcccacag aacctacaag 780
 ccattttgca tattgtcttt gggttgatag agcagctgtt ttcttattat gctccacagt 840
 cttcataatt tcaacctgtt gttgtgccat catttaataa agccattttc ccttaatgtc 900
 ttgcttagga tatatctagg atttggtttt ttgtgttttt gtgttttttg gctatttaag 960
 tagaccacaa atgaacaact taatatatat gtgtatcctt t 1001

<210> 158
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-331-275 : polymorphic base T or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-331-275.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-331-275.mis2, potential complement

<220>
 <221> primer_bind
 <222> 756..775
 <223> upstream amplification primer, complement

131

<220>
 <221> primer_bind
 <222> 290..310
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-331-275 potential probe

<400> 158
 taagaaacta cggcttgga ggtgtactaa gccaagggcc agaacacaaa atcagggtcct 60
 aacactaagt gccatcctct ttgttttcta ccagattgct ttctttattc accatttcttc 120
 ctggctcagt ggtcaacctg gtagagtccct gctcaatata tgggcggggc ttctggttct 180
 catthttgttt tctaacaagg aaaatgaaga aataggcata atggagttaa aatgagtctt 240
 aaagggtcaca gtctgccaac acttgtcacc ttttgacaag tgtccagttt ctacttggac 300
 agctctaagg ccaaaggagt ttactacctg ctgcagcagt cctgggtcctt aacaactgct 360
 acaaaattct gcctccccgt aatttctacc agtttagtcc gatttttcagg cacacataaa 420
 ataagcccgga ttccccctact gtctgaaagc agctcttatg tctgccattc tactcgaata 480
 ttcccatctt aaacattgca kacctggtag gggagataaa cagagcccca gtggcagggg 540
 tacttacaca gacacaggta ttatacagga tactcaagca gtccttggac atttcatcac 600
 ttactgaaag tgaaagggtg atgactgggt atttttctca atgaaaagat agtacaacag 660
 ttaccacatt tttttcagca taagaactgt tataatcccc tccaagatga ttatttttcc 720
 tttaatatata ttcttccagc ccctgtctac caaagggttt catagtgcc atcagaacct 780
 acaagcccat ttgcatattg ctttttggtt gatacagcag ctgttttctt attatgctcc 840
 acagtcttca taatttcaac ctggtgttgt gccatcattt aataaagcca ttttccctta 900
 atgtcttgct taggatatat ctaggatttg tttttttgtt tttttgtgtt ttttggctat 960
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<210> 159
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 12-334-320 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 483..502
 <223> 12-334-320.mis1, potential

<220>
 <221> misc_binding
 <222> 504..523
 <223> 12-334-320.mis2, potential complement

<220>
 <221> primer_bind
 <222> 184..202
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 616..634
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 491..515
 <223> 12-334-320 potential probe

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<400> 159
ccagcctggg caacagagtg agactccatc tcaaaaaaaaa gaaaaggata acgtgataga      60
cttatagggg ggggcagcct ccagggatga aacatctgaa tgaccaaagg agccagtcac      120
gccaggattt tggaggaaaag caccagga gaggatgcag aaagggcaaa cgctccctgg      180
aaagattctt agtcaagagt ccttcactcc cagtcctacc acaaactggg tcaccttgaa      240
caagtcacgt aacttctgag gctcagctgc cacatctaca aaatgggaat aaagacatct      300
tacctgccac attgtgagag gtttcaacca aagggtctgtt aagggtctggg atcctcccca      360
aatctcacca tagacacctg atactcatca cttggcaccc gtcttggaag aggggaacct      420
gcacagagaa ccctgggtca tgcttttgat ttttaatttc atgctgcact agaaatagct      480
tcttttgttc ctggttgacc caggagcctc tcctgccac ctggggccta ttctagttaa      540
cagctgctta tcccctcagg tacaaaagcc aacaaggaaa ggacatcagg aaacattgtt      600
ctgggaataa ccagacacct atctgccacc atctccccc atcccgtgac cacacacggg      660
agactggagg actcagcctg tcctgtagtc agataatgta catggtttat ttaaagagtc      720
aaaaggggcc gggcgcagtg gctaacgcct gtaatcctag cactctggga ggctgggggtg      780
ggtggatcac ctgagctcaa gagtttcaga ccaatctggc caacatggtg aaaccctgtc      840
tctacaaaaa atacaaaaat tagccgggtg tggtgggtgga cgctgtaat cccagctact      900
tgaggaggctg aggcaggaga attgcttgaa cctgggaagt ggaggttgca gtgagctgag      960
atcgtgccac tgcactccag cctgggcaac aacaacgaaa a                                     1001

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<210> 160

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 12-334-391 : polymorphic base A or G

<220>

<221> misc_binding

<222> 483..502

<223> 12-334-391.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 12-334-391.mis2, potential complement

<220>

<221> primer_bind

<222> 113..131

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 545..563

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 12-334-391 potential probe

<400> 160

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gtcaagagtc cttcactccc agtcctacca caaactgggt caccttgaaac aagtcacgta      180
acttctgagg ctcagctgcc acatctacaa aatgggaata aagacatctt acctgccaca      240
ttgtgagagg tttcaaccaa agggctggtt aggtctggga tcctcccca atctcaccat      300
agacacctga tactcatcac ttggcacccg tcttggaaga ggggaacctg cacagagaac      360
cctgggtcat gcttttgatt ttttaatttc tgctgcacta gaaatagctt cttttgttcc      420

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133

tggttgaccc aagagcctct tcctgccacc tggggcctat tctagttaac agctgcttat	480
cccctcaggt acaaaagcca acraggaaag gacatcagga aacattgttc tgggaataac	540
cagacaccta tctgccacca tctcccccca tcccgtagc acacacggga gactggagga	600
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ggcgagtggt ctaacgcctg taatcctagc actctgggag gctgggggtg gtggatcacc	720
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ggcaggagaa ttgcttgaac ctgggaagtg gaggttgag tgagctgaga tcgtgccact	900
gcactccagc ctgggcaaca acaacgaaaa ctccgtctca aaaaaaaaaa aaaaaaaaaa	960
aagagtcaaa aggatcttgg tccctgggtt gggccactga t	1001

<210> 161

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-335-417 : polymorphic base G or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-335-417.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-335-417.mis2, potential complement

<220>

<221> primer_bind

<222> 85..102

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 534..552

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-335-417 potential probe

<400> 161

agcctttgct gcttttgttc ctgcaatttg gaacactgtc cccatcccag cctctcacct	60
ctacccttac ctccctcact acctatacct tcctatccat ccttcaagac cccaaaaacc	120
atccctgatt ccttcagaaa ggcagtttat tgccatctt atcagactga aagcagtggc	180
tgtgtcttat ttatggttaa ttccctagaa gctggactga tacattccat ttaactaaaa	240
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gaaggcacct gggggctgcc aagcaatgag gtggggggta ggaatcatga atccgcata	360
ttttaaaaac tgccccagat cctgatgtaa acggtacaag agagtctgag aaacacaggg	420
ctcccctcaa acagtcctga cttcagcatt cctggaaaaa tgaaaatcct ttccttttgc	480
ctctaattgt ttccctgctg statcccagg ttaaaaaaaa atagataaaa tcagggggat	540
ttttctggga cttggctggg ctgggaaaca agcctgggtt ctaatacagg ctccagccct	600
gacgtactat gggccccctgc cctcctctgg ggcctccatt accacggcca cccccaccct	660
tatcaattgt gtgccccctga ggtagtgaat gtcccgctct gagcattagt tccccatct	720
tccactagtc gtcgtcagct ctgacgctct atgagctatg catacccgta gctccccgcc	780
gaccccgatg gtccccctccc ctccctccca aggtccatcc gccagggtgc agccgacgca	840
ctcctaattgc taaggccgcc ctctcatcga ccgccccctc ctggcctcga ctacagccca	900
aaggataggg tctctgcccc gcctgctctt taagcctagc cggggcggtc agcgcaagcg	960

134

cactgggtcg catcgaggcc ccgccccctg agcctgggta g

1001

<210> 162

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-337-189 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-337-189.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-337-189.mis2, potential complement

<220>

<221> primer_bind

<222> 313..331

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 792..812

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-337-189 potential probe

<400> 162

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tagagctaca	acggggagcg	attagggcca	aactttgtcc	aggggtggaag	cgagcgggcc	180
cgtgaagtgg	ggccagcctg	ggcagccgac	cgtgtcgttg	cctcggggcc	tttccaggca	240
ctggcctaag	tcctggcgat	aaagtgcgac	cgatttcctt	gtgggcgttt	tgaggctttc	300
ggtgatctga	cccgtctgtc	attcattctt	cattcattca	tgtgatgaat	gaatacagta	360
ctaagcgcg	ctaattacta	ggtagagaag	tgatcaagac	aaacactgtt	cctacggtac	420
agggaaaagt	gatgggctgt	agaatgtaga	agcccggggc	ggagaacagg	gacagcttcc	480
ggaacgaaat	cgcgagccca	ratcaggagt	ggtggcgaga	gttccaaaga	gaagacagca	540
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ctctgaatct	gtttcacgcc	cagggaagag	atgacagtgg	ccggggctag	gctacaaact	660
ctggaaatgg	agataaataa	aggaattcaa	agtactatat	acttaggcag	caaaatccat	720
aggatttggg	gagagtgaga	tgtaggaaac	aagtactcaa	ggcttgggta	cctgggtggg	780
gttcatcaga	ggagaagcag	atttgtggga	gacaacaaca	aattctattc	tggttgatg	840
gagactcgca	ggaaaaaatt	ggatattcta	gtttgaagg	aggaaagtat	tgctgtgaag	900
atgtagattt	gaatgtcatc	agcaaaacat	aaataaagcc	aaggagggt	tgaggctgta	960
gaatgagaaa	aacaaagggc	ccacttagca	ccttcattctg	a		1001

<210> 163

<211> 881

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

135

<222> 381
 <223> 12-340-130 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 361..380
 <223> 12-340-130.mis1, potential

<220>
 <221> misc_binding
 <222> 382..401
 <223> 12-340-130.mis2, potential complement

<220>
 <221> primer_bind
 <222> 252..272
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 681..701
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 369..393
 <223> 12-340-130 potential probe

<220>
 <221> misc_feature
 <222> 205,247,340,499,507
 <223> n=a, g, c or t

<400> 163
 aaaaattagc cacgtgtgat ggcattgaacc tgtagtccca gctactcggg agactgaggc 60
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 ctccagcctg tgacacagtg caactctatc tctaaaatca tcccaacaat ttttaaaagc 180
 tgtaattaaa aaaaattctg ttaanacaaa ttctagggtta atataaacag aaaaaaataa 240
 atgttangaa aggaatactc ccgaatctta acagtgggtg aattttggtg acaagtccca 300
 agacagtttt tcacattttc cttgacaaac accttttccn ttttaaaatg agaaaaatta 360
 ggacctttgt tttccaaaaa rgtccaattt tcacttaaag catttaaaaa ttatctatat 420
 gctgagaata tgactaagcc catatgttta aagacattcc ctatatacgt atgtattttt 480
 tattattgtt taaatcaang ctaggangct accccagaac aaaaagaaaa attcttcctt 540
 agccccctct agctataggc caatacttag gcagcatgtc caagacacct caagccaaat 600
 gaagaaggaa gattccatag cattttttta attaaaaagc cagcaggcaa atctttgaga 660
 ctagacagtt cagcttgagg gtctgagaaa gcctctgctc atctcaaacc agcaacaaat 720
 ctttagaaaag taattccat gccatgagat tgctcgtggc atgaatgtga cactataatt 780
 caacatcctg aattaagaga gatgtgttat tttagcttaa agcagcagat taaaaataaa 840
 aatcctaaac tactacacca cagattgtca attctagaga a 881

<210> 164
 <211> 961
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 461
 <223> 12-340-210 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 442..460

136

<223> 12-340-210.mis1

<220>

<221> misc_binding

<222> 462..481

<223> 12-340-210.mis2, potential complement

<220>

<221> primer_bind

<222> 252..272

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 681..701

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 449..473

<223> 12-340-210 potential probe

<220>

<221> misc_feature

<222> 205,247,340,499,507

<223> n=a, g, c or t

<400> 164

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aggaggatca	ctagagccca	ggggttcaag	gctgcagtga	gctaggatcg	taccactgca	120
ctccagcctg	tgacacagtg	caactctatc	tctaaaatca	tccaacaat	ttttaaagc	180
tgtaatataa	aaaaattctg	ttaanacaaa	ttctagggtta	atataaacag	aaaaaaataa	240
atgttangaa	aggaatactc	ccgaatctta	acagtgggtg	aattttggtg	acaagtccca	300
agacagtttt	tcacattttc	cttgacaaac	accttttccn	ttttaaatg	agaaaaatta	360
ggacctttgt	tttccaaaaa	agtccaattt	tcacttaaa	catttaaaaa	ttatctatat	420
gctgagaata	tgactaagcc	catatgttta	aagacattcc	ytatatacgt	atgtattttt	480
tattattgtt	taaatcaang	ctaggangct	accccagaac	aaaaagaaaa	attcttcctt	540
agccccctct	agctataggc	caatacttag	gcagcatgtc	caagacacct	caagccaaat	600
gaagaaggaa	gattccatag	cattttttta	attaaaaagc	cagcaggcaa	atctttgaga	660
ctagacagtt	cagcttgagg	gtctgagaaa	gcctctgctc	atctcaaacc	agcaacaaat	720
ctttagaaag	taattcacat	gccatgagat	tgctcgtggc	atgaatgtga	cactataatt	780
caacatcctg	aattaagaga	gatgtgttat	tttagcttaa	agcagcagat	taaaaaataa	840
aatcctaaac	tactacacca	cagattgtca	attctagaga	agcactgggc	tcagctttct	900
gcacatctgt	atttattgtt	aactgcactt	gcaggaggga	aaagaaagaa	gtctcatgac	960
t						961

<210> 165

<211> 973

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 473

<223> 12-340-222 : polymorphic base G or T

<220>

<221> misc_binding

<222> 453..472

<223> 12-340-222.mis1, potential

<220>

<221> misc_binding

137

<222> 474..493
 <223> 12-340-222.mis2, potential complement

<220>
 <221> primer_bind
 <222> 252..272
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 681..701
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 461..485
 <223> 12-340-222 potential probe

<220>
 <221> misc_feature
 <222> 205,247,340,499,507
 <223> n=a, g, c or t

<400> 165
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 aggaggatca ctagagccca ggggttcaag gctgcagtga gctaggatcg taccactgca 120
 ctccagcctg tgacacagtg caactctatc tctaaaatca tcccaacaat ttttaaaagc 180
 tgtaattaaa aaaaattctg ttaanacaaa ttctaggtta atataaacag aaaaaataa 240
 atgttangaa aggaatactc ccgaatctta acagtgggtg aattttggtg acaagtccca 300
 agacagtttt tcacattttc cttgacaaac accttttccn ttttaaaatg agaaaaatta 360
 ggacctttgt tttccaaaaa agtccaatth tcaacttaaag catttaaaaa ttatctatat 420
 gctgagaata tgactaagcc catatgttta aagacattcc ctatatacgt atktattttt 480
 tattattgtt taaatcaang ctaggangct accccagaac aaaaagaaaa attcttcctt 540
 agcccccttct agctatagcc caatacttag gcagcatgtc caagacacct caagccaaat 600
 gaagaaggaa gattccatag cattttttta attaaaaagc cagcaggcaa atctttgaga 660
 ctagacagtt cagcttgagg gtctgagaaa gcctctgtc atctcaaacc agcaacaaat 720
 ctttagaaaag taattcacat gccatgagat tgctcgtggc atgaatgtga cactataatt 780
 caacatcctg aattaagaga gatgtgttat tttagcttaa agcagcagat taaaaataaa 840
 aatccctaaac tactacacca cagattgtca attctagaga agcactgggc tcagctttct 900
 gcacatctgt atttattgtt aactgcactt gcaggaggga aaagaaagaa gtctcatgac 960
 ttgaggcaac aat 973

<210> 166
 <211> 975
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 491
 <223> 12-340-240 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 471..490
 <223> 12-340-240.misl, potential

<220>
 <221> misc_binding
 <222> 492..511
 <223> 12-340-240.mis2, potential complement

<220>

<221> primer_bind
 <222> 252..272
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 681..701
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 479..503
 <223> 12-340-240 potential probe

<220>
 <221> misc_feature
 <222> 205,247,340,499,507
 <223> n=a, g, c or t

<400> 166
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 ctccagcctg tgacacagtg caactctatc tctaaaatca tcccaacaat ttttaaaagc 180
 tgtaattaaa aaaaattctg ttaanacaaa ttctagggtta atataaacag aaaaaataa 240
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 agacagtttt tcacattttc cttgacaaac accttttccn ttttaaaatg agaaaaatta 360
 ggacctttgt ttccaaaaa agtccaattt tcacttaaag catttaaaaa ttatctatat 420
 gctgagaata tgactaagcc catatgttta aagacattcc ctatatacgt atgtattttt 480
 tattattgtt yaaatcaang ctaggangct accccagaac aaaaagaaaa attcttcctt 540
 agccccttct agctataggc caatacttag gcagcatgtc caagacacct caagccaaat 600
 gaagaaggaa gattccatag cattttttta attaaaaagc cagcaggcaa atctttgaga 660
 ctagacagtt cagcttgagg gtctgagaaa gcctctgctc atctcaaacc agcaacaaat 720
 ctttagaaaag taattcacat gccatgagat tgctcgtggc atgaatgtga cactataatt 780
 caacatcctg aattaagaga gatgtgttat tttagcttaa agcagcagat taaaaataaa 840
 aatcctaaac tactacacca cagattgtca attctagaga agcactgggc tcagctttct 900
 gcacatctgt atttattgtt aactgcactt gcaggaggga aaagaaagaa gtctcatgac 960
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<210> 167
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-341-99 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-341-99.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-341-99.mis2, complement

<220>
 <221> primer_bind
 <222> 403..422
 <223> upstream amplification primer

139

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<220>
<221> primer_bind
<222> 927..947
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-341-99 potential probe

<220>
<221> misc_feature
<222> 133,141,738,898
<223> n=a, g, c or t

<400> 167
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aatatgacta agcccatatg tttaaagaca ttccctatat acgtatgtat tttttattat      120
tgtttaaadc aangctagga ngctacccca gaacaaaaag aaaaattctt ccttagcccc      180
ttctagctat aggccaatat ttaggcagca tgtccaagac acctcaagcc aaatgaagaa      240
ggaagattcc atagcatttt ttaaattaaa aagccagcag gcaaattctt gagactagac      300
agttcagctt gagggctctga gaaagcctct gctcatctca aaccagcaac aaatctttag      360
aaagtaattc acatgccatg agattgctcg tggcatgaat gtgacactat aattcaacat      420
cctgaattaa gagagatgtg ttatttttagc ttaaagcagc agattaaaaa taaaaatcct      480
aaactactac accacagatt rtcaattcta gagaagcact gggctcagct ttctgcacat      540
ctgtatttat tgttaactgc acttgcagga gggaaaagaa agaagtctca tgacttgagg      600
caacaatgaa aactgccctg aacatatgcc tgctttgctt tgtataatag agacctagg      660
tcacacctta gaaaagggtga agtaattatt atacagtata taaccatttt atagcctggt      720
ttcatcatga attttcnca tattactata actttaacat tatattaaca acttcataaa      780
attcaacaaa atagatagaa taaccattat cttctcctgg tagatagtca ttacaaataa      840
tgttacacct aacgggtcttg gtatacaca gctttatctc attttgactt acgtcttnca      900
tcagagtcac agaaatggaa acaacagggc aaaaatgagta gtaatgttta aagctctgaa      960
gtatactaca ccaattcttc tcaaaagaga tcacattcat c                                     1001

<210> 168
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-342-32 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-342-32.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-342-32.mis2, potential complement

<220>
<221> primer_bind
<222> 513..532
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 81..101
<223> downstream amplification primer

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<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-342-32 potential probe

<400> 168
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 gtttgtggaa gggggcttct ggggtactggg aatgttctat ttcctaattt gggtagtagt 180
 gcaaaagtga atgtattttg tggttaattat tgggtgactt ttctgtatga aggttatact 240
 tcagtaacaa agtctataaa aatacacaca taaacacagt atgttggtga tggtaggggt 300
 aaacagagcg tcatactttg ttcctgggga tataaactga caaaacttct taggtaggta 360
 aacttcagat ttataaacia taaaaaacat acgttcttgt tccaaaggta tatactcaca 420
 tgtatacaaa aatatgtaaa agatctttac tgcaaccttg tctgtaagag aaatgggtgtg 480
 gaaaaattat aaatgccagt yaactggggc ctgggtaaat aaattatggc acaatcacac 540
 caggaaacac taaccattta attttttttt gagagctcat caccagggt agagtgcagt 600
 ggtatgatct tggctcacgg caacctctgc ctcccggtt caagcaattc tctgcctca 660
 gcctcctgag tagctgggat tacaagtggc tgccaccgtg cccatctaatt tttgggtattt 720
 ttagtagaga cagggtttca ccatcttggg cagggtgggc tcgaactcct gacctcacga 780
 tccacctgcc ttggcctccc aaagtgtctg gattacaggc gtgagccact gcgcccggcc 840
 taaaattgtt ttaattaaaa aaaaaaaaag aagaagaaa aaggtagaga atagtgtagc 900
 cgtgtatatg gtatatcact ctatgtgcgg agaaaataaa ctaagggtgga ggtgggtggg 960
 aatatttaca cacacacaca cacacacaca caaaaaaac a 1001

<210> 169
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-344-349 : polymorphic base G or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-344-349.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-344-349.mis2, complement

<220>
 <221> primer_bind
 <222> 154..173
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 685..705
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-344-349 potential probe

<400> 169
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 accacaaatg aacaacttaa tatatatgtg tatecttttc atgtttgtat taaactagtt 120

141

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cctcaagata cattttcaaa agtagaacta ctagaatcta aagtataggc atcttttttt 180
tgttcatttg ttttggtttt ttaaagagg tcttactctg tcaactcagg gcacaatcac 240
agctcactgt agtctcgaa tcctaggctc aagcaatttt cctcctcac cctcccgagt 300
ggctaggact gcatgcgcgt gtaccacgcc tggctaaaag ttaaaagtat aagcatctca 360
attgctcttg ttataaatcc ccattgaaag ttctactgca gcaaacaaaa ataccatttt 420
taccagactc attaactgag catttctttt tttgttgctg ttatctgtgt tgggcaaatg 480
gctcttaatg tctgatctat kactaattct tataaagaaa ctactacttc cctgtgagca 540
ggaacaggaa agtagcataa aaacgaaact taattttcat gagcccaaaa ccaaaagatg 600
atgaaactga gtatgaacca tggacaaagt gctttatttg gcacttgctt ctatttttta 660
aaattgtttc cttcactcc taagctgcta ggaatgctaa aatgctaggt ctcttctca 720
gatcccaatg ggcagccctg ccaagctagc ttgactagat gggttgtctc ataactctga 780
gacaacgcag acgctctgca tcccttatca ccacctttca acctactggg gctctgtgat 840
tgatttattt aacgacttca gagcagggtg aaacactgct ctgcatgtct cactatatat 900
ctcactattt ctatgcctc cttttttaa aggaattggg attcactcat tcatcaagta 960
ttgttcagca tctactctag agcagatata gtgggtgagg a 1001

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<210> 170

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-345-453 : polymorphic base G or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-345-453.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-345-453.mis2, potential complement

<220>

<221> primer_bind

<222> 53..70

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 558..578

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-345-453 potential probe

<400> 170

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cagatcccaa tgggcagccc tgccaagcta gcttgactag atgggttgct tcataatcct 60
gagacaacgc agacgctctg catcccttat caccaccttt caacctactg gggctctgtg 120
attgatttat ttaacgactt cagagcaggg tgaacactg ctctgcatgt ctactatat 180
atctcactat ttctagatcc tccattttta aaaggaattg ggattcactc attcatcaag 240
tattgttcag catctactct agagcagata cagtgggtgag ggaaaaaaag tctcagcctt 300
catggaacct ataaatctag tgggaagaag agagactaaa caagtgcacc aacaaataat 360
tacaatatgc tacttgctat gagggatcat agagaacatg aaagaccaag ttagaatata 420
cagctgagac attaaaaatg aatataaatc ctcttaataa ccactactgc atgcacaaat 480
gaggccttat acagtatgtc statgtgggt aaaaaaaaaa tcttttaaat taaaaaacg 540
caaagtgggt aggaggcat tcaccaaaca ttaactgaag tcatctctgg cttttaacac 600
cagagtaaaag tgcattcact tttttatttt aaattaaata ccgaagctgg gtgcggtggc 660

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142

tcatgcctgt	aatcccagca	cttgggaggc	tgagggtgggc	agatcacttg	agggtcaggag	720
ttcgagacca	gcctgggtcaa	catgggtgaaa	ccccatctct	actaaaaaaaa	aaaatacaaa	780
aattagccgg	gtatgggtggt	gggcgcctgt	aatcccagct	acttgagagg	gtgaggcagg	840
aaaatcactt	gagctcagga	ggcggagggt	gcagtgaacc	aagatcatgc	cactgcactc	900
cagcctgggc	aacagagcga	gagactgtct	caaaaaaaaa	aaaattgaat	acctaaaaag	960
aattatttgt	aacgtgtaag	ttataaaaaa	taataataga	a		1001

<210> 171

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-346-204 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-346-204.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-346-204.mis2, potential complement

<220>

<221> primer_bind

<222> 684..704

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 248..267

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-346-204 potential probe.

<220>

<221> misc_feature

<222> 664,706

<223> n=a, g, c or t

<400> 171

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ccccatcaca	gagattacaa	ggggaagtgg	ctagagggcc	tcaggcagaa	tttttttttt	120
tttttttttt	tgagacacag	tctcactctg	ttgcccaggc	tgaggtgcag	tggcgtgatc	180
tcagctcact	gcaacctctg	cctcctgggt	tcaagcaatt	ctggtggccg	ctccacagac	240
attacaaaac	acgaggcaac	actccaccct	gaggtctgaa	gacccaaaca	caagcattag	300
tgccccatga	gcaatcgaaa	gagaccttaa	gaaagtattt	taaaaatgat	taaaaacaga	360
atatgcagca	gaaaaaagat	attaacatca	tggctaagca	gtttccgaat	tgagccagac	420
agaacatcta	gaaatgcaaa	atatatttgc	ttgaaattaa	aaactcaaat	gataaagcag	480
aagacaggtc	gctgagggaa	rtccccagag	tgagtgaag	agaagagggc	cccatggcac	540
caggccgatg	gctgggtggc	acttttaggt	cccagagcac	tttccttctc	atgctggtag	600
gcagggtgcc	gactagccgg	ggggccaata	ggggaaagag	tattatcctt	cttttgcaag	660
aaanacagag	gctcagagat	tcagtgatcc	attcaagctc	ttccancaag	ccttccaatg	720
tcctgttcag	agctctctca	aggggactgt	gagagacaca	agctaaagga	gagtgcttgg	780
gtcaaaaaaa	ccaaagccac	cttttttgtg	atgagacagt	gtctttgctc	tgtcaccag	840
gccggatgtg	cagtggcttg	atcttagttc	actgcaacct	ctacctcccg	gggttcaagt	900

143

attctccac ctcagcctcc tgagtagcag ggattacagg tgccccacca acatgcctgg 960
 ctaatttttg tatttttagt agagacgggg tttcaccatg t 1001

<210> 172
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-364-55 : polymorphic base G or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-364-55.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-364-55.mis2, potential complement

<220>
 <221> primer_bind
 <222> 447..464
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 849..867
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-364-55 potential probe

<220>
 <221> misc_feature
 <222> 180
 <223> n=a, g, c or t

<400> 172
 tactcacaag taattttaca ttttttttgt acggagtctt caaaatctgg tgtatatttt 60
 actctcacag catgtgcatg ttttcattag gacaagccat atttcaagta ctcatgggcc 120
 actgtgtgcc tggtagcttc tggactaaac aagcatgagt ctggaggata attattaatn 180
 cctgcagaga tgaggaggagg aggagcaagg tattggggct ccagagatgc ctgggcaaag 240
 tgggtactaa agtttgacca aagtcttttg agttaatttg ggacatgttg caaacagtga 300
 aagcagacca tggcagactt tgaacacctg aattgatttg gtaagttaca gggagccttg 360
 ggagcagggg ttgagcagga gacagaactg cattctcgag caggagccaa agaattgata 420
 ctaatgcaaa atctttaatc acaaagtctc ctgtgagtgt cttgacacca cagatacatt 480
 ttctgttgag ttgtcttaga kaactaattt gaggtatgat ttcatccac ttacttgat 540
 gtaatcaaat tcttctttta cacgatgact cttagggtgac caatttatga cgtttggtg 600
 tctgttttag taccttaaca agaaatatcc gacataggag aggagaaaag gttgtcatca 660
 atgtaccaag taagtctact gagagggtgg ggggtgggag agagacatgt tgtattgttg 720
 ttaaatcctg gattctaaac catTTTTatt ttgtatttt tataatacag tatttaagga 780
 caagaataca ccatctccat ttatagaaac atttactgag gatgatgaag cttcaagggc 840
 ttctaagccg gatcataatt acatggatgc catgggattt ggaatgggca attgctgtct 900
 ccaggtagt ttcaaatat acagagaggc aaagtgttcc atccatttct gttttttaac 960
 ttctttatat atgcatgttt cctgttccaa aaatcacatt t 1001

<210> 173

144

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<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-364-108 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-364-108.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-364-108.mis2, potential complement

<220>
<221> primer_bind
<222> 394..411
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 796..814
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-364-108 potential probe

<220>
<221> misc_feature
<222> 127
<223> n=a, g, c or t

<400> 173
atatttttact ctacagcat gtgcatgttt tcattaggac aagccatatt tcaagtactc      60
agtggccact gtgtgcctgg tagcttctgg actaaacaag catgagtctg gaggataatt      120
attaatncct gcagagatga gggagggagg agcaagggtat tggggctcca gagatgcctg      180
ggcaaaagtgg gtactaaagt ttgaccaaag tctttggagt taatttgga catgttgcaa      240
acagtgaag cagaccatgg cagactttga acacctgaat tgatttggtg agttacaggg      300
agccttggga gcaggggttg agcaggagac agaactgcat tctcgagcag gagccaaaga      360
attgatacta atgcaaaatc tttaatcaca aagtccctt gtagtgtctt gacaccacag      420
atacattttc tgttgagttg tcttagagaa ctaatttgag gtatgatttc attccactta      480
cttgtagtga atcaaattct ycttttacac gatgactctt aggtgaccaa tttatgacgt      540
ttggttgtct gtttttagtac cttaacaaga aatatccgac ataggagagg agaaaagggt      600
gtcatcaatg taccaagtaa gtctactgag aggtgggtggg gtgggagaga gacatgttgt      660
attgttgttt aatcctggat tctaaacat ttttattttt gtatttttat aatacagtat      720
ttaaggacaa gaatacacca tctccattta tagaaacatt tactgaggat gatgaagctt      780
caagggcttc taagccggat catatttaca tggatgccat gggatttgga atgggcaatt      840
gctgtctcca ggtatagttt caaatataca gagaggcaaa gtgttccatc catttctggt      900
ttttaacttc tttatatatg catgtttcct gttccaaaaa tcacatttta atgaggttga      960
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<210> 174
<211> 1001
<212> DNA
<213> Homo Sapiens

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145

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<220>
<221> allele
<222> 501
<223> 10-364-267 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-364-267.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-364-267.mis2, potential complement

<220>
<221> primer_bind
<222> 235..252
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 637..655
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-364-267 potential probe

<400> 174
ttggggctcc agagatgcct gggcaaagtg ggtactaaag tttgaccaa gtctttggag      60
ttaatttggg acatgttgca aacagtgaaa gcagaccatg gcagactttg aacacctgaa      120
ttgatttggg aagttacagg gagccttggg agcaggggtt gagcaggaga cagaactgca      180
ttctcgagca ggagccaaag aattgatact aatgcaaaat ctttaatcac aaagtccct      240
tgtagtgtct tgacaccaca gatacatttt ctgttgagtt gtcttagaga actaatttga      300
ggtatgattt cattccactt acttgatatg aatcaaattc ttcttttaca cgatgactct      360
taggtgacca atttatgacg tttgggtgtc tgtttttagta ccttaacaag aaatatccga      420
cataggagag gagaaaaggt tgtcatcaat gtaccaagta agtctactga gaggtgggtg      480
ggtgggagag agacatgttg wattgttgtt taatcctgga ttctaaacca tttttatttt      540
tgtattttta taatacagta ttaaggaca agaatacacc atctccattt atagaaacat      600
ttactgagga tgatgaagct tcaagggctt ctaagccgga tcatatttac atggatgcc      660
tgggatttgg aatgggcaat tgctgtctcc aggtatagtt tcaaataac agagaggcaa      720
agtgttccat ccatttctgt tttttaactt ctttatatat gcatgtttcc tgttccaaaa      780
atcacatttt aatgaggttg aaatggtagc tggatatgct ttctgaaaaa caatgaagtt      840
atattagtaa attcattgga agctgtctat gactaatagt tctacagact ctgttgttca      900
ccacaaaggt atatacggtatatacctt tataactgta atttcagtta acttaaaatg      960
caatatattc tgtcattgtt tcccttctct ttttatatgc c                                1001

<210> 175
<211> 997
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 497
<223> 10-367-20 : polymorphic base G or T

<220>
<221> misc_binding
<222> 477..496
<223> 10-367-20.mis1, potential

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<220>
 <221> misc_binding
 <222> 498..517
 <223> 10-367-20.mis2, potential complement

<220>
 <221> primer_bind
 <222> 478..495
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 889..908
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 485..509
 <223> 10-367-20 potential probe

<400> 175
 agcgttggtta acttgcccct ctctgccag caccttcctt ctctgacttc actgcttggg 60
 gagcatgcta atgattccct ggtgttaata actttgcaat tcttaaacag gtgacattcc 120
 aagcctgcag tatactctgag gccagatacc tttatgatca gttggctact atctgtccaa 180
 ttgttgtaag tagaaattac ctcttatttt aaatactact tcgtatgaaa taagatagca 240
 tgtgcagaat ttactgacag tgtgctattt aagtcagtt aagacctcag tcagagatgg 300
 actaatataa atagtatgta ggtttaggta taatgaactg agagtctaca ctgtagaagt 360
 ttactcttgc tagtacaaca ttgatttggt aaatgtgaag tttgaatgtg gccattttcc 420
 ctccccata cttcatgtcc tcacattaga gagaggatga ttttaagtga tcaaacccaa 480
 ggaactggat tcttcckggt atatttctact gtaagatagg cacaggtaga tgtgctctgt 540
 atgggttgca taaacatgct ttttgatcag aaatataact gcatggagct ttttttagca 600
 tgtaagtgc actttgaatt tgcaggagct gacttttgtt tgtttttaga tggctttgag 660
 tgctgcacct cccttttacc gaggctatgt gtcagacatt gattgtcgct ggggagtgat 720
 ttctgcatct gtagatgata gaactcgga ggagcgagga ctggaggtgg gaattgtttt 780
 tccttaatac cccttttaag tcaagcaggt aaaatggatc ttttgtaact acttgcaatt 840
 tcaggatgtc tccctgcaat ttttatctga aatggggaaa aagatttggg ctagggtggg 900
 agttaatttt tatcgatgt tgatgtctgt atttgtttta gcttcattta aaattagtag 960
 tccgattttt ctatattttg gaagtgcgta tggctgt 997

<210> 176
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-351-389 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-351-389.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-351-389.mis2, potential complement

<220>
 <221> primer_bind
 <222> 113..132

147

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 518..537

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-351-389 potential probe

<400> 176

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gtgatctgct tttaaaagat aaaagtatat ttaaatacata ccagaaaaaa aggggtattta      60
aattgccttc agatttttaa aaacataatt ttccttaata atacttttta gggctcacta      120
actttttttc tgtatcttat gttgaggttt ttatataatt atcatatata aaaatatatt      180
ccactcattt tatatagcat attcatttat atatatattt aatcttttagc cattgaagaa      240
caataactat aggatcagta aatcccgata tgactcaata gacagctatt tatctaagtg      300
tgggtgagaaa tataatgaca tcgacttgac gatagataaa gagatctacg aacagctgtt      360
gcaggaaggt ggggtttctac tccatcttcc tgggtttgaa tgtacgcctt tagttcttca      420
aagctctttt acactttttt gctgactcct ggtctgggtt ctatttttag tgcaaagtct      480
ttaacttctc tcatgaggct rcttgttcct aaagtttcag gttccaaata cttgtgagat      540
tttcttgatt tttagcaaaa ggagcttact ttggaggctt gtgtctaggt ccacaccagt      600
gccccagcag gcattgtgta agtagtgaat aaaacgctga cactcccga gtgtccgcag      660
gataaaatac tgggtgaggt gaggatacta atcaaaccag ctatttcaag cttctagaca      720
ccctttcttc aaacttcctg agctatcctg tcgtctttct ggactaagag gaagtgggtat      780
ctctcgcttt gcagtgaagt cccatgtgat ctctttttgc aggcattgat catctcctgg      840
cccagcatgt tgctcatctc tttattagag acccactgac actgtttgaa gagaaaatac      900
acctggatga tgctaataag tctgaccatt ttgaggatc ttctcagttt tatttttatt      960
tatttatgta ttgacttctg agagtctgga atcctctggt t                                1001

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<210> 177

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-353-102 : polymorphic base A or T

<220>

<221> misc_binding

<222> 481..500

<223> 10-353-102.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-353-102.mis2, potential complement

<220>

<221> primer_bind

<222> 400..417

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 800..819

<223> downstream amplification primer, complement

<220>

<221> misc_binding

148

<222> 489..513

<223> 10-353-102 potential probe

<400> 177

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ctttccccc ccaaactcac aaaaggagat ataaatecctt ccagtcttgc catcgggtcc      60
caagatgggc aggacggaga aagaactctc tctcagtgtg ttgagaaaca gctacccttc      120
ttaggtctctt gggtcacgga agcagcagca ttcccaggag aggaggaaga aaggaaacaa      180
ctgtcatgtg acagggttct cagatgaaag tgtccagtgt cacctggaaa ggcaggctgg      240
ctcctaaaat tctcagggat gaagggtggg gccccgtggc tcttcagatg ctgctctgta      300
gctgggagat agggagtagg agctgggtga gattaagctt gcagtgatag ggcctcatag      360
cttttggttaa aacttggtct gttttgtttt cctaaaagag cactctcgaa gaaaatcttc      420
aattgtacct ttttgtcttt gtcaattgaa atttggtatg gacagtgagc agtcttcttc      480
cttaattaaa taccagatca wcttaatat ttcttggtat tgtgaaaagt tggttttctt      540
ctctgctttt gtatcacaga atattcagtc cacaaattgg cagacaatga gatttaagcc      600
ccctcctcca aactcagaca ttggatggag agtagaattt cgacccatgg aggtaagaca      660
catgcatcag caagaactga ctcaaaagta ctctttcgcc agctgttcat cacccttctg      720
atgctgctat gagaaggctc ttatatataa aataaaaatt aagtatgtgc atggtagcaa      780
gtcagtccaa gttaaggagg gttgatttct gagaatagat gtgggcaaag ggcttccaga      840
cccagatggg gaattaggag atggcttggg aatgacatga tctgaggaag ggcctgggtc      900
aggggaagagc atgtttgtgt agttgggtca taacttctct gggcttctgc ttgtctaggt      960
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<210> 178

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-354-72 : polymorphic base A or G

<220>

<221> misc_binding

<222> 482..500

<223> 10-354-72.mis1

<220>

<221> misc_binding

<222> 502..521

<223> 10-354-72.mis2, potential complement

<220>

<221> primer_bind

<222> 430..447

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 830..849

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-354-72 potential probe

<400> 178

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ttcaattgta cttttttgtc tttgtcaatt gaaatttggg atggacagtg agcagtcctc      120
ttccttaatt aaataccaga tcactttaat attttcttgg atgtgtgaaa agttgggttt      180
cttctctgct tttgtatcac agaatatcca gtccacaaat tggcagacaa tgagatttaa      240
gccccctcct ccaaactcag acattggatg gagagtagaa tttcgaccca tggaggtaag      300

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149

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acacatgcat cagcaagaac tgactcaaaa gtactctttc gccagctggt catcacccctt 360
ctgatgctgc tatgagaagg ctcttatata taaaataaaa attaatgatg tgcattggtg 420
caagtcatgc caagtttaagg aggggttgatt tctgagaata gatgtgggca aagggtcttc 480
agaccagat ggggaattag ragatggctt ggggaatgaca tgatctgagg aagggtcttg 540
gtcaggggaag agcatgtttg ttaggttggt tcataacttc tctgggcttc tgcttgctta 600
gggtgcaatta acagactttg agaactctgc ctatgtgggt tttgtgggtac tgctcaccag 660
agtgatcctt tcctacaaat tggattttct cattccactg tcaaaggtaa ggatatgttt 720
ctttatgggt atgggtatag atctatctgt agatatattt atttatatat gctattttatt 780
tcccacctaa ttctatttga aattgtttac cctttgcaat aaaatgtttc tccatcagcc 840
ctattcttta tttcttttta aacctaaagt taatttctag acgctttcca ttcaagatga 900
ttgatggcta gaagtagtcc tacacattga tttcatccac caaaaaatcc cagggttgatt 960
acaatgttaa attaggatgg ggaggggaaag tgtaactgct g 1001

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<210> 179

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-354-320 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 10-354-320.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-354-320.mis2, potential complement

<220>

<221> primer_bind

<222> 182..199

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 582..601

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-354-320 potential probe

<400> 179

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ctccaaactc agacattgga tggagagtag aatttcgacc catggaggta agacacatgc 60
atcagcaaga actgactcaa aagtactctt tcgccagctg ttcacacccc ttctgatgct 120
gctatgagaa ggctcttata tataaaataa aaattaagta tgtgcatggt agcaagtcag 180
tccaagttaa ggagggttga tttctgagaa tagatgtggg caaagggtt ccagaccag 240
atggggaatt aggagatggc ttgggaatga catgatctga ggaagggtc gggtcaggga 300
agagcatgtt tgtgtagtgt gttcataact tctctgggct tctgcttgct taggtgcaat 360
taacagactt tgagaactct gcctatgtgg tgtttgtggg actgctcacc agagtgatcc 420
tttctacaa attggatttt ctcatccac tgtcaaagg aaggatatgt ttctttatgg 480
tgatgggtat agatctatct rtatgatata ttatttatat atgctattta tttcccacct 540
aatttcattt gaaattgttt accctttgca ataaaatgtt tctccatcag cctatttctt 600
tattttcttt taaacctaa cttaatttct agacgcttct cattcaagat gattgatggc 660
tagaagtagt cctacacatt gatttcaccc accacaaaat cccagggttga ttacaatgtt 720
aaattaggat gggggaggaa agtctaactg ctggaatgcc ggtaaaagtc tctcagtag 780
aactgaactt gagatatttc tgaagaattc ggatgggatt gaactctcag aaaaacaaat 840

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150

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tggagttaat ctgcccccca aaagacccaa aaacaagctt tctgggagga gtttgccagc   900
aaaacaactc caggtgatga gggagcagag ctgtgggttg tggagcagta gctgaggagg   960
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<210> 180
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-354-360 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-354-360.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-354-360.mis2, potential complement

<220>
 <221> primer_bind
 <222> 142..159
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 542..561
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-354-360 potential probe

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<400> 180
catggaggta agacacatgc atcagcaaga actgactcaa aagtactctt tcgccagctg   60
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tgtgcatggt agcaagtcag tccaagttaa ggagggttga tttctgagaa tagatgtggg   180
caaagggtt ccagacccag atggggaatt aggagatggc ttgggaatga catgatctga   240
ggaagggcct gggtcaggga agagcatggt tgtgtagttg gttcataact tctctgggct   300
tctgcttgtc taggtgcaat taacagactt tgagaactct gcctatgtgg tgtttgtggt   360
actgctcacc agagtgatcc tttcctacaa attggatttt ctcattccac tgtcaaagg   420
aaggatatgt ttctttatgg tgatgggtat agatctatct gtagatata ttatttatat   480
atgctattta tttcccacct ratttcattt gaaattgttt accctttgca ataaaaatgtt   540
tctccatcag ccctattctt tattttcttt taaacctaa ctttaattct agacgtttc   600
cattcaagat gattgatggc tagaagtagt cctacacatt gatttcatcc accacaaaat   660
cccagggtga ttacaatggt aaattaggat ggggaggga agtgtaactg ctggaatgcc   720
ggtaaaaagt tcttcagtag aactgaactt gagatatttc tgaagaattc ggatgggatt   780
gaactctcag aaaaacaaat tggagttaat ctgcccccca aaagacccaa aaacaagctt   840
tctgggagga gtttgccagc aaaacaactc caggtgatga gggagcagag ctgtgggttg   900
tggagcagta gctgaggagg tgaacgcctt tggtttcttg gccagggttc ctcttggcag   960
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<210> 181
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

151

<220>
<221> allele
<222> 501
<223> 10-355-87 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-355-87.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-355-87.mis2, potential complement

<220>
<221> primer_bind
<222> 415..434
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 821..840
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-355-87 potential probe

<400> 181
agtgtggtgg tgcaggcctg taatcccagc tgcttgggag gctgaggcac aaagaattgc 60
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gcaacagagc gagactccat ctcaaaaaaa cagaagaaga actgggttct agtcctgcct 180
tctgccttcg ttaccctggg actcctgggt agacactgct atataaaggg aaccagccac 240
ctgccctccc aacactgtat atctgttgca aggctcagtc acagagggtc tttgaaatgc 300
agacgttcca catgaatata agttttgggt tttaagtttc tcttaaaatt ccctgattgg 360
ttgaaaaatc acataccaat ccatgattga gtgatacagt cctcacataa ataaaaagcc 420
tgttcctccc actgggaagc atttgagcag aaagtagaat ccctaaggga atgagtccta 480
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tcgtgattct ttttttcct taggttgatg agaacatgaa ggtagcacag aaaagagatg 600
ctgtcttgca gggaaatggtt tatttcagga aagatatttg caaagggtatt acattatctt 660
agattttcaa tgtcagctta tgctgcaaca agctgctaaa gctccctga ccctcttctc 720
cggcaggtgg caatgcagtg gtggatggtt gtggcaaggc ccagaacagc acggagctcg 780
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ggccctgtac agtacgcctc actgtgcaca tcccccgga gggagttcat aaagtgtcct 900
gcttcttgta ggaaggtgtg tttcctggac tgatcccaat tctgaactct taccttgaaa 960
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<210> 182
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-358-60 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-358-60.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-358-60.mis2, potential complement

 <220>
 <221> primer_bind
 <222> 442..460
 <223> upstream amplification primer

 <220>
 <221> primer_bind
 <222> 870..889
 <223> downstream amplification primer, complement

 <220>
 <221> misc_binding
 <222> 489..513
 <223> 10-358-60 potential probe

<400> 182
 tttctggagt cacaaaggat agccgtagaa ccctacctca cccctcaaat ggtatactgc 60
 caatttccca cttcattcac tctacttact gttctttatt ctctccacct ctttgatcaa 120
 agatcgctca aggacctac agtcctctga ggcagtctca tgacactggc atttgtagtc 180
 ctagccctct ggccaaatgg gagggcacat gttcttgtag acatgtgtctg gtcctctgtc 240
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 gtatgtgttc tcattgcctg cctgcaacct agaattcctg cccaggagga gttcttcaaa 360
 cgctatgaaa gatgttccca ccccttgcca tgcagctaca ctaaaaggac atattgattt 420
 ctctccagaa ttgtgtttat gctgaccact aaatatcaac ttattaaaaa aaaaacttac 480
 gtggttttaa ttttttttcc rctccccctc cgcccacagg agaactaatg acagttgcca 540
 gatggatgag ggagtttatt gcaaaccatc ctgactacaa gcaagacagt gtcataactg 600
 atgaaatgaa ttatagcctt attttgaagt gtaaccaaat tgcaaatgaa ttatgtgaat 660
 gccagaggt acttggtatca gcatttagga aagtaaaata tagtggaagt aaaactgact 720
 catccaacta gacattctac agaaagaaaa atgcattatt gacgaactgg ctacagtacc 780
 atgcctctca gccagcccgt gtgtataata tgaagaccaa atgatagaac tgtactgttt 840
 tctgggccag tgagccagaa attgattaag gctttctttg gtaggtaaat ctagagttta 900
 tacagtgtac atgtacatag taaagtattt ttgattaaca atgtatttta ataacatatt 960
 taaagtcatc atgaactggc ttgtacattt ttaaattctt a 1001

<210> 183
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-468-63 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-468-63.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-468-63.mis2, complement

<220>
 <221> primer_bind
 <222> 439..458

153

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 946..966

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-468-63 potential probe

<220>

<221> misc_feature

<222> 376,386,618

<223> n=a, g, c or t

<400> 183

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cagtgc aaag acccagaacc cagccttcct tcacctgaaa cagctgcagc gtgcacacac      60
acttcttg tg catatatctc tgggtctattt attttcaaaa ctaagtataa tccaaattga      120
atgctgga at cagatttttc cattctgaat gtgtttaaat aacatggcca aggataattt      180
ctttctgt tt tcttgacatt tataggtagt ataaaatatg tgacttccaa ataaacataa      240
accatcac ac ttcacgaaaa aagagatcct tcgactttta actgcctggt tcctatctta      300
attacaag ta tttctaaaga aaaccattaa gttctagagc ttacagtaca tggtttttaa      360
attgtata ag tgctgnttaa gagtanttga ttgccttttc ttgggtttaat attaaaccag      420
ggtgttct gc caaagaccgc atagtttctc tgatatgggt ccaaagggat attcctttcca      480
ctgaaacac t gatgtatac yagtaaatgc ttcctaattg tagatgataa atatttttgt      540
tgcttgtag a tagaattttt ccatctagtg taagcttagg attgttttct tttcccag      600
gacatgtac a gtttcacnta ctccacttaa aaaaaatcgt tagctcagat aaagtgtgtg      660
gcacatgaaa t gaatttttg caattcacca ccgaaatccc tgctttatat ctcttcagtg      720
gaacactaaa c caacttctt tcccaagtac actgatttga tctttacaaa ttatatgaat      780
gtattaaatt atcacatgtg ccctgaaact gtgtacatct attatgtatc attagagaga      840
tggaaaaaaa aaaaaagaaac tgcttagtaa agtagaaaaa atagttttaa agtaattttg      900
taaggcta at ggaagactta ctgtataaaa caaaaaggat ttaaccaca ttcaaattat      960
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<210> 184

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-468-388 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-468-388.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-468-388.mis2, potential complement

<220>

<221> primer_bind

<222> 113..132

<223> upstream amplification primer

<220>

<221> primer_bind

154

<222> 620..640
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-468-388 potential probe

<220>
 <221> misc_feature
 <222> 50,60,292,676
 <223> n=a, g, c or t

<400> 184
 ttaagttcta gagcttacag tacatggttt taaaattgta taagtgctgn ttaagagtan 60
 ttgattgcct tttcttggtt taatattaaa ccagggtggt ctgccaaaga ccgcatagtt 120
 tctctgatat gggtccaaag ggatattcctt tccactgaaa cactgtatgt ataccagtaa 180
 atgcttccta atggtagatg ataaatattt ttgttgcttg tagatagaat ttttccatct 240
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 ttaaaaaaaa tcgcttagctc agataaaagt tgtggcacat gaaatgaatt ttgccaatc 360
 accaccgaaa tccctgcttt atatctcttc agtggaacac taaaccaact tctttcccaa 420
 gtacactgat ttgatcttta caaattatat gaatgtatta aattatcaca tgtgccctga 480
 aactgtgtac atctattatg yatcattaga gagatggaaa aaaaaaaaag aaactgctta 540
 gtaaagtaga aaaaatagtt ttaaagtaat tttgtaaggc taatggaaga cttactgtat 600
 aaaacaaaaa ggattttaac cacattcaaa ttattgactg ttttggggct tttcaggaat 660
 cacttaaaaa gcaccnaagt tcacagccag gcacggtggc tcatgcctgt aatcccagca 720
 ctttgggagg ctgaggtggg cagatcactt gaggtcagga gtttgagaca agcctggtca 780
 tcatggcaaa atctcatctc tactaaaaat acaaaaatta gacctgggtg catgtgcctg 840
 taatcccagc tactgaggag tctgaggcat gagaaacgct tgaacctggg aggcggaggt 900
 tgcagtgagc caagatcgtg ccactgcatt ccagcctggg gaacagagca agtctttgtc 960
 tcaaaaaaaa aaaaaaaaaa agcactaagt tcatgacagg t 1001

<210> 185
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-468-491 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-468-491.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-468-491.mis2, potential complement

<220>
 <221> primer_bind
 <222> 10..29
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 517..537
 <223> downstream amplification primer, complement

<220>

155

<221> misc_binding
 <222> 489..513
 <223> 12-468-491 potential probe

<220>
 <221> misc_feature
 <222> 189,573,901,905
 <223> n=a, g, c or t

<400> 185
 ccaaagaccg catagtttct ctgatatggt tccaaaggga tattctttcc actgaaacac 60
 tgtatgtata ccagtaaatg cttcctaata gtagatgata aatatttttg ttgcttgtag 120
 atagaatttt tccatctagt gtaagcttag gattgttttc tttttcccag tgacatgtac 180
 agtttcacnt actccactta aaaaaaatcg ttagctcaga taaagtgtgt ggcacatgaa 240
 atgaattttg ccaattcacc accgaaatcc ctgctttata tctcttcagt ggaacactaa 300
 accaacttct tcccaagta cactgatttg atctttacaa attatatgaa tgtattaaat 360
 tatcacatgt gccctgaaac tgtgtacatc tattatgtat cattagagag atggaaaaaa 420
 aaaaaagaaa ctgcttagta aagtagaaaa aatagtttta aagtaatttt gtaaggctaa 480
 tggaagactt actgtataaa rcaaaaagga ttttaaccac attcaaatta ttgactgttt 540
 tggggccttt caggaatcac ttaaaaagca ccnaagttca cagccaggca cgggtggctca 600
 tgcctgtaat ccagcactt tgggaggctg aggtgggagc atcacttgag gtcaggagtt 660
 tgagacaagc ctggtcatca tggcaaaatc tcatctctac taaaaataca aaaattagac 720
 ctggtggcat gtgcctgtaa tcccagctac tgaggagtct gaggcattgag aaacgcttga 780
 acctgggagg cggaggttgc agtgagccaa gatcgtgcc ctgcattcca gcctggggaa 840
 cagagcaagt ctttgtctca aaaaaaaaaa aaaaaaagc actaagttca tgacaggtta 900
 nggttagccc ctcccacccc cccccaaggt catgtgactt caaatctggg ttgtagataa 960
 agtttagatt agatgtttca gtttctaaca tatatgttcc t 1001

<210> 186
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-469-132 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-469-132.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-469-132.mis2, potential complement

<220>
 <221> primer_bind
 <222> 370..387
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 812..832
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-469-132 potential probe

156

<220>

<221> misc_feature

<222> 16,226,688,735

<223> n=a, g, c or t

<400> 186

gcccgcgggc	cccgtncccc	gccgggcacc	cgtgtctggc	cgcccgcgct	gcctttgtct	60
tgccctacgc	ccccggccct	atcgcggtcc	gcgttctcca	ctgcgcccgg	gggtcctcga	120
gcgcctccc	gccccgggag	catcgtcctt	gctttcgcc	agtcgcgctc	cagggccatc	180
ctcctgacta	gactcctttc	ttgttcattc	attcttttgg	gttttncccc	ttcattccat	240
aaacacggat	tgggcgctgg	gagggcgatga	gcatgaaaaa	gtgacattag	gtgctgcgag	300
tcttcaacct	agtgtatctg	cagaccggca	actaccatga	tccaccttac	aggctcaaaa	360
ttcgcttttg	cggtcaatat	gaaagagatt	taagttttcc	tagtaggcct	gctgctttta	420
gaaatcaggt	cttcaggatg	tccacttctg	ccctacctca	tgcagggtgc	ttttccttaa	480
acctctccaa	cttctcatct	ycctccccct	ccaaaacaca	cacacttcac	agctataaat	540
tgaaaccagt	aaattacggc	tcagtttcct	acatggggga	ggaaccttcc	ctttcctgtt	600
taattctaag	tgggaatgca	tttagagttt	caacattagg	atttgcttgt	gtctttccat	660
ggcctaggtc	cagcaactaa	actttacnaa	accagtgttc	tgccatagaga	tgaaatgtct	720
ctagattctc	agtanggttg	aaccattgtt	tattggaatg	atctggaatg	cagcaatgtt	780
aaaactgttg	atttagtgct	atctgccaaa	actttttgtg	ccttccccctt	ctgtttttga	840
aaattacgtg	tgtatgcagt	acacattaaa	tgacttcttg	agaagtccat	ctctgttttt	900
gttttttagct	tttgccttag	atggcttgcc	acctgtgtaa	attgtttatc	ttttggccag	960
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<210> 187

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-469-245 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-469-245.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-469-245.mis2, potential complement

<220>

<221> primer_bind

<222> 257..274

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 699..719

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-469-245 potential probe

<220>

<221> misc_feature

<222> 113,575,622,936

<223> n=a, g, c or t

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<400> 187
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attccataaa cacggttg ggctgggag ggcgtgagca tgaaaaagt acattagggtg      180
ctgcgagctc tcaacctagt gtatctgcag accggcaact accatgatcc accttacagg      240
ctcaaaattc gcttttgccg tcaatatgaa agagatttaa gttttcctag taggcctgct      300
gcttttagaa atcaggtcct caggatgtcc acttctgccc tacctcatgc aggtgtcttt      360
tccttaaacc tctccaactt ctcattcttc ctcctctcca aaacacacac acttcatagc      420
tataaattga aaccagtaaa ttacggctca gtttctaca tgggggagga accttccctt      480
tcctgtttaa ttctaagtgg raatgcattt agagtttcaa cattaggatt tgcttggtgc      540
tttccatggc ctaggtccag caactaaact ttacnaaacc agtggtctgc ctagagatga      600
aatgtctcta gattctcagt anggttgaa cattgtttat tggaaatgatc tggaaatgcag      660
caatgttaaa actgttgatt tagtgtcatc tgccaaaact ttttgtgctt tccctttctg      720
tttttgaaaa ttacgtgtgt atgcagtaca cattaaatga cttcttgaga agtccatctc      780
tgtttttgtt tttagctttt gccttagatg gcttgccacc tgtgtaaatt gtttatcttt      840
tggccagtgt tgttatcaat cttggcctaa gtgtgacgt gctgttacac cagtgcagaa      900
tatctccttt caaaaagtta gttttttttt tttttnctaa gattgggatt ctacctcta      960
cagctgaaga aattgtgctg ttttaaatta ggaaagtatg a                               1001

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<210> 188

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-472-435 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-472-435.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-472-435.mis2, potential complement

<220>

<221> primer_bind

<222> 68..86

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 533..553

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-472-435 potential probe

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<400> 188
gatttgtaaa atgtgaagtt tgaatgtggc cattttccct ccccatact tcatgtcctc      60
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atttcactgt aagataggca caggtagatg tgctctgtat ggggtgcata aacatgcttt      180
ttgatcagaa atataactgc atggagcttt ttttagcatg taagtgcacac tttgaatttg      240
caggagctga cttttgtttg ttttagatg gctttgagtg ctgcattctc cttttaccga      300
ggctatgtgt cagacattga ttgtcgtggg ggagtgattt ctgcattctg agatgataga      360
actcgggagg agcaggagct ggaggtggga attgtttttc cttaatagcc cttttaagtc      420

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158

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aagcaggtaa aatggatctt ttgtaactac ttgcaatttc aggatgtctc cctgcaattt 480
ttatctgaaa tggggaaaaa ratttggtct aggtggggag ttaattttta tcgtatgttg 540
atgtctgtat ttgttttagc ttcattttaa attagtagtc cgatttttct atattttgga 600
agtgtctgat gctgttttta ccaaaaggct ttttggtgcc acatgagtgt tttgtatatg 660
gtgctttctg ctgtggaaag tataatttgt tgtcagagat tctttttcca tgtaaaagggt 720
taggcattga ctaataagggt tgagatggca cctcttggtt gcatgttgaa ctgtaaagta 780
acccttgcat ctctccaaca aggggtgtgc atcagaacca cccatggaaa tctttgaaaa 840
tagacaccca gaccctatcc tagacctact aaataagaat ctctaggatg ggacccgaac 900
aagggtgttt ttaaaggagc cctcataagt ggttttgata ttctcaacca gggctatact 960
actactgctc tggctcttcat gtaattgttc ataaattgtt g 1001

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<210> 189

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-473-311 : polymorphic base A or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-473-311.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-473-311.mis2, potential complement

<220>

<221> primer_bind

<222> 192..210

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 740..758

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-473-311 potential probe

<400> 189

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taatttttat cgtatgttga tgtctgtatt tgttttagct tcatttaaaa ttagtagtcc 60
gattttttcta tatttttgaa gtgctgatgg ctgtttttac caaaaggctt tttggtgcc 120
catgagtgtt ttgtatatgg tgctttctgc tgtggaaagt ataatttggt gtcagagatt 180
ctttttccat gtaaaagggt aggcatgac taataagggt gagatggcac ctcttggttg 240
catgttgaac tgtaaaagtaa cccttgcatc tctccaacaa ggggtgtgca tcagaaccac 300
ccttggaat ctttgaaaat agaccccag accctatcct agacctacta aataagaatc 360
tctaggatgg gaccgaaaca aggggtgttt taaaggagcc ctcataagtg gttttgatat 420
tctcaaccag ggctatacta ctactgctct ggtcttcatg taattgttca taaattgttg 480
aacatgcttt ctaagtagaa mtaaaactta aaggataatt attttgatag gtttatctta 540
cgttatagat ttatttatatt atttgctttt aaccttagta tttattttcc ctagcttaat 600
aagaatgaaa gtgatctgct tttaaaagat aaaagtatat ttaaatacata ccagaaaaaa 660
agggtattta aattgccttc agatttttaa aaacataatt ttccttaata atacttttta 720
gggtcacta actttttttc tgtatcttat gttgaggttt ttatataatt atcatatata 780
aaaatatatt ccactcattt tatatagcat attcatttat atatatattt aatcttttagc 840
cattgaagaa caataactat aggatcagta aatcccgata tgactcaata gacagctatt 900
tatctaagtg tggtgagaaa tataatgaca tcgacttgac gatagataaa gagatctacg 960

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159

aacagctgtt gcaggaaggt gggtttctac tccatcttct t 1001

<210> 190
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-473-483 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-473-483.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-473-483.mis2, potential complement

<220>
 <221> primer_bind
 <222> 20..38
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 568..586
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-473-483 potential probe

<400> 190
 cagagattct ttttccatgt aaaagggttag gcattgacta ataaggggtga gatggcacct 60
 cttgttttga tgttgaactg taaagtaacc cttgcatctc tccaacaagg ggtgtgcatc 120
 agaaccaccc atggaaatct ttgaaaatag acaccagac cctatcctag acctactaaa 180
 taagaatctc taggatggga cccgaacaag ggtgttttta aaggagccct cataagtggg 240
 tttgatattc tcaaccaggg ctatactact actgctctgg tcttcatgta attgttcata 300
 aattgttgaa catgctttct aagtagaaat aaactttaaa ggataattat tttgataggt 360
 ttatcttacg ttatagattt atttatttat ttgcttttaa ccttagtatt tattttccct 420
 agcttaataa gaatgaaagt gatctgcttt taaaagataa aagtatattt aaatcatacc 480
 agaaaaaaag ggtattttaaa ytgcttccag attttaaaaa acataatttt ccttaataat 540
 acttttttag gctcactaac tttttttctg tatcttatgt tgagggtttt atataattat 600
 catatataaa aatatattcc actcatttta tatagcatat tcattttatat atatttttaa 660
 tcttttagcca ttgaagaaca ataactatag gatcagtaaa tcccgatatg actcaataga 720
 cagctattta tctaagtgtg gtgagaaata taatgacatc gacttgacga tagataaaga 780
 gatctacgaa cagctgttgc aggaagggtgg gtttctactc catctttctg ggtttgaatg 840
 tacgccttta gttcttcaaa gctcttttac acttttttgc tgactcctgg tctgggttct 900
 attttttagt caaagtcttt aacttctctc atgaggctac ttgttcctaa agtttcagggt 960
 tccaaatact tgtgagattt tcttgatttt tagcaaaagg a 1001

<210> 191
 <211> 998
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele

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<222> 501
<223> 12-475-85 : polymorphic base T or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-475-85.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-475-85.mis2, potential complement

<220>
<221> primer_bind
<222> 566..585
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 108..126
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-475-85 potential probe

<220>
<221> misc_feature
<222> 555,666,713
<223> n=a, g, c or t

<400> 191
acaccattga atatgcttgg taaaattctc ggtctgcagg acaaattgcta acaagtttag      60
taatgtgact gcagccttcc cagctaattct gctggcaagc gagccctgtg aaaaggcaga      120
tgcaggacga gcccttttcta tgaaaatcag gctgacctca tttgatagtt atgcagcctg      180
tgtcgatctc ttcccagggc agcaggtagc aggccagaat cagaacccca agtcaggagc      240
tttaacttat ctgagatttt catccttttag catgaatttc aaatatggca gggaaggaga      300
ttgaattcac aaaaacctaa atcttccaaa tcccacaggt tacagttact ctggttggtg      360
gatccactat aacacccagg tacgattcct gaatgggaac ctgatgctgc ctttgtgaga      420
tgtggttatg acacagtgtc tgcactcaga ttcgtatgat ggtggaatgg cattaactt      480
ggaggtcttg aagccctgtc ktcctgtccc tggaggcata ggtgaccccc agtgagcact      540
agcagtcact ttggnactta gaattcctgt atttagcatt gactctcact tagtctcttt      600
agaaaaactct cttttttctc tctgttaggt tgattagtct aacttcagtt cctaggaact      660
aaaatnccctg aattttctcat aggcagtctg aatttagggc agcctaattt atnaacatgc      720
cttagaagga aatcatgtgt gcattcttgc ttgctcagcc caagaagtgt atcaggccct      780
gagcggggca ccgcccactg ggggatgtgt tctctgtctt gtcccatgc taaagcccta      840
aactctctctg cacctagagg gaaccgctgc agaaaattctc catgattctc acccactaca      900
gtgccccagc tctggctact gcagggcagt tgatccaaag cagcttctgt ctggggatca      960
ggatactgtt tcttgtcaac cacgtggtga ctagaact      998

<210> 192
<211> 985
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 485
<223> 12-475-446 : polymorphic base G or A

<220>

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<221> misc_binding
 <222> 465..484
 <223> 12-475-446.mis1, potential

<220>
 <221> misc_binding
 <222> 486..505
 <223> 12-475-446.mis2, potential complement

<220>
 <221> primer_bind
 <222> 911..930
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 453..471
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 473..497
 <223> 12-475-446 potential probe

<220>
 <221> misc_feature
 <222> 47,196,202..203,900
 <223> n=a, g, c or t

<400> 192
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 gcctgcactc ttagctgctc cccacacctat taccgcccac ataggcagga ggaaaagagc 120
 tctgtgacag ttttaaatagg ctccaaacag agatgagatt gaggggtggcg aggaagagaa 180
 gaaagaatag agaaanggga tnnnggtggta atgcaggaag taggcttttt gttttttaat 240
 gaaaatatga atatgtcatc agccacagat ccacgcttaa gcattttttg gtacccata 300
 gcaggttaatt ctcttctagt gaaatgccag cactctttca aaacgacacc attgaatatg 360
 cttggtaaaa ttctcgtctc gcaggacaaa tgctaacaag tttagtaatg tgactgcagc 420
 cttcccagct aatctgctgg caagcgagcc ctgtgaaaag gcagatgcag gacgagccct 480
 ttctrtgaaa atcaggctga cctcatttga tagttatgca gcctgtgtcg atctcttccc 540
 agggcagcag gtagcaggcc agaatcagaa cccaagtca ggagcttta cttatctgag 600
 attttcatcc ttagcatga atttcaaata tggcagggaa ggagattgaa ttcacaaaaa 660
 cctaaatctt ccaaattccca caggttacag ttactctgtt ggtgggatcc actataacac 720
 ccaggtacga ttctgaatg ggaacctgat gctgcctttg tgagatgtgg ttatgacaca 780
 gtgtctgcac tcagattcgt atgatggtgg aatggcatta aacttggagg tcttgaagcc 840
 ctgtcgtcct gtccctggag gcataaggta ccccagtgga gcactagcag tcactttggn 900
 acttagaatt cctgtattta gcattgactc tcacttagtc tctttagaaa actctctttt 960
 ttctctctgt taggttgatt agtct 985

<210> 193
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-477-100 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-477-100.mis1, potential

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<220>
<221> misc_binding
<222> 502..521
<223> 12-477-100.mis2, potential complement

<220>
<221> primer_bind
<222> 580..600
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 62..82
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-100 potential probe

<220>
<221> misc_feature
<222> 368
<223> n=a, g, c or t

<400> 193
tcagttactg tgacctacca tatcatgggt gaattcctcc atggttaagac cctactgtct 60
agaagtatgg tgtagcaga tgtactcatt gattgggtact gtctgtagtt tcattttgaa 120
gcataaacct gagtaacatt cagtaagact ctgtatgttc agaaaagatg tcacaatatt 180
aattgagcct ctaacatcac tatttatgtt tctgaacatt ttacatact gtcaaggcat 240
ctgaatatat tcttaaagtt agaaaactgt atatgaagca ttactgatat tgctgggtatt 300
actggaaaga ccatatccta acgagcttgc taattagtac tctgtttcta catttcatga 360
tataatcnag gtgtttttaa aaaaacattt taacagcttt attgagttat aattaacata 420
aagttaactg cacatattta aaatgtacaa tttggttaagt ttgatatat gtatacatca 480
taaaatcacc tctgataata rgtatattca ttatctccaa aaatgtcatc atgccccttt 540
ggtaatttct tcctctggcc atcccatgca gctgatttgc tttctgtagt ttgcattttc 600
tagattttca tatttaagaa atcatagttt gcatttgata tctagtttca tatacctagg 660
aaatcatcca gcatacctc ttttgggtctg ccttcttaga gtctacataa atattttgag 720
atccatccat gttgttacat gtgtcagtag ttcatcctt ttcgtcgtg agtaatatatt 780
cattccatgg ttataccagt ttgtttatac attcaccatt tgtgttgcat tcagtttttc 840
actattataa aaaaattata tgaacattaa catacaagtt tgtatgtatg gactaatgct 900
tttcttcac ttattaccct aggagtagcg tgttggttaac tttttaagga aactataata 960
ccaaactttt ccagggtggt tataccattt tgcattctca c 1001

<210> 194
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-331 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-331.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-331.mis2, potential complement

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<220>
<221> primer_bind
<222> 812..832
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 294..314
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-331 potential probe

<220>
<221> misc_feature
<222> 600
<223> n=a, g, c or t

<400> 194
gtgtaacaaa ggaggaaagg tgagaaatac cattggatag tatgtgaagg ttattgtgca      60
gttttagtgtt gtaaatgcag tgaatagggt tagccagctt gtagaagtct ttgtctagtt      120
ctcaaaaagt agaggttatg ttgtacttta aaagcatgag aaaagtagaa tcgaaaaaaaaa      180
gtgtattagt cttctatacc tatctcctac agaaaaaatc ttttaagact tatcagttac      240
tgtgacctac catatcatgg ttgaattcct ccatgttaag accctactgt ctagaagtat      300
gggtgttagca gatgtactca ttgattggta ctgctgtag ttccattttg aagcataaac      360
ctgagtaaca ttcagtaaga ctctgtatgt tcagaaaaga tgtcacaata ttaattgagc      420
ctctaaccatc actatttatg tttctgaaca tttttacata ctgtcaaggc atctgaatat      480
attcttaaag ttagaaaact rtatatgaag cattactgat attgctggta ttactggaaa      540
gaccatatcc taacgagctt gctaattagt actctgtttc tacatttcat gatataatcn      600
agggtgtttt aaaaaaacat tttaacagct ttattgagtt ataattaaca taaagttaac      660
tgacacatatt taaaatgtac aatttggtaa gttttgatat atgtatacat cataaaatca      720
cctctgataa taagtatatc cattatctcc aaaaatgtca tcatgccctt ttggtaattt      780
cttcctctgg ccatcccatg cagctgattt gctttctgta gtttgcattt tctagatttt      840
catatttaag aaatcatagt ttgcatttga tatctagttt catataccta ggaaatcatc      900
cagcatatcc tcttttggtc tgccttctta gagtctacat aaatattttg agatccatcc      960
atgttggttac atgtgtcagt agttcattcc ttttcgtcgc t                               1001

<210> 195
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-332 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-332.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-332.mis2, potential complement

<220>
<221> primer_bind
<222> 813..833

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<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 295..315
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-332 potential probe

<220>
<221> misc_feature
<222> 601
<223> n=a, g, c or t

<400> 195
agtgtaaaca aggaggaaag gtgagaaata ccattggata gtatgtgaag gttattgtgc      60
agtttagtgt tgtaaatgca gtgaataggt ttagccagct tgtagaagtc tttgtctagt      120
tctcaaaaag tagaggttat gttgtacttt aaaagcatga gaaaagtaga atcgaaaaaa      180
agtgtattag tcttctatac ctatctccta cagaaaaaat cttttaagac ttatcagtta      240
ctgtgacctt ccatatcatg gttgaattcc tccatgttaa gacctactg tctagaagta      300
tggtgttagc agatgtactc attgattggt actgtctgta gtttcatttt gaagcataaa      360
cctgagtaac attcagtaag actctgtatg ttcagaaaag atgtcacaaat attaattgag      420
cctctaacat cactatttat gtttctgaac atttttacat actgtcaagg catctgaata      480
tattcttaaa gttagaaaac ygtatatgaa gcattactga tattgctggt attactggaa      540
agaccatata ctaacgagct tgctaattag tactctgttt ctacatttca tgatataatc      600
naggtgtttt taaaaaaaca ttttaacagc tttattgagt tataattaac ataaagttaa      660
ctgcacatat ttaaaatgta caatttggtt agttttgata tatgtataca tcataaaatc      720
acctctgata ataagtatat tcattatctc caaaaatgtc atcatgcccc tttggtaatt      780
tcttctctcg gccatcccat gcagctgatt tgctttctgt agtttgcatt ttctagattt      840
tcatatttaa gaaatcatag tttgcatttg atatctagtt tcatatacct aggaaatcat      900
ccagcatata ctcttttggg ctgccttctt agagtctaca taaatatttt gagatccatc      960
catgttggtt catgtgtcag tagttcattc cttttcgtcg c                                1001

<210> 196
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-44 : polymorphic base C or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-44.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-44.mis2, potential complement

<220>
<221> primer_bind
<222> 524..544
<223> upstream amplification primer, complement

<220>
<221> primer_bind

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<222> 6..26
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-477-44 potential probe

<220>
 <221> misc_feature
 <222> 312
 <223> n=a, g, c or t

<400> 196
 gtctagaagt atgggtgtag cagatgtact cattgattgg tactgtctgt agtttcattt 60
 tgaagcataa acctgagtaa cattcagtaa gactctgtat gttcagaaaa gatgtcacia 120
 tattaattga gcctctaaca tcactattta tgtttctgaa cttttttaca tactgtcaaag 180
 gcatctgaat atattcttaa agttagaaaa ctgtatatga agcattactg atattgctgg 240
 tattactgga aagaccatat cctaacgagc ttgctaatta gtactctgtt tctacatttc 300
 atgatataat cnaggtggtt ttaaaaaaac attttaacag ctttattgag ttataattaa 360
 cataaagtta actgcacata tttaaaatgt acaatttggt aagttttgat atatgtatac 420
 atcataaaat cacctctgat aataagtata ttcattatct ccaaaaatgt catcatgccc 480
 ctttggtaat ttcttctctc sgccatccca tgcagctgat ttgctttctg tagtttgcat 540
 tttctagatt ttcataattta agaaatcata gtttgcatct gatattctagt ttcataatac 600
 taggaaatca tccagcatat cctcttttgg tctgccttct tagagtctac ataaatattt 660
 tgagatccat ccatgttggt acatgtgtca gtagttcatt ctttttcgtc gctgagtaat 720
 atttcattcc atggttatac cagtttggtt atacattcac catttggtgt gcattcagtt 780
 tttcactatt ataaaaaaat tatatgaaca ttaacataca agtttgatg tatggactaa 840
 tgcttttctt catcttatta ccctaggagt agcgtgttgt taacttttta aggaaactat 900
 aataccaaac ttttccaggg tgggtatacc attttgcatt ctcactagca gagtatgcca 960
 gttcagttca tccacattct tgtaaacacc ggtatgggca g 1001

<210> 197
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-478-223 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-478-223.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-478-223.mis2, potential complement

<220>
 <221> primer_bind
 <222> 704..723
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 234..254
 <223> downstream amplification primer

<220>

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<221> misc_binding
<222> 489..513
<223> 12-478-223 potential probe

<220>
<221> misc_feature
<222> 35,194,272,317,458
<223> n=a, g, c or t

<400> 197
tcttgctctg tcacccaggc tagagtgcag tgacnaccat cacagtgtgc tgcagccgca      60
gcctcccagg ctcaagctgt ttagatcgta tttctaagtt gcgcttcaaa aacgcattga      120
cacaggctca ggctaggtct cttaaaataa gatatagagc acaaattaat tatttcttaa      180
taggcattac aaangattca ggttccttct ataggtcata gcgtattctg taacacaaaa      240
agcaaagttg tcgcatctct ctatcctttt tnagctgtca ctggacattg attcaacagc      300
atttattgtc cgtaanccc ctaccacccc ccagaagttc ccttggtgcc ttgacagtg      360
tgtgcatgcy tgtatgctag agagagaggg ggagagcact tcagttgatt ctgggtttcc      420
ttcagacacc acctttgaga aactgcctta aagagtgntg tggtcattaa ttagatgaag      480
gggagaaaagg aaggcattat rgtcaaaaaga acagtgtaac aaaggaggaa aggtgagaaa      540
taccattgga tagtatgtga aggttattgt gcagtttagt gttgtaaatt cagtgaatag      600
gttttagccag cttgtagaag tctttgtcta gttctcaaaa agtagagggt atgttgtact      660
ttaaaagcat gagaaaagta gaatcgaaaa aaagtgtatt agtcttctat acctatctcc      720
tacagaaaaa atcttttaag acttatcagt tactgtgacc taccatatca tggttgaatt      780
cctccatggt aagaccctac tgtctagaag tatggtgtta gcagatgtac tcattgattg      840
gtactgtctg tagtttcatt ttgaagcata aacctgagta acattcagta agactctgta      900
tgttcagaaa agatgtcaca atattaattg agcctctaac atcactatct atgtttctga      960
acatttttac atactgtcaa ggcattctgaa tatattctta a                                1001

<210> 198
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-478-320 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-478-320.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-478-320.mis2, potential complement

<220>
<221> primer_bind
<222> 801..820
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 331..351
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-478-320 potential probe

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<220>
<221> misc_feature
<222> 132,291,369,414,555
<223> n=a, g, c or t

<400> 198
cattaacagt aattttttat tgtatttctt ttcttttttt taatattatg tatttatgta      60
tttattttatt tattttattta ttttgagaca ggggtctttct tgctctgtca cccaggctag      120
agtgcagtga cnaccatcac agtgtgctgc agccgcagcc tcccaggctc aagctgttta      180
gatcgtattt ctaagttgcg cttcaaaaac gcattgacac aggctcaggc taggcttctt      240
aaaataagat atagagcaca aattaattat ttcttaatag gcattacaaa ngattcaggt      300
tccttctata ggtcatagcg tattctgtaa cacaaaaagc aaagttgtcg catctctcta      360
tcttttttna gctgtcactg gacattgatt caacagcatt tattgtccgt taancccccta      420
cccacccccca gaagttccct tgtgcccttt gcacgtgtgt gcatgcgtgt atgctagaga      480
gagagggggga gagcacttca rttgattctg gttttccttc agacaccacc tttgagaaac      540
tgccttaaag agtngtgtgg tcattaatta gatgaagggg agaaaggaag gcattatggt      600
caaaagaaca gtgtaacaaa ggaggaaagg tgagaaatac cattggatag tatgtgaagg      660
ttattgtgca gtttagtggt gtaaatagcag tgaatagggt tagccagctt gtagaagtct      720
ttgtctagtt ctcaaaaagt agagggttatg ttgtacttta aaagcatgag aaaagtagaa      780
tcgaaaaaaaa gtgtattagt cttctatacc tatctcctac agaaaaaatc ttttaagact      840
tatcagttac tgtgacctac catatcatgg ttgaattcct ccatgttaag accctactgt      900
ctagaagtat ggtgtagtca gatgtactca ttgattggta ctgtctgtag tttcattttg      960
aagcataaac ctgagtaaca ttcagtaaga ctctgtatgt t                                1001

<210> 199
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-479-289 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-479-289.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-479-289.mis2, potential complement

<220>
<221> primer_bind
<222> 213..230
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 678..698
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-479-289 potential probe

<220>
<221> misc_feature
<222> 444,957..958
<223> n=a, g, c or t
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<400> 199
ctctcctggt actccccctt ctctcactcc actccagcca tactagcctc cttactgttc      60
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ggaatggctg aatttcctta cctccttcaa atccttgctt aatccctcct tctcaaagag      180
acctaaacac cctggccacc ttctttaata taatattctg accatgcacc taacctcaca      240
cctgcataccc ctgctctaata ctgtcttttt cataatgttt atcaacttct gactttctat      300
atagttatatt attgtgcatg ttgtgtgect ccccttgcta aaatgtaagc tccacaaggg      360
caggcatgct tgtttgttat agtcagtgat gtatcctaag cacctagaac agtacttgcc      420
tgatgggtgag tgctcaatga acantttgca gaaaaatgaa tgaatgaatg ccaggcattc      480
ataagcccac aaaaaaaatc katgtgtcat tctacacctt cactgtagcc taatgcttca      540
tgctccaaaa agaaagaaga ggcattcattt tctctgtttc ctgtgctcca cctctcgcac      600
attccccact ctctagctg ctgtctttcc cctgactttt ttgtctagta acaagaactc      660
cctgcctggg gaaagtcggc attttcttct caatttactt ctaaataatta gtgcttttgt      720
ttaccctgtg aagcagatgg taacagttaa tgtaataacc agactgtctc ctctctcttg      780
tttgacacag tagatgtcat gagccatatt ttcccttggg tatatttgtt aaatagaaga      840
caggagatct gctatatggt caacattagg tctggtcact gcttttatat tgtaaacact      900
gtgtttcctt tcatatattt acatcatttg gaaacatttg ccctagtcc agcaatnnag      960
gctaagagat aaggatccaa atgaaagaaa gaggataaaa a                               1001

<210> 200
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-482-237 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-482-237.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-482-237.mis2, potential complement

<220>
<221> primer_bind
<222> 720..737
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 223..243
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-482-237 potential probe

<220>
<221> misc_feature
<222> 552,561,757,831,845
<223> n=a, g, c or t

<400> 200
ttctcttggg actcatatca ctaatctagg caagttaaga atgttttctc tgtttgggct      60
gagacaatat tgagaaagtt actccaccta atcctatagg aaattaattg atttttgtgc      120

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169

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agtattaaaa ttgagattaa tgtgttataa ataaaaagca gcctgctctg tgctacagaa 180
aactagatca gggagaggcc acatttattt taatttctaa aagtgtaaac ctttcatagt 240
atcatgtgaa attcttttagt atgaatagac atttcaaagt aggaggaaaa aaacctattt 300
tctcaaaata tatgaaatgt tagcagaatt tgatacagct ttagacaaaa ctgctaaaaac 360
attttctttt tggaacatag aacaatttaa ttattacagt atccacagtc atcaaatata 420
tatatattta aatcatcaaa tatatatggt taaaatatag ttgtgtgtgt gatgttatgt 480
atgtataatg tcatgtacac raaagcacat acagtttcta ctttgtactt actgggtccc 540
taaaagtgtc tnggagatta nccatgtcaa acagtgggtt tcctatttgt gatgtcatca 600
ttagacatat ctaacatggg agtccatctt taaaaatctg agccatatgt aattttatta 660
catctgtatt agaatctcat attcagtttt ctacttttta aaacacagct cctcttttag 720
tcttgtcagt caggttgtcc tatgttactg tgggtgnttt aaaaattaag tagcatcact 780
atggctaaca cctctttggg tgctccaagt ttgggaagtg aatgccatcc naacttgatg 840
gttgnagatt tcttttaaaa aaaaatttgt cattaccatt ttgctgtgag aggaaacagt 900
cttctgggca gaaggcattg agtccctaac tttaaaacag tttataacct agaggggtgac 960
tacttggcat gatctctgtg ggggtggatgc agtgatctgc g 1001

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<210> 201

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-482-285 : polymorphic base T or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-482-285.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-482-285.mis2, potential complement

<220>

<221> primer_bind

<222> 768..785

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 271..291

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-482-285 potential probe

<220>

<221> misc_feature

<222> 600,609,805,879,893

<223> n=a, g, c or t

<400> 201

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cccgcaactc tcaactgtctt tctctatttt attaaagtct tgaaattttt ctcttggggac 60
tcatatcact aatctaggca agttaagaat gttttctctg tttgggctga gacaatattg 120
agaaagttac tccacctaat cctataggaa attaatgtat ttttgtgcag tattaataatt 180
gagattaatg tgttataaat aaaaagcagc ctgctctgtg ctacagaaaa ctagatcagg 240
gagaggccac atttatttta atttctaaaa gtgtaaacct ttcatagtat catgtgaaat 300
tcttttagtat gaatagacat ttcaaagtag gaggaaaaaa acctattttc tcaaaatata 360

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170

tgaaatgtta	gcagaatttg	atacagcttt	agacaaaact	gctaaaacat	tttctttttg	420
gaacatagaa	caattttaatt	attacagtat	ccacagtcac	caaatatata	tatatTTTaaa	480
tcatcaaata	tatatgttta	waatatagtt	gtgtgtgtga	tgttatgtat	gtataatgtc	540
atgtacacaa	aagcacatac	agtttctact	ttgtacttac	tggtccccta	aaagtgcctn	600
ggagattanc	catgtcaaac	agtggttttc	ctattttgtga	tgatcatcatt	agacatatct	660
aacatgggag	tccatcttta	aaaatctgag	ccatatgtaa	ttttattaca	tctgtattag	720
aatctcatat	tcagttttct	acttttttaa	acacagctcc	tcttttagtc	ttgtcagtca	780
ggttgctcta	tgttactgtg	ggtgntttaa	aaattaaagta	gcatcactat	ggctaacacc	840
tctttgggtg	ctccaagttt	gggaagtga	tgccatccna	acttgatggg	tgtagatttc	900
ttttaaaaaa	aaatttgta	ttaccatttt	gctgtgagag	gaaacagtct	tctgggcaga	960
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<210> 202

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-482-482 : polymorphic base T or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-482-482.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-482-482.mis2, potential complement

<220>

<221> primer_bind

<222> 965..982

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 468..488

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-482-482 potential probe

<220>

<221> misc_feature

<222> 67,797,806

<223> n=a, g, c or t

<400> 202

tctgcagtaa	gagaaatggt	ctactctata	ctatccatta	gggagtagga	aactgatttt	60
tttatnttta	tgtaagtaa	ttttaaatcc	acacagccac	atgtgcttag	tgactagcat	120
aatggacaac	acaatttttt	gtgttccttt	ggtgacaggt	gacattttct	ccctgtatga	180
gagtcctccc	agttttacccc	gcaactctca	ctgtctttct	ctattttatt	aaagtcttga	240
aattttttctc	ttgggactca	tatcactaat	ctaggcaagt	taagaatggt	ttctctgttt	300
gggctgagac	aatatttgaga	aagttactcc	acctaattcct	ataggaaatt	aattgatttt	360
tggtcgagat	taaaattgag	attaatgtgt	tataaataaa	aagcagcctg	ctctgtgcta	420
cagaaaaacta	gatcagggag	aggccacatt	tatttttaatt	tctaaaagtg	taaacccttc	480
atagtatcat	gtgaaattct	wtagtatgaa	tagacatttc	aaagtaggag	gaaaaaaacc	540
tattttctca	aaatatatga	aatggttagca	gaatttgata	cagctttaga	caaaactgct	600

171

```

aaaacatttt ctttttggaa catagaacaa tttaattatt acagtatcca cagtcatcaa 660
atatatatat atttaaatca tcaaatatat atgtttaaaa tatagttggtg tgtgtgatgt 720
tatgtatgta taatgtcatg tacacaaaag cacatacagt ttctactttg tacttactgg 780
tcccctaaaa gtgcttngga gattanccat gtcaaacagt ggttttccta tttgtgatgt 840
catcattaga catatctaac atgggagtc atctttaaaa atctgagcca tatgtaattt 900
tattacatct gtattagaat ctcatattca gttttctact ttttaaaaca cagtcctctt 960
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<210> 203

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-483-322 : polymorphic base T or A

<220>

<221> misc_binding

<222> 479..498

<223> 12-483-322.mis1, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-483-322.mis2, potential complement

<220>

<221> primer_bind

<222> 802..820

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 311..331

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-483-322 potential probe

<220>

<221> misc_feature

<222> 253,301..302,345,368,400,565,570,968,973,978

<223> n=a, g, c or t

<400> 203

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agacactttg aaatgtcttt gcttaaaaac aattggttta agtgcaactgc aaaagcatta 60
catgggtctag cctcataata atttccctt tttggagacc caggattcag tgtgggctct 120
gccagattt cagagatcta ggcaaaaaag aaataatccc tatatgaata aaattgggtct 180
cctcatacaa tcccatgata gagttctata attttatgtt tgatttggca tccatcttta 240
tttccctct agncaccact agactttttc tgtctgtacc ttgagatata aattttgcta 300
nntgattttt catctaagag ttgtttcctt caatatgcag gtttnagggc tatttagctg 360
acaactgncc aggttaatga aacaggttat catgagtttn gcaagtctaa gacaggggaa 420
aacaaaagga ggtcttagga atctataaga tgtacttcta tcagtatgcc taatacatct 480
atgtatctat gtgttatgwa cacgtttcac tactaaaaac atataaaaga gctgtaatta 540
attggcttgc agaaaaataa aggtngcttn aaatccaatg ctttatcaga gaaaagaaaa 600
gactagccaa atgctttttc aagtttatgt gatttaagta aaatctttaa taaataagct 660
agctttaaaa ttactggcaa agtaatatta gaaatgtctt aagaattgcc agcatacatt 720
ttcgtttgca tttatggatc aagtcatttc atatttatcc ctgccaaata ctgtaagggt 780
tcaaagtttg gcatagggtt acaaaactat aaaccagcc taaaacagaa tgatttttgt 840

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172

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ttgtgttaat ttttaataaa taagacattg atattgggtt aatgaaaata gctacatctt   900
gaattattta gtaaaattac tgtaacttct aatcttgtgg ccttagggag tctagtccac   960
aggcaatnaa ggnnttcntt ttgggaaatg actgttatca t                          1001

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<210> 204

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-484-46 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-484-46.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-484-46.mis2, potential complement

<220>

<221> primer_bind

<222> 528..546

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 86..106

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-484-46 potential probe

<400> 204

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tgtgagcaag aagtgtgggg agtggttgta aaggggcaca gtatttacac aacatctgtt   60
ttgtaaacac aaagccctct gaaaagggga tactagaaat gaggtgtctt tggcaggtgc   120
agtgatggca agactgcaca caattaattc ttgaaaacaa atcccatcta tttagttctt   180
caatttggtg tagattaggg tgcctgggtt tcacactgcc cgaggtcaaa cccaacccag   240
tggaaggagg agcttccaag tccctcttct ttccagatga agcaataaac aagcaccctc   300
gcttcagggtg agtatggctt tgtgttgaaa tgcagatgcc cttcactaga cccctgactt   360
ctgagagtat agtatttctg tctagaaatc ctttttgagc attaactgag ttttggtctt   420
cttcctaagt aaccagagaa gatagcagat gtgcacctgt tcacatcttc agtaccacca   480
ggcttcttgg ttgttgatgc rtgcaccagg cttgatttgt caattctcca agtcgtcaca   540
aagttattcg ctgagccact gcgaataact cttttaatag ggagattatt ttcagtccta   600
ggtctgtaaa tgcctactgg gatttttttt tctcttagtt atttctcctt ttttgccttc   660
tctaaccatc agtatctgtg atttgcccat cttactctat ataacttata aaatagggtgc   720
agtacctgat atataataa ggcaactctc tccattaact tcaagttctg ttggtttggt   780
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acttctcagc gttcattcct ttaacaggcc ctcacgtttg ctatgtgcag agccttttgg   960
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<210> 205

<211> 1001

<212> DNA

<213> Homo Sapiens

173

<220>
 <221> allele
 <222> 501
 <223> 12-490-312 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-490-312.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-490-312.mis2, potential complement

<220>
 <221> primer_bind
 <222> 189..209
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 621..641
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-490-312 potential probe

<220>
 <221> misc_feature
 <222> 437,543,597,604,664,732,872,932
 <223> n=a, g, c or t

<400> 205
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 cgggggctgt atcacaaaca ctgcgcggcg tgcgcgcgcc gcggcccaca ccgcttcctc 120
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 tacagccctg atggagnctg tctgctgaaa actcacttcc agatgtcgaa acctggccct 480
 ggggtgcagtc tacagaatga watcgagcag tagtggacct atgcaggcaa agcattgtca 540
 ganggggagt aactcttgtt aaatatgact tcagttgata cgtgatggga tttttgnttt 600
 ttttctttgt aacagaaaag gctaaagaca ctgagagatc aagggtttaa ttgggcataa 660
 ctgnccctgt ggtgcagcag cgccggcgcc ctttttgagg ttgtccaaag ctctgggacc 720
 cccgctgggg gnagctggtt cagaattcgg gggggtagga tagggtagg gaggtccctt 780
 atgtgagtgt gagccgggat ctaggacaga gtaactccaa ttacagtgtt aaactcttac 840
 taggttcagt gtcgcgtagg gctttggcta gnactagaat ttagtctatt attgaaccgc 900
 ccaggtccat gattcctaac aggtgcatgg gnaaaagtgt atggtgtgca gcagggtgat 960
 gggaaaactg ctttgcaaag tgtaaatcaa ggtctacatc a 1001

<210> 206
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-491-295 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-491-295.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-491-295.mis2, potential complement

<220>
 <221> primer_bind
 <222> 777..795
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 266..286
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-491-295 potential probe

<220>
 <221> misc_feature
 <222> 128,300,307,312,357
 <223> n=a, g, c or t

<400> 206
 tgcaggcaga aatgaaaaaa gaaatcctga aactttaaga atcggggata atatcagata 60
 agtatgttgc ttaaatttga ctaattttaa ccatttttat aaattagtca ctcagcatga 120
 agacatcnaa aaattcttcc taaattctaa acactatgta catttgaatg ctgagttagt 180
 cccaggattc atccccaaaa tatcactgac cagtatgatt taatattagt atttgccctc 240
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 catcttntgc tncctgtttg ttactctgag atgatectct gcctgaaaat atctaangca 360
 gatacttttc tcagctttgc aatgcaaatg atattatga gttccctagg aatgttttgt 420
 gtgcttatca aatttcagct aaacacattt atttatatga taaatatgat aacccaaaagg 480
 ttccatgtat tatcttttca rtattcatgt tatactgtac aagcactgta ttatacaaat 540
 actgtataat atagtattgt aagggtacaaa aatacaataa actaaccata cttcaactct 600
 gcgggggttgc tgtgggagag ctctgcaggg ttgctgtgca agccccaggt aagtgattaa 660
 gtcagacaat aactacatca gtgcttctca aattttcatg tgccctgcaga ttatcggttg 720
 ggggcgggga gtttttaata tgcattctga cttagtaggc ctggtgtcag gccagagatt 780
 ctgcgtctct cccaagcttt caggtgatac agatgctgac tgggtggacca cattttgagt 840
 agcaagatgc taaagcttct tacaactcta aactttcaaa atcctttata aaaggatagc 900
 tataatgtat atgtgaaatg gactatggaa acataaaaata ataaaagctt actattgtca 960
 gtcacttggg aagtgtcact tttggaagtt agtcacttcc c 1001

<210> 207
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-493-417 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 481..500

175

<223> 12-493-417.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-493-417.mis2, potential complement

<220>

<221> primer_bind

<222> 90..109

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 514..534

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-493-417 potential probe

<220>

<221> misc_feature

<222> 590,704,1000

<223> n=a, g, c or t

<400> 207

aatgttaatt	tttctcacct	ttattttcaa	taggtggaat	acatgttggt	atcttttgat	60
catgaaaata	aaaaagtcg	gttggtcctg	tctggggaga	aagttcttga	aactctgcaa	120
gagaaggggg	aaaggacaaa	cccaaagtaa	gctctcatgt	gctgatttag	tgtttctgaa	180
actgctaaaa	cttctagaat	atagagtttt	ttctcaatta	ttggaggcag	gatagcctaa	240
cagtttaagag	tacaggctct	ggtttcaggt	tgccatagtt	tcaaatacatg	gttcctttac	300
tcaatagctg	aataaccttg	ggcaagttag	ttaacttttc	tgtgcctcag	ttctctcatc	360
tgtaaagtaa	agatcatagc	aataacctacc	taagggtgtg	gaattaaata	cattaatata	420
tgaagcactt	tgtacagtaa	actaaatata	aagcctgttt	tttattaaaa	catttttggg	480
aaaaaatgta	ttgcagaagc	stataactgg	gatcacaaac	catgatgcaa	gatataagtt	540
gcagatgggc	tttgtttggc	tttgtttggc	tggcatgatt	tttttttgan	gacggagtct	600
cactctgtcg	tccgggctgg	agtgcagtgg	cacgatctca	gctcactgca	agctccacct	660
cctggcttca	cgccattctc	ctgcctcacc	ctcccgagta	gctngggact	acaggcgccc	720
gccaccacgc	ctggctaatt	ttttgtattt	ttagtagaga	cggggggttc	accgtgttag	780
ccaggatggt	ctccatttcc	tgacctcatg	atctgcccgc	ctcagcctcc	caaagtgtcg	840
ggattacaag	catgagccac	cgcaccgggc	ctggtgtgtt	tttaagggtat	tcctacattt	900
aagtagacag	agacggggag	gggaggggaa	tatatactcc	tctgctcatt	ttccactcat	960
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<210> 208

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-494-373 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-494-373.mis1, potential

<220>

<221> misc_binding

176

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<222> 502..521
<223> 12-494-373.mis2, potential complement

<220>
<221> primer_bind
<222> 127..144
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 571..591
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-494-373 potential probe

<220>
<221> misc_feature
<222> 2,4,8,15,19,33,36,296,311,640,899
<223> n=a, g, c or t

<400> 208
antncagncc gggcnatana gttagatcct gtntcnaaaa aaaaaaaaaa agaaaagaaa      60
agaaaaaCaAaa agtcttgggt tctagtccca ctttactgct gattaacatt ttaacttgaa      120
gagtgattca atcactcggt tgccccactt gaaaaaaaaa aaaagctgga gtacatatct      180
agaatcctta ccacacgaac attctatatt tttggttctt tgactctaaa atggtcagct      240
taaaagagtg ttttccatcc ctcttttggc tgttagagcc atccctgggtg actttnaccc      300
ctttcccctg naaccctttca tatgtttatt gagcatccac tccagtgtg cactggtggt      360
tgttttcacg gggttactgg taccctccac cctcacccct ctttctccct gcagaaagct      420
tttctaatac tttcagccgt ggtcaatttc aggtgatagc aatggtaatc atttattgag      480
tacttaccaa atgctagaga ytgacacagg ctatgtcatt tttcaatac caagccctgt      540
gaaatgggta ctatcagacc atttttacac ctgtggctta gaagacttaa atgtctagtg      600
taagggcggt tgtagtggta ggcagaggca ggtctcaaan ccctcgcta cctaactcag      660
acacacttgg caatactata tatctcttta agcctttcag aggatatgtt ttaggagggtg      720
gattgttcca ttttatatat atatgaacat gatagacaga cagatagata gataaataga      780
tagagataat tttaaacgtg ctcactttca tttatgaaaa tttacatttg ataactaaaa      840
gagccttgca attccagcat ctccctcatg gtggcagtag aagactaagt catgtacanc      900
gcagcctcca gcaccaacaa ctaaccaga agaaacctcc ttaataaatc agcttttggt      960
caagattggt gttacgtaaa atgcaaaatt aggaccctcg g                                1001

<210> 209
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-495-166 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-495-166.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-495-166.mis2, potential complement

<220>

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177

<221> primer_bind
 <222> 336..355
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 784..802
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-495-166 potential probe

<220>
 <221> misc_feature
 <222> 146,405,641,702,965
 <223> n=a, g, c or t

<400> 209
 tagagactga cacaggctat gtcatttttt caataccaag ccctgtgaaa tgggtactat 60
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 gtggtaggca gaggcaggtc tcaaanccct cgctaccta actcagacac acttggaat 180
 actatatatc tctttaagcc ttccagagga tatgttttag gaggtggatt gttccatttt 240
 atatatatat gaacatgata gacagacaga tagatagata aatagataga gataatttta 300
 aacgtgctca ctttcattta tgaaaattta catttgataa ctaaaagagc cttgcaattc 360
 cagcatctcc ctcatgggtg cagtagaaga taaatcagct tttgggtcaag attggtgtta 420
 caacaactaa ccagagaaga acctccttaa taaatcagct tttgggtcaag attggtgtta 480
 cgtaaaatgc aaaatttaga ycctcggaag gggaaaaaaa gagtctcaag tatctagggt 540
 attgacccca gaaacaaaag aaatttgaca aacttgcaaa acagagacaa caacttccta 600
 tgggggtaaa aaaaacaaag caactacttg ttgctgcccc ncccgtttag taactggcct 660
 tggtagtctt ccagcagcaa gcacaatagc cttgtccaca gnatgctttt cccatttcct 720
 cggtcccctt gaaaccaagc ttttgagaac aaatagttca tttctccttt ctttaatttg 780
 tctgaagggt ttttaacacg cgataactgg catatagaaa tttcacatat ttttcttgat 840
 cactatggcc tatcaacccc cgctgatga ttaaatgaag gacgatgtat ccaaggttct 900
 taaagaactt ggttgcaacg aatgaacaca aaaaacacca gacaataaac atgtattgaa 960
 ttatnatctg ggtacagtag acaccattgg gcagacttca g 1001

<210> 210
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-495-272 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-495-272.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-495-272.mis2, potential complement

<220>
 <221> primer_bind
 <222> 230..249
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 678..696
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-495-272 potential probe

<220>
 <221> misc_feature
 <222> 40,299,535,596,859
 <223> n=a, g, c or t

<400> 210
 taaggggcgt tgtagtggta ggcagaggca ggtctcaaan ccctcgcccta cctaactcag 60
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 gattgttcca ttttatatat atatgaacat gatagacaga cagatagata gataaataga 180
 tagagataat ttttaacgtg ctccactttca tttatgaaaa ttacatttg ataactaaaa 240
 gagccttgca attccagcat ctccctcatg gtggcagtag aagactaagt catgtacanc 300
 gcagcctcca gcaccaacaa ctaaccacaga agaaacctcc ttaataaatc agcttttgggt 360
 caagattggt gttacgtaaa atgcaaaatt aggaccctcg gaaggggaaa aaaagagtct 420
 caagtatcta ggttattgac ccagaaaaca aaagaaattt gacaaaactg caaaacagag 480
 acaacaactt cctatggggg waaaaaaaaac aaagcaacta cttgttgctg cccancccggt 540
 ttagtaactg gccttggtag tcttccagca gcaagcacia tagccttgct cacagnatgc 600
 ttttccatt tcctcgggtc ccttgaaacc aagcttttga gaacaaatag ttcatttctc 660
 ctttcttaat ttgctctgaa ggtttttaac acagcgataa ctggcatata gaaatttcac 720
 atatttttct tgatcactat ggcctatcaa cccccgcctg atgattaaat gaaggacgat 780
 gtatccaagg ttcttaaaga acttggttgc aacgaatgaa cacaaaaaac accagacaat 840
 aaacatgtat tgaattatna tctgggtaca gtagacacca ttgggcagac ttcagaatta 900
 gcccccggaa gttttgcttt tgcttgactc ttggtcatag ctgattggac tagaagtgaa 960
 cacctgactc aggaggagga agttcattgg ctgaccagga g 1001

<210> 211
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-495-424 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-495-424.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-495-424.mis2, potential complement

<220>
 <221> primer_bind
 <222> 78..97
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 526..544
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-495-424 potential probe

<220>
 <221> misc_feature
 <222> 147,383,444,707
 <223> n=a, g, c or t

<400> 211
 tagacagaca gatagataga taaatagata gagataattt taaacgtgct cacttttcatt 60
 tatgaaaatt tacatttgat aactaaaaga gccttgcaat tccagcatct ccctcatggt 120
 ggcagtagaa gactaagtca tgtacancgc agcctccagc accaacaact aaccagaag 180
 aaacctcctt aataaatcag cttttggtca agattggtgt tacgtaaaat gcaaaattag 240
 gaccctcggg aggggaaaaa aagagtctca agtatctagg ttattgacct cagaaacaaa 300
 agaaatttga caaacttgca aaacagagac aacaacttcc tatgggggta aaaaaacaa 360
 agcaactact tgttgctgcc cancccgttt agtaactggc cttggtagtc ttccagcagc 420
 aagcacata gccttggtcca cagnatgctt ttcccatttc ctcggtcccc ttgaaaccaa 480
 gcttttgaga acaaatagtt yatttctcct ttcttaattt gctctgaagg tttttaacac 540
 agcgataact ggcatataga aatttcacat atttttcttg atcactatgg cctatcaacc 600
 cccgcctgat gattaaatga aggacgatgt atccaagggt cttaaagaac ttggttgcaa 660
 cgaatgaaca caaaaaacac cagacaataa acatgtattg aattatnatc tgggtacagt 720
 agacaccatt gggcagactt cagaattagc ccccggaagt tttgcttttg cttgactctt 780
 ggtcatagct gattggacta gaagtgaaca cctgactcag gaggaggaag ttcattggct 840
 gaccaggagc caattagggg ctctctcttg agaactctga ctaagagaca gagatgcagg 900
 ttatttagtc cagttgcggg tgtagcatta gacagatata aaaccaaga actcttggtgta 960
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<210> 212
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-500-220 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-500-220.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-500-220.mis2, potential complement

<220>
 <221> primer_bind
 <222> 283..303
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 711..731
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513

<223> 12-500-220 potential probe

<400> 212

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tcccatctct tgaaaaaaa aagcaactgg aaagaattac tatttttttaa aaaatacttt      60
taaacccttt ttagagacag ggtctcacta tgttgctcag gctggctctg aactcctggg      120
ctgaaatgat cgtcctcctg ctgcctcagc cttccaggtg gctggaatta cagacacaaa      180
ccaccatgct cagcttttga aagagttctt aaaggaattc taattagtgg cctcagacaa      240
attctagaga ggttcagtca catccataaa acaagtatta tagattgtgc ttatttaatg      300
gtgagtattc tcaccagtag agcagatggt gaatatccaa ggtagtgatt taaaagacca      360
aatgaagatt aatcccagca ggatggtgaa gaaatggaaa ttatggaaat cctgaagcat      420
ggaaagctct ggaaaattca atgtttgtgt aataatttag aagaggagaa tagtttatat      480
aggaaagata tacaataatc raagaaataa tagaattttt ccttaataag tcttccttaa      540
ggatgagaca aatatttaac tcaaatttag gcatttatta atctcaaaga gaaaattaac      600
tgtccggaca ggagaaaaaa ttaggagaca tgaaaagggg ggaaaatcaa ctgatattac      660
ttttcatttg caacattaaa tgctagatgg aaagaagttt tcagaatctc gagaggtaaa      720
gaattaacaa ccacagaatt atcttctcag ccaaattatt ctttaaattt caggtgatcc      780
taacaaaact gaatggatca agttagggtc aaaagtatgc cagaagtctt atctagtgtc      840
ttggtttgtt tgggctgctg taacaaaaat accttacagt ggtggtgctta taaacaacag      900
gaatgtattg ctcacagttc tggaggctgg gaagttcacg atcaagtcac cggcagtttc      960
ggtgtgtggt gagagctttt gctctctggt tcatacatgg t                                1001

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<210> 213

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-501-155 : polymorphic base T or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-501-155.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-501-155.mis2, potential complement

<220>

<221> primer_bind

<222> 636..655

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 168..188

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-501-155 potential probe

<400> 213

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acagctctac tgagctttac catctgaaca cagctaagaa tttgggattt taggaacaga      60
actgtaaatc ttaaaacaag caaaaagtgc tttctccttg gtagaaatac ctgtggccaa      120
gccagacct tcagatccta acttgggata caactgattg ttacttaacc tgctgctaac      180
ctaaagacta gttttctgct catctagtcc cctgtgtgaa taagaggttt cctcctggtc      240
ccaggatgcc tctgctgctc agctcatctc tgaggctgtc tgtgagcctt cagttcagaa      300
attgagggaa aatccattgc cttggatgtc tccttccaaa tcaccaccca aaacaaaaat      360

```

181

```

taggagacgt agaaatccag gatgtgttgt ggggttaggcc atattctgag gagttggaag 420
gtttcttggg gacctgaagt ctctgaaga gaaaatgtgg aaataagtgt ccttcaagcc 480
attgtagtgc ttgacatggg kgaaagaggc cagggggagg gggacctgtg gtgccagggc 540
ctttcagagc ttggctagat gaggggggtcc ttctcagaac tgtaaataag ctgctcagtt 600
gcatgatatt cagaggccct gctaatagagc tttttgtttg ggtaaagcct cccctgcttt 660
ccctgaagat aagccactga gttctatcag ctgctgtctt ctctccatta tgctttcgta 720
taaataattta acatttccta taaacaattc tggaagtaca tgccaagtga tacttatgga 780
agtgtaaaga gatgtttcag ttcaggctgc tataactacc acagactgag tgacttacac 840
aactgacatt tgttactgtt agggaggctg gaagtgcagg agcaaggcac tggcggattc 900
agctcctggt gagcgtctct catggtttgc agatggttgt cttgctgcgt cccatgtgtt 960
ggagagatca tttctcttgt atctctcctt atctaaggac a 1001

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<210> 214

<211> 998

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-503-52 : polymorphic base T or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-503-52.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-503-52.mis2, potential complement

<220>

<221> primer_bind

<222> 535..552

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 80..100

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-503-52 potential probe

<220>

<221> misc_feature

<222> 105,135,165,402,424,522,569,587,843,873

<223> n=a, g, c or t

<400> 214

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gaatcatgta ttctgtcatt tgatattaca tcttttaata tttgataagt gtctttaatt 60
tgcatacaaa atgtcttgat tccatttaat cttgatgccc atcanggtat ccacgatgta 120
attcttagaa cagancatat aatattacat ctgtctattg aattnctcca aaaaatgtat 180
atatcctctg tacaatacta aaaatgggta tcatatttct attcacagaa gcaatgtttt 240
catgtattaa actaagacta tgagctgagt acttcacatg tttgacataa tcatttttgg 300
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caggcaatta gcatttttat gtcaatatta tctgtttcca anttcattaa taatttcacg 420
aggntagatc atatctagtt tttcttttca catttcaata aagtcagtat aacttttttc 480
tgttgatata acatcattct kaatgtgaac atacttaata antgttacat acttggtcac 540
aatcggctac atctggtata taataaaana tcaagggtatt ttgcttnect tttttttaat 600

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182

tgagacattc	ttgctctgtc	gccaggctg	gagtgcaagt	gtgtgttctc	agctcactgc	660
aacctccatc	tccaggggtg	aagtgattcg	cccacctcag	cctcccgagt	agctgggact	720
acaggtgtgt	gccaccacac	cagctaattt	ttgtattttt	agtagagagg	ggtttcacca	780
cattggccat	gctgggtctg	aactcctgac	gtcaagtgc	ccaccgcct	ccgactccca	840
aangtgctgg	gattacaggc	atgagccact	gcngccagct	tgctcacata	cttatttcaa	900
gcttttgaaa	tgtctaacat	ttccctttct	tcacttttgt	cttcacaatt	caaaacagat	960
tctttagtta	actctgaatt	tggttaattgt	tctattct			998

<210> 215

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-503-62 : polymorphic base T or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-503-62.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-503-62.mis2, potential complement

<220>

<221> primer_bind

<222> 545..562

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 90..110

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-503-62 potential probe

<220>

<221> misc_feature

<222> 115,145,175,412,434,532,579,597,853,883

<223> n=a, g, c or t

<400> 215

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gtctttaatt	tgcatacaaa	atgtcttgat	tccatttaaat	cttgatgcc	atcanggtat	120
ccacgatgta	attcttagaa	cagancatat	aatattacat	ctgtctattg	aattnctcca	180
aaaaatgtat	atatcctctg	tacaatacta	aaaatggtta	tcataattct	attcacagaa	240
gcaatgtttt	catgtattaa	actaagacta	tgagctgagt	acttcacatg	tttgacataa	300
tcattttttg	tggaaataat	ggccacacat	ctttgtatac	acaagccata	tttgctctat	360
tatcatttcc	caggcaatta	gcatttttat	gtcaatatta	tctgtttcca	anttcattaa	420
taattttcac	aggntagatc	atatctagtt	ttttctttca	catttcaata	aagtcagtat	480
aacttttttc	tgttgatata	wcatcattct	taatgtgaac	atacttaata	antgttacat	540
acttgttcac	aatcgggtac	atctgggtata	taataaaaana	tcaagggtatt	ttgcttncct	600
tttttttaat	tgagacattc	ttgctctgtc	gccagggtg	gagtgcaagt	gtgtgttctc	660
agctcactgc	aacctccatc	tccaggggtg	aagtgattcg	cccacctcag	cctcccgagt	720
agctgggact	acaggtgtgt	gccaccacac	cagctaattt	ttgtattttt	agtagagagg	780
ggtttcacca	cattggccat	gctgggtctg	aactcctgac	gtcaagtgc	ccaccgcct	840

183

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ccgactccca aangtgctgg gattacaggc atgagccact gcngccagct tgctcacata   900
cttatttcaa gcttttgaaa tgtctaacat ttccctttct tcaactttgt cttcacaatt   960
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<210> 216

<211> 1013

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-504-54 : polymorphic base A or G

<220>

<221> misc_binding

<222> 479..498

<223> 12-504-54.misl, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-504-54.mis2, potential complement

<220>

<221> primer_bind

<222> 446..463

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 993..1013

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 487..511

<223> 12-504-54 potential probe

<220>

<221> misc_feature

<222> 108,180..181,663,712,768

<223> n=a, g, c or t

<400> 216

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ggattacaga tggccaccac catgcccaac tattttttgt atttttcgtg gagacagggg   180
ntttcaccat gttggcctga gtggtcttga actcctgacc tcaagtgatc tgcccacctc   240
ggcctcccaa agtgctggaa ttataggcat gagccatcgt gccagcgtg gttgtgctta   300
ttttaaatc ttaatttggt tgttccagta ttctcgttg atatcgtgta tgttcagtgt   360
gtgtttttct ttttgcaagt gttctaacct caggtatttt aagctgtgag ctgatgttcc   420
cctggagtta tcaggtacca atgtgacata ccaataccag gtcctacttt ctgtgttcc   480
tatgttttta agattaagra gttgagtccc agagagtccc ttaggtgttg gaacgatagt   540
caacaagcca tctgttgccc ctccactagg cattactctg ctagggattc tcctctaaag   600
cctttgaaag ggagccggtg gtcatctcat aagtgtatgca ccatttaccac cacatgagga   660
ggnactggag gagtgaagtgc tcagggaagc tggtcagcct ccccttttta gncgtgggtg   720
attgctgctg cctcctgact cacagtgggt atgggacagg caatggtncc aaaggaaaaga   780
ggagagaaaa ggagagcaga acctagcagc actctaccta ttattctaac tctgcattcc   840
tccccacca aagtttatga tggcctttag tgtctccagg agtttctcac agtttttttc   900
tagggctgat tccccagggc atctgtggcc tgtgcctgat cttgtctgta cttcaggggc   960
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184

<210> 217
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-504-96 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-504-96.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-504-96.mis2, potential complement

<220>
 <221> primer_bind
 <222> 406..423
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 953..973
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-504-96 potential probe

<220>
 <221> misc_feature
 <222> 68,140..141,623,672,728
 <223> n=a, g, c or t

<400> 217
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 tcagcctncc cgagtagctg ggattacaga tggccaccac catgcccacac tattttttgt 120
 atttttcgta gagacaggn ntttcacccat gttggcctga gtggtcttga actcctgacc 180
 tcaagtgatc tgcccacctc ggcctcccaa agtgctggaa ttataggcat gagccatcgt 240
 gcccagcgtg gttgtgctta ttttaaattc ttaatttggt tgttccagta tttctgcttg 300
 atatcgtgta tgttcagtgt gtgtttttct ttttgcagtg gttctaacct cagggtatttt 360
 aagctgtgag ctgatgttcc cctggagtta tcaggtagca atgtgacata ccaataccag 420
 gtccactctt ctgtgttcc tttgttttta agattaagga gttgagtcac agagagtcac 480
 ttaggtgttg gaacgatagt yaacaagcca tctgttgccc ctccactagg cattactctg 540
 ctagggattc tctctaaag cctttgaaag ggagccggta gtcactctcat aagtgatgca 600
 ccatttacca cacatgagga ggnactggag gagtgaagtc tcaggggaagc tggtagcct 660
 ccccttttta gncgtgggtg attgctgctg cctcctgact cacagtgggt atgggacagg 720
 caatggtncc aaaggaaaaga ggagagaaaa ggagagcaga acctagcagc actctaccta 780
 ttattcctaac tctgcattcc tccccacca aagtttatga tggccttttag tgtctccagg 840
 agtttctcac agtttttttc tagggctgat tccccagggc atctgtggcc tgtgcctgat 900
 cttgtctgta cttcaggggc cagcagtggg ggataggtta ctgaaagttt ttgagttttg 960
 ctgtgagaag attaatcttt cagcagagtg caataaaagg a 1001

<210> 218
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-504-428 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-504-428.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-504-428.mis2, potential complement

<220>
 <221> primer_bind
 <222> 75..92
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 622..642
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-504-428 potential probe

<220>
 <221> misc_feature
 <222> 292,341,397
 <223> n=a, g, c or t

<400> 218
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 caggtaccaa tgtgacatac caataccagg tcctactttc tgtgttcctt atgggttttaa 120
 gattaaggag ttgagtccca gagagtccct taggtgttgg aacgatagtc aacaagccat 180
 ctgttgcccc tccactaggc attactctgc tagggattct cctctaaagc ctttgaaagg 240
 gagccggtag tcatctcata agtgatgcac catttaccac acatgaggag gnactggagg 300
 agtgagtgtc cagggaaagc ggtcagcctc cccttttttag ncgtgggtga ttgctgtctgc 360
 ctctgactc acagtgggta tgggacaggc aatggtncca aaggaaagag gagagaaaag 420
 gagagcagaa cctagcagca ctctacctat tattctaaact ctgcattcct cccacccaa 480
 agtttatgat ggcctttagt stctccagga gtttctcaca gtttttttct agggctgatt 540
 cccagggca tctgtggcct gtgcctgac ttgtctgtac ttcaggggcc agcagtgggg 600
 gatagggtac tgaaagtgtt tgagttttgc tgtgagaaga ttaatcttct agcagagtgc 660
 aataaaaagga ggaaggaaac cctgttacta gtttaagtaa gcaataatgg agatctggat 720
 taatagtgtt tatgttgaag tgagaagatt ttttttttaa gtataaatga tttatttgtt 780
 agttgagccc aagcttgaag aagctgctct tttattttgc ctcttttttt tcttacatat 840
 gtttattctt agccttttct tttcttttct ttcttttttgc ttttttttgc agtgaattct 900
 acaaaactaag cactggaaga atgtcgagat gttacagtga aaaagggaagc taaatgaggc 960
 cagattggag agcaaattgt tattattttaa aacttatgga c 1001

<210> 219
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 474

186

<223> 12-507-53 : polymorphic base C or T

<220>

<221> misc_binding

<222> 454..473

<223> 12-507-53.mis1, potential

<220>

<221> misc_binding

<222> 475..493

<223> 12-507-53.mis2, complement

<220>

<221> primer_bind

<222> 422..441

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 982..1001

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 462..486

<223> 12-507-53 potential probe

<220>

<221> misc_feature

<222> 153,560,925,934

<223> n=a, g, c or t

<400> 219

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agtgtagcta ctccccctgt gctcccaccc ccaccatata ccagtgggtc ttaaacttta      60
acatgcatca taatcaccca gagagtttgt taaaacaggg attgctgggc tccacctcca      120
gagtttctga ttacagtaaat ctggggcaag ccnttgataa tgtgtttcct aacaagtcct      180
caactcatag tgacactact agtccaggga tcaactctga gaatcactgc catataccaa      240
tatttctcag tactgactgc acctggggat tttaaagaga atacaactgc caaaaattac      300
cagtgtctag gtctgttccc actgattctg atttaattgg ttgggaatga ggccaggata      360
cctgtatttt ataaaagtgc ttcaggagat tctaagggtat acttaggttc aagaagcact      420
tccttacact caatctccac cgtcattca gagaaactca tgtagtttct gttycacctt      480
ccattaaagc cttcaatggt aagctattat caagatattt ttatatagac tgggatgcct      540
attagtctta gtcaccaccn aaaatgtaag tcactaagta tttatcctct cccttactct      600
tactatttct ccatgatatt tctccactaa tccatacctg ctectacttt gccttccacc      660
atgagtaaaa gttccttgag gcctccccag aagcagacgc cgccatgctt cctgtacagc      720
ctgcagagcc atgagccaat taaaccactt ttcttataaa ttaccagtc tcaggatatt      780
ctttatggca atgcaagaaa ggactgatac aggttaataaa tcattcatte attcaaataa      840
agttaccata gtgttgggga tacagaaaag agacagcccc ttaaggagct caaagtcctc      900
agaataccct tcctttattg tgatnttagt gccnactttt gaagacaaaa aagaagtaag      960
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<210> 220

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-507-92 : polymorphic base A or G

<220>

<221> misc_binding

187

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<222> 481..500
<223> 12-507-92.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-507-92.mis2, potential complement

<220>
<221> primer_bind
<222> 410..429
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 970..990
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-507-92 potential probe

<220>
<221> misc_feature
<222> 141,548,913,922
<223> n=a, g, c or t

<400> 220
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atcacccaga gagtttggtta aaacagggat tgctggggctc cacctccaga gtttctgatt      120
cagtaaatct ggggcaagcc nttgataatg tgtttcctaa caagtcccca actcatagtg      180
acactactag tccagggatc aactctgaga atcactgcca tataccaata tttctcagta      240
ctgactgcac ctggggattt taaagagaat acaactgcca aaaattacca gtgctcaggt      300
ctgttcccac tgattctgat ttaattgggt gggaatgagg ccaggatacc tgtattttat      360
aaaagttctt caggagattc taagggtatac ttaggttcaa gaagcacttc cttacactca      420
atctccaccc gtcattcaga gaaactcatg tagtttctgt ttcaccttcc attaaagcct      480
tcaatgttaa gctattatca rgatattttt atatagactg ggatgcctat tagtcttagt      540
caccaccnaa aatgtaagtc actaagtatt tatcctctcc cttactctta ctatttctcc      600
atgattttctc tccactaatc catacctgct cctactttgc cttccaccat gagtaaaagt      660
tccttgaggc ctccccagaa gcagacgccg ccatgcttcc tgtacagcct gcagagccat      720
gagccaatta aaccactttt cttataaatt acccagtctc aggtatttct ttatggcaat      780
gcaagaaagg actgatacag gtaataaatc attcattcat tcaaataaag ttaccatagt      840
gttggggata cagaaaagag acagccccctt aaggagctca aagtcctcag aatacccttc      900
ctttattgtg atnttagtgc cnacttttga agacaaaaaa gaagtaagag tcttatttcg      960
tgaacatgtg gcaaattgtat gactcattac gtttatgggt c                               1001

<210> 221
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 500
<223> 12-507-159 : polymorphic base G or T

<220>
<221> misc_binding
<222> 480..499
<223> 12-507-159.mis1, potential

<220>

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188

<221> misc_binding
 <222> 501..520
 <223> 12-507-159.mis2, potential complement

<220>
 <221> primer_bind
 <222> 341..360
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 901..921
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 488..512
 <223> 12-507-159 potential probe

<220>
 <221> misc_feature
 <222> 72,479,844,853
 <223> n=a, g, c or t

<400> 221
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 tggggcaagc cnttgataat gtgtttccta acaagtcccc aactcatagt gacactacta 120
 gtccagggat caactctgag aatcactgcc atataccaat atttctcagt actgactgca 180
 cctggggatt ttaaagagaa tacaactgcc aaaaattacc agtgctcagg tctgttccca 240
 ctgattctga ttaattgggt tgggaatgag gccaggatac ctgtatttta taaaagttct 300
 tcaggagatt ctaagggtata cttagggtca agaagcactt ccttactctc aatctccacc 360
 cgtcattcag agaaactcat gtagtttctg tttcaccttc cattaaagcc ttcaatgtta 420
 agctattatc aagatatttt tatatagact gggatgccta ttagtcttag tcaccaccna 480
 aaatgtaagt cactaagtak ttatcctctc ccttactctt actatttctc catgatttct 540
 ctccactaat ccatacctgc tctactttg ccttccacca tgagtaaaag ttccttgagg 600
 cctccccaga agcagacgcc gccatgcttc ctgtacagcc tgcagagcca tgagccaatt 660
 aaaccacttt tcttataaat taccagctct cagggtatttc tttatggcaa tgcaagaaag 720
 gactgatata ggtaataaat cattcattca ttcaaataaa gttaccatag tgttggggat 780
 acagaaaaga gacagcccct taaggagctc aaagtcctca gaataccctt cctttattgt 840
 gatnttagtg ccnacttttg aagacaaaaa agaagtaaga gtcttatttc gtgaacatgt 900
 ggcaaatgta tgactcatta cgtttatggg tccactaagt ttaaattagg aggaagttcc 960
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<210> 222
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-507-177 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-507-177.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-507-177.mis2, potential complement

189

<220>
 <221> primer_bind
 <222> 324..343
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 884..904
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-507-177 potential probe

<220>
 <221> misc_feature
 <222> 55,462,827,836
 <223> n=a, g, c or t

<400> 222
 ggattgctgg gctccacctc cagagtttct gattcagtaa atctggggca agcctttgat 60
 aatgtgtttc ctaacaagtc cccaactcat agtgacacta ctagtccagg gatcaactct 120
 gagaatcact gccatatacc aatattttctc agtactgact gcacctgggg atttttaaaga 180
 gaatacaact gccaaaaatt accagtgtctc aggtctgttc ccactgattc tgatttaatt 240
 ggttggggaat gaggccagga tacctgtatt ttataaaagt tcttcaggag attctaaggt 300
 atacttaggt tcaagaagca ctcccttaca ctcaatctcc acccgtcatt cagagaaact 360
 catgtagttt ctgtttcacc ttccattaaa gccttcaatg ttaagctatt atcaagatat 420
 ttttatatag actgggatgc ctattagtct tagtcaccac cnaaaatgta agtcactaag 480
 tattttatcct ctcccttact sttactatct ctccatgatt tctctccact aatccatacc 540
 tgctcctact ttgccttcca ccatgagtaa aagttccttg aggcctcccc agaagcagac 600
 gccgccatgc ttccctgtaca gcctgcagag ccatgagcca attaaaccac ttttcttata 660
 aattaccagc tctcagggtat ttctttatgg caatgcaaga aaggactgat acaggtaata 720
 aatcattcat tcattcaaat aaagttacca tagtggtggg gatacagaaa agagacagcc 780
 ccttaaggag ctcaaagtcc tcagaatacc cttcctttat tgtgatntta gtgccnactt 840
 ttgaagacaa aaaagaagta agagtcttat ttcgtgaaca tgtggcaaata gtatgactca 900
 ttacgtttat gggtccacta agtttaaatt aggaggaagt tcctaataag tatttttaag 960
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<210> 223
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-508-29 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-508-29.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-508-29.mis2, potential complement

<220>
 <221> primer_bind
 <222> 473..491
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 907..925
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-508-29 potential probe

<220>
 <221> misc_feature
 <222> 847
 <223> n=a, g, c or t

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<400> 223
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ataccagcc attcctcaaa ttgttttttt tttttttttt tgaggcggag tcttgctctg    120
tcaccaggc cagagtgcag tgccgcgatc tcggctcact gcaagctctg cctcctgagt    180
tcacgccatt ctccctgcctc agcctcctta gtagctggga ctacaggcgc ccgccagcat    240
gcctagctaa ttttttgat ttttagtaga gatggggctt caccgtgtta gccaggatgg    300
tcttgatctc ctgaccttgt gatccgcccg cctcgccctc ccaaagtgtc gggattacag    360
gcatgagcca ccgtgccctg cctgccattc ctcaaattct aagctccctg aaactcttac    420
ccttaaggtg gagtatcaaa agttttttaa agcaagaaaa gaaaattttt atcttatgct    480
agtggtaaat gccattttaa racttaaadc ctaaaagctt gtatttacct ttaaacttca    540
ttgtcacagg tatttctctg tctgctgtat attcagcatt gtactgagta cttacatcgc    600
ctcagttaaa attcctttgtt tttgttgcc taatttcaga ttaacataaa agtacctcac    660
ccttgtttaa acctgcatta aatgacttgg attactgtgt ctggagtgtt cctagcaaca    720
ctatttcaca caciaagcaa agtacatact agccttttgt atgtgtcttt gtccttggtt    780
caacagctca gggatagtag tgtattaatg acttttattc tggctcttta tatgtgtctt    840
tgtcctntga tttgacagct gagaatagtg gtttttattc tagtaggata aaatttagcc    900
ttttagcact agaagtctaa gagattttta ttttcatttg taaaaatagt gcacatttaa    960
aatctgaatg tcttgccagag tggtcaggca tttttttatt g                                1001

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<210> 224
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-509-42 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-509-42.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-509-42.mis2, potential complement

<220>
 <221> primer_bind
 <222> 460..479
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 889..909

191

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-509-42 potential probe

<220>

<221> misc_feature

<222> 678,728,796,824

<223> n=a, g, c or t

<400> 224

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gactttttaa	tatgcagtta	cgattcagaa	tgctcatata	gacaggctct	aatcggaat	180
aaacataaat	gtgttgaggt	ggtgggggtg	tttaacaaaa	agctaaaagt	ttgaagaacc	240
tctttgagga	ctagtgcaga	aagatcaagg	tgactgcaga	gaaggagcac	ttcagaaggc	300
attacatttt	agtttgaaaa	accgtcagga	aattccttgag	gcttccaact	gatgattatt	360
ctattgaaaa	gtaaatttgg	ttttctttct	catttggtaa	atattctgat	gtttttctgt	420
ttcattttgct	taatgagatc	atgaagtgat	tatactttaa	ttgaggagag	tttggtttgt	480
taacatttta	aatgtcatcc	rtttggcatt	taaaactgat	atttaaaact	cagaatgagc	540
tttaactttt	tgttcttttg	ccctacccat	gttttaaaact	tgtgggctaa	gagtgaattt	600
gaaaactaag	gattttcaatt	tttttcaaag	ttaggaaact	aacaattaaa	gttattgcaa	660
cttagtttat	ataattgnct	acaagttcct	gctcatttgg	taaaaaataa	atgatgcact	720
cagtaagnca	aggaagtatc	tcttagactt	tctttaggaa	gcatgttttc	tagttaagca	780
aataacttaa	ttccangtag	cagatgccag	gcagatgagt	tggnagtcta	agtgagttaa	840
ggaggaagta	ctgaagaagg	aacatttcct	cctagctggg	agagtttaga	atgctacaca	900
gagtaagtgg	gttcctgcct	gggcctgagg	gatgggccag	ttcatctgtt	aaaatctatg	960
actgtaacta	ttgttacagc	ccagcttcca	tgatataatg	t		1001

<210> 225

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-509-126 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-509-126.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-509-126.mis2, potential complement

<220>

<221> primer_bind

<222> 376..395

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 805..825

<223> downstream amplification primer, complement

<220>

<221> misc_binding

192

<222> 489..513
 <223> 12-509-126 potential probe

<220>
 <221> misc_feature
 <222> 594,644,712,740
 <223> n=a, g, c or t

<400> 225
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 tcagaatgct catatagaca ggctctaatac ggaaataaac ataaatgtgt tgaggtggtg 120
 ggggtgttta acaaaaagct aaaagtttga agaacctctt tgaggactag tgcagaaaga 180
 tcaaggtgac tgcagagaag gagcacttca gaaggcatta catttttagtt tgaaaaaccg 240
 tcaggaaaatt cttgaggctt ccaactgatg attattctat tgaaaagtaa atttggtttt 300
 ctttctcatt tggtaaataat tctgatgttt ttctgtttca ttgcttaat gagatcatga 360
 agtgattata ctttaattga ggagagtttg gtttggttaac attttaaatg tcatccgttt 420
 ggcatttaaa actgatattt aaaactcaga atgagcttta actttttggt cttttgccct 480
 acccatgttt taaacttgtg rgctaagagt gaatttgaaa actaaggatt tcaatttttt 540
 tcaaagttag gaaactaaca attaaagtta ttgcaactta gtttatataa ttgnctacaa 600
 gttcttgctc atttggtaaa aaataaatga tgcactcagt aagncaagga agtatctctt 660
 agactttctt taggaagcat gttttctagt taagcaaata acttaattcc angtagcaga 720
 tgccaggcag atgagttggn agtctaagtg agtgaaggag gaagtactga agaaggaaca 780
 ttctctccta gctgggagag ttaggaatgc tacacagagt aagtgggttc cgtcctgggc 840
 ctgagggatg ggccagttca tctgttaaaa tctatgactg taactattgt tacagcccag 900
 cttccatgat ataatgttag gacccttcc atgaaatgaa agcataatca atttgagata 960
 gtttcatcca gtattataac ttttccctgc ttcatatagg t 1001

<210> 226
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-510-59 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-510-59.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-510-59.mis2, potential complement

<220>
 <221> primer_bind
 <222> 539..559
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 107..127
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-510-59 potential probe

<220>

193

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<221> misc_feature
<222> 7..8,169,196,281,468,470,821
<223> n=a, g, c or t

<400> 226
tttggcnnct ttctccacta ccacctatcc tectatctct ctcttctttc tattacacac      60
aatgaatgag tccctacctc tgtgctgggc atcattctag aaataaaaag gtaagcaatg      120
tagacagaga tagtgaataa atacatatta ataatgtttt aaaactttna aaaattgata      180
taaactttca tatcancaaa atgtataaat cttaaataata aactcaatga atcacttgag      240
tgagcttaag tgtaagctca aacaataact taatagtttt ncataagtgc tagaaatctt      300
atccaggaat aattgaaatt ttaccaatga gcataatata ccaaataaaa taaatgggct      360
ttggtttgaa ttgtcatttt gaagaccatt actcagatat ttgaaagttg ttagtttggg      420
gcaagggtcat cacaccatgg cctgtgggac taggggctaa taatggtnn ttatattttt      480
gaaagggttta agacaaaaac rgaagaagaa aaagaaggag aaagagaagg aacagagact      540
atatgtggac ttcaatgctg aaacatactt attatcttgt ttcttataga aaaatttgct      600
aaccctggag ctacagagta aaagtcaact ggaagccaag acagtgattt cttttctttg      660
ttcttttagcc tagtaagcca gatgtgtcaa caggttcttt ttgactggca ttaacatctt      720
gctcaataat aaaaggcctt aaatttttac taacttatat cagccccacc tagtgaaatt      780
aaatacaagg aatagtttagc tgaaacactg tgtaccagaa nccattaagt caggacagtc      840
tgagggttggt gacctcaatt ttgatatgaa ctggattttt tagacacgta ggaatagtta      900
tggtatatt taactatttt catggctatg gtgtatgttt ttaagacttt ccatagata      960
ttgtcattat ctactggctg gggcctttag aacagatggg a                                1001

<210> 227
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-511-74 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-511-74.mis1, potential complement

<220>
<221> misc_binding
<222> 483..500
<223> 12-511-74.mis2

<220>
<221> primer_bind
<222> 558..575
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 125..145
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-511-74 potential probe

<220>
<221> misc_feature
<222> 102,561,637
<223> n=a, g, c or t

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194

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<400> 227
tgcagccctg ccctcagcca aggatctgta gggaaactccc acttagactt ctaggaactc      60
atctttgcag ctccctcctt actggtacca tgccctgcaa anttccaaac tttttgcac      120
cctgaacttc agtctctgcc tcttcagctc agggagactg ctgtgctctg tttgggctcc      180
acttcatggc ctctgttggt caaaaagttg cccccaacc tggggcaaat gtgctgctca      240
cttcataaggc ttcctttctc tgaaggagca cagttctatg ctgccttgct tccaacgtcc      300
gaaaatagct gtcatttatt ttgtcattta aaaaccttga attacagtaa gggaaagcat      360
attcataaat gaaatgatgt aaagacttta agtctacctt acatctagtt tttttctttt      420
ttgctaattg gactattcct cttttcattc atgtccttta agtttgttta tggaaaaaaa      480
ttatgacgac cacactcttc ygtggttata ggaactttca caccattac aacattatgc      540
atztatattc tgacgacctt ngatgggaca cacaaaacct gattcttgca actttgccat      600
gaactttgtg atttccagag actggttaacc acttagncce cacaaacttc taattctcta      660
cacagattat ctctctttcc ttgactctta tggtttgtaa ataaatgtct tttacacaca      720
actctgaagc gcgtcagatt ttatggtacc ccataagggt ataatgccta tagaaatggg      780
accaaattga aattttggaa atctctcttg gctttgtaga ctagtgggtc gtaacttccc      840
aagtcacact tctgatacac ctgtgaggga ttactgcttt gtgccacact agatgacctg      900
caaggttttc taaccataga taaagccagt ctgtgattct catggacaaa ttttatgtgt      960
ttgttggaac caggcatcca gaggttcctc attttgctctg t                                1001

<210> 228
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-325-311 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-325-311.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-325-311.mis2, potential complement

<220>
<221> primer_bind
<222> 191..208
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 596..613
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-325-311 potential probe

<400> 228
gcggaggggt catcttcacc atctacaatg tgacaacagg tgggcccaca tgtgaactgc      60
catggggaag atgggcttgt ccacaccact gcgtaacccc ttctccagcc agtcccatca      120
actcaagccc gtttctgggt gttcttgggc cccctgccct gccccatttg cctcagctgt      180
gcaaagccct tgtgtcaact cctgtccctg tgttagccca gagtccatct cataatgcag      240
agatggaaac tgaggcctag agcaggccag gggctgtctg cagggtccat gaccactcac      300
ctgccctgcc ctactccagg gaaggtggag gtcacaaatg cccgggagac ggtgccggcc      360
agccacgccc cgagcctgct ggaccagtgt gcacaggctc tgccactggg cacaggtgac      420
gccccatgga ggtcccccac tcccaccccc caggccacta ggactaatca gaacaccccc      480

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195

gcaaaggagc agcgccctcac rgacaggctg tgactccctg gcacgggggg acacggagcc	540
tgtggggaac cccagcccc aacctgcagg gattgagaag gtcccccttg ggaacgggct	600
ctctgaggtg atccaggag agggaccagg ctggacaaag gcctggaggg ttcagtggag	660
atgggttggc ggggcagggt ggggctcctg gggccagttt gtgtaggggc ccttgggctt	720
ggccatggac tttgtgggga gccacagggt atttgagcag ggaggggacgt ggtcgggtgt	780
gggctccaga aagctcactc tggctgctgt aactgggggg ccacatgtag gggatgatggc	840
aaacctggga aggcctggaa gccacagggt tgagagctgg gatgtgccat gcaggggccc	900
agtggatcgg ggtgccggg gagctccgtg gctatgccga ggcccaccgc cgccatggcc	960
gcctgccctg ggcgcagctg ttccagccca ccatcgcgct g	1001

<210> 229

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-327-120 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 10-327-120.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-327-120.mis2, potential complement

<220>

<221> primer_bind

<222> 382..400

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 805..824

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-327-120 potential probe

<400> 229

ggccactagg actaatcaga acacccccgc aaaggagcag cgccctcacgg acaggctgtg	60
actccctggc acgggggggac acggagcctg tggggaaccc ccagcccca cctgcaggga	120
ttgagaaggt ccccttggtg aacgggctct ctgaggtgat ccaggagag ggaccaggct	180
ggacaaaggc ctggagggtt cagtggagat ggggtggcgg ggccagggtgg ggctcctggg	240
gccagtttgt gtagggcccc ttgggcttgg ccatggactt tgtggggagc cacagggtgat	300
ttgagcaggg agggacgtgg tcgggtgtgg gctccagaaa gctcactctg gctgctgtaa	360
ctgggggggc acatgtagg gtgatggcaa acctgggaag gcctggaagc cacagggttg	420
agagctggga tgtgccatgc agggggccag tggatcgggg tgcccgggga gctccgtggc	480
tatgccgagg cccaccgccg ycatggccgc ctgccctggg cgcagctggt ccagcccacc	540
atcgcgctgc tccgaggggg gcatgtggtg gccctgtcc tcagccggtt cctgcacaac	600
agcatcctgc ggccttcctt gcaggcgta accctgcggt gagccccaca tgggtggcct	660
gggttccttg gttcaaggcc atatcctgtc tgggcccagt ccacacccca gctctgcctc	720
agtcctctt acactggagg attgacctc ggggtgctgg ccaggacaaa gactactttt	780
catggccctt ccagctcccc gtggcagagc ctaacttggg gttaggctgc ggggagttta	840
ttgcccaagt gataggactc caaggtgtgg atttgggctc tgccaccgc cctggggccc	900
cggcctcctt cttcctctct ctggcatggc aggagggctt caactgccac tctcacctgc	960
cccaccacg ccactgacag gccctcccag gagtgagatg a	1001

<210> 230
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-331-179 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-331-179.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-331-179.mis2, potential complement

<220>
 <221> primer_bind
 <222> 326..345
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 728..747
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-331-179 potential probe

<400> 230
 gccaggagtt caataccagc ctgaacaaca tggcgaaatc ctgtctacta aaaatacaaa 60
 aataattagc tgtacgtggt ggcgaacaca tgtagtctca gctactcagg agactaagga 120
 ccaagaatca cttgaaccca ggaggcagag attgcagtga gctgagactg cgccattgca 180
 ctccagcctg ggcaatagag tgagactctg tctaaaaaaa aaaaaaaaaa aaaaaaaatc 240
 cttaacttac ttttccactt aaggtattag tcaactctgt gctgtataag gtaatatcca 300
 caggttttgg gaattaggat gtgggtggat ctttctgtgg tgggggggtg gggcaacatt 360
 caaccatta catagggtga cccaaccaa cctgtgcccc aacctctctc cagggttcaa 420
 cttctcaaca gagtctatgg ccaggcctga agggagggtg aacgtgtacc accaccttgt 480
 agagacgctc aagtttgcca rggggcagag gtggaggctg ggggaccctc gaagccaccc 540
 gaagctccag gtgaggttgc tgaggttgc tgggtggtg gccgtcctc tccctggctc 600
 aggacttggc atgaaatgag ggtcaggcct ggtaggggga agttggaggg atatgtatgt 660
 ggttctaggc cagggcagga ctgaaaggga tcccggggtg gcaggtagag gggtcagggtg 720
 caggagtggc accatatctc aaaggacctg gagggtagag agagtctaga cctagctggg 780
 cttgaggagg acctggccac aaggtagagg acagactgga ggtggccccc atgggggctg 840
 atctcatcct gcccttgggt ctgcggatc tgccctggccc ctactgacc ctgccacctg 900
 cccaccacc ccagaatgcc tcccgggacc tgctggggga gacctgggcc cagctcatcc 960
 gccaacagat cgatggccgg ggggaccacc agctcagcca c 1001

<210> 231
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501

197

<223> 10-331-357 : polymorphic base G or T

<220>

<221> misc_binding

<222> 481..500

<223> 10-331-357.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-331-357.mis2, potential complement

<220>

<221> primer_bind

<222> 148..167

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 550..569

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-331-357 potential probe

<400> 231

cactccagcc tgggcaatag agtgagactc tgtctaaaaa aaaaaaaaaa aaaaaaaaaa	60
tccttaactt acttttccac ttaaggtatt agtcactctt gtgctgtata aggtaatatc	120
cacaggtttt ggggaattagg atgtgggtgg atctttctgt ggtgggggggt gggggcaaca	180
ttcaacccat tacatagggg gacccaacc aacctgtgcc ccaacctctc tccagggttc	240
aacttctcaa cagagtctat ggccaggcct gaaggagggt tgaacgtgta ccaccacctt	300
gtagagacgc tcaagtttgc caaggggcag aggtggaggc tgggggaccc tcgaagccac	360
ccgaagctcc aggtgaggtt gctgaggttg ctgggctggt gggccgtcct cctccctggc	420
tcaggacttg gcatgaaatg agggtcaggc ctggtagggg gaagtggag ggatatgtat	480
gtggttctag gccagggcag kactgaaagg gatcccgggg tggcaggtag aggggtcagg	540
tgcaggagtg gcaccatata tcaaaggacc tggaggggtga gcagagtcta gacctagctg	600
ggcttgaggg agacctggcc acaaggtaga ggacagactg gaggtggccc ccatgggggc	660
tgatctcatc ctgcccttgg ttctgctggc tctgcctggc ccctactga ccctgccacc	720
tgccaccca cccagaatg cctccgggga cctgctgggg gagaccctgg cccagctcat	780
ccgccaacag atcgatggcc ggggggacca ccagctcagc cactacagct tggccgaggc	840
ctggggccac gggacaggca cgtcccatgt gtctgtgctg ggggaggatg gcagcgccgt	900
ggctgccacc agcaccatca acacaccgtg cgtagggcct gggggaaggc ggatggcttc	960
actcctctc tcctagacct gcacaccccc agccccatgt c	1001

<210> 232

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-334-263 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 10-334-263.mis1, potential

<220>

<221> misc_binding

<222> 502..521
 <223> 10-334-263.mis2, potential complement

<220>
 <221> primer_bind
 <222> 240..257
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 658..675
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-334-263 potential probe

<400> 232
 tgcacacccc cagcccatg tcccctcact tgtccccacg gggcagcacc ttgcttttgc 60
 cctttttctc ctctctatt tcaaaagagg cccccacccc tgacatctct ggctggaaag 120
 gctgctgctg ggggtggccc gaccaagat ttacctggga atgggtagcc tctctcagaa 180
 ggggtgccctg atgtgggggc acaggtgggt ctttggggac ccctcctggg tgggtgccagg 240
 gagagaatag cggcttcagc atgcttcggg gcagctgtaa aacgaggggg tcctgcaaag 300
 cgtgcagggt aagtgggtgc tgggtgggag cccgggtcct agcccaggct cttctgcctc 360
 cacggctgca gctttggagc gatgggtgtat tcaccacgga caggcatcat cctcaacaac 420
 gagctcctgg acttatgcga gcgatgcccc cgggggtccg gcaccacccc ctcacctggg 480
 gagaacaaag cttcccaccc rgggtccaca agggccccc accaggggag aggagggagg 540
 gggctgggct ggggttgcat gctaaccct ggatgggtca ctgcacttgc caagacgctg 600
 tttgctcagc agtgagtggg gacaggggtg gtggagctcc cggaaggtgc tggcccccag 660
 ttccaggcga gcgttcccca tctccatgg tgcctccat cttgatcaac aaagcccagg 720
 ggtcgaaagt agtgattggc ggggctggcg gggagctcat catctctgct gtggcccagg 780
 tgagtctggg gctcctggct cgagtgtctc ctctctgggc agcatactgt ctgactgtct 840
 ctggagtggg gatgtgagg ctgatgtagg gtagcagggt gcccccttct tccctgaaac 900
 cctcatctct ccccaggcc atcatgagca agctgtggct tggctttgac ctgagagcgg 960
 ccattgcagc ccccatcctg catgtcaaca gcaagggtctg t 1001

<210> 233
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-321-226 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-321-226.misl, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-321-226.mis2, potential complement

<220>
 <221> primer_bind
 <222> 276..293
 <223> upstream amplification primer

<220>

199

<221> primer_bind
 <222> 692..711
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-321-226 potential probe

<400> 233
 gcacaggtgg gtctttgggg acccctcctg ggtggtgccg gggagagaat agcgggcttca 60
 gcatgcttcg gggcagctgt aaaacgaggg ggtcctgcaa agcgtgcagg gtaagtgggtg 120
 tctggtggga gccccgggtc ctagcccagg ctcttctgcc tccacggctg cagctttgga 180
 gcgatggtgt attcaccacg gacaggcatc atcctcaaca acgagctcct ggacttatgc 240
 gagcgatgcc cccgggggttc cggcaccacc ccctcacctg gtgagaacaa agcttcccac 300
 ccagggtcca caagggtccc ccaccagggg agaggagggg gggggctggg ctgggggttgc 360
 atgctaaccc ctggatgggt cactgcactt gccaaagacg tgtttgctca gcagtgtgtg 420
 gagacagggg ggggtggagct cccggaaggt gctggccccc agttccaggc gagcgttccc 480
 catcctccat ggtgccctcc rtcttgatca acaaagccca ggggtcgaag ctagtgtattg 540
 gcgggggctgg cgggggagctc atcatctctg ctgtggccca ggtgagtctg gggctcctgg 600
 ctcgagtgtc tctctctctg gcagcatact gtctgactgt ctctggagtg gggatgtgag 660
 ggctgatgta gggtagcagg gtgccccctt tctccctgaa accctcatct ctccccagg 720
 ccatcatgag caagctgttg cttggctttg acctgagagc ggccattgca gccccatcc 780
 tgcatgtcaa cagcaagggc tgtgtggagt acgagcccaa cttcagccag gtgaggctga 840
 ggtccgagct ggatgcctag ggcagagccc actccccaaa tccgtgctgc tcaaagccac 900
 ctgggaggaa ctcagtcact gagattctta ggccagggtac acttcaactt tggggggccat 960
 aggagttggg gaccttgatg ggtgaggctg tcagtggcct c 1001

<210> 234
 <211> 858
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-183-98 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-183-98.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-183-98.mis2, potential complement

<220>
 <221> primer_bind
 <222> 581..598
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 136..155
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-183-98 potential probe

200

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<400> 234
ctgagacccc agaggggtccc tcccagcatc ttcaaagcaa caggattttg tgcctgcaga      60
tcctttctttg cagcacacac caccaccctt gaccaggacc cctagaatgc ccagcatccc      120
tgaggaggcc ctgtggtagt ttccagctccc tctggggggc cagaatgaac ctggcctgtg      180
gtgaggatgt aagcaccaat ggccaattgg gtccaaagga agacaccggg tcaaactctg      240
aaaccaatca gattctccca cggccttctt gccatcagac gacactgggt caggggtggt      300
tgctatgtac agggcagagc cacccaatcc ccacgcagga gctgtgtcct gccatgctgg      360
cctcctcctg gccatcacat caggccaagc aggggagagg aatgggaatg cccatgcacc      420
cctatcaact ctgcagacac agaaccatgc acagctcttg ggaggagtca gatgagctgc      480
tcaaagcccg ggagggaccc rcacagtggg cagcatagca gggacgggtg tttagccaag      540
gcagggatgg caggtgactc actcaggatc ttcaaaggag ccgctgcatt tccgtgctct      600
ttccagataa gaaggacatg tcggtgatga tgagcgagac ggacatgaac gccatcgag      660
gcacgctgaa gctgtacttc cgtgagctgc ctgagccccct cttactgac gaggttctacc      720
ccagcttcgc agagggcatc ggtgagcatt ggaggccttg gcctcgtggg agacgtctcc      780
tccatgtgca ctgctgccct tggaggctgt gaaaagtga ggtgtgggaac ctgagctgtg      840
accctctgc catgggtcg                                     858

<210> 235
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-185-78 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-185-78.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-185-78.mis2, potential complement

<220>
<221> primer_bind
<222> 424..444
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 855..875
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-185-78 potential probe

<220>
<221> misc_feature
<222> 661,672,954
<223> n=a, g, c or t

<400> 235
gctgagaaag ccacagttct ggcagctggc agagctgaaa gagaagggaa aatctatgca      60
cagggccctt ggatttccac ccatattccc caggaaagga tacagttcca ggaagggctc      120
tctctgatct cccggaatga aatctgagat gaaccacagg gccttatggc ttacctgtac      180
ctcctttttg tagtttccag ctggcctggc acagactgac aaccccaaat ggatgggtcga      240
aatccactgt tctccagtcc ctctcaaacc tcaccggcaa gaaggaaaga aactaaaccc      300

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201

cgagggccca	ttatattcca	gcggggctct	agggattcca	cactcattca	gttcctttac	360
atcataagaa	gtgggtatta	taatatcaga	tccactgtaa	aaggtgatcc	cgaagcaaat	420
ggtagagcag	gagctgaat	aggggcacct	ccaacagcca	catccacccc	accacagctc	480
ccaggggttt	ctttctaata	ycagggtgg	cctataccct	gggactatag	ggggccttgg	540
tgtgctaaat	cttcagagac	atTTTTaaac	ggTcaagacg	cctcttggcg	actggaagaa	600
gttcctgacc	tcgcggcatt	ccctccttcc	catccccact	accacaccaa	tcctatgcca	660
ngcctgtctg	tngtcaggga	agaagtcacg	ctggacaact	ctggcagcct	cctgtcgccc	720
tcccctgcca	gcaatccttc	tgtgccacag	ctgtgtgtcc	acactctaaa	gcacacatcc	780
caccaggcca	ctctcctgta	aaataatgcc	tactgtccc	aggccaaata	ccccagcgcc	840
gatacctgct	tcttcaaata	caggctccaa	cccacccctc	catctcattt	ccatttttacg	900
tgcacacata	gtcacacact	ctcacatacc	cacactttgg	ctcctactgt	tcctatcccc	960
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<210> 236

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-186-154 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-186-154.mis1, potential

<220>

<221> misc_binding

<222> 502..520

<223> 12-186-154.mis2, complement

<220>

<221> primer_bind

<222> 348..368

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 784..803

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-186-154 potential probe

<220>

<221> misc_feature

<222> 3

<223> n=a, g, c or t

<400> 236

ttntttttct	tttttttgag	acggagtctc	gctctgttgc	ccaggctggc	gtgcagtggc	60
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tcccgccctca	tcctcccaag	tagctgggac	tacaggcacc	caccaccacg	ctcggctaata	180
tttttgtatt	tttagtagag	acagggtttc	accgtgttag	ccaggatggg	ctcgatctcc	240
tgaccttgtg	atccgccccg	cttggcctcc	caaagtgtctg	ggattatagg	cgtgagccac	300
cgcgcccggc	ccctcccttg	actcttgact	gaaggacctt	tgtctttgtg	aacatcaatt	360
ctcaggacct	ttcacccctg	ggacgtgaaa	tgctgagaat	ttgggagatg	acagtctggg	420
gactgggatt	aatggaatcc	agtgaccac	aaacctaagg	ttctcagctc	ccttggggag	480
ttggaatgtc	agctattcag	rtctagggct	ttccatggag	taaatcctaa	actctggggt	540

202

```

ggagacttta agcctccaag gaccttcaca gctaaggccc agggactagg gcgaggagag 600
tctttgatcc tcagagtctt ggagtttggc cagtggactc tgaggaatgg agtctctgag 660
cactgaaggt ccaacttttg cttcagcagt aaaggatctt ggccttcaag tctaaggaca 720
gtgggcaatt agtaggtcag gcatggggaa ctcatagcca aacgtgcagg gctccaaaga 780
cctcatttgc cctgtcagca gctcaggcca tgtggcatca cccgatgcat ctagatgtct 840
ccggaatctc aggccttgca gggtgagggt ctcgggccat tagttttttt tgttttgttt 900
tgttttgttt ttttggttg ttgttggtga gacaaagttt cactctgtca cccaggctgg 960
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<210> 237

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-186-397 : polymorphic base C or T

<220>

<221> misc_binding

<222> 482..500

<223> 12-186-397.mis1

<220>

<221> misc_binding

<222> 502..521

<223> 12-186-397.mis2, potential complement

<220>

<221> primer_bind

<222> 105..125

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 541..560

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-186-397 potential probe

<400> 237

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ccttgtgatc cgcccgctt ggcctcccaa agtgctggga ttataggcgt gagccaccgc 60
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aggacctttc accctgggga cgtgaaatgc tgagaatttg ggagatgaca gtctggggac 180
tgggattaat ggaatccagt gaccacaaa cctaagggtc tcagctccct tggggagttg 240
gaatgtcagc tattcaggtc tagggctttc catggagtaa atcctaaaact ctgggttgga 300
gactttaagc ctccaaggac cttcacagct aaggcccagg gactagggcg aggagagtct 360
ttgatcctca gagtcttgga gtttgccag tggactctga ggaatggagt ctctgagcac 420
tgaagggtcca actttggctt cagcagtaaa ggatcttggc cttcaagtct aaggacagtg 480
ggcaattagt aggtcaggca yggggaactc atagccaaac gtgcagggtc ccaaagacct 540
catttgccct gtcagcagct caggccatgt ggcattcacc gatgcatcta gatgtctccg 600
gaatctcagg ccttcgaggg tgaggttctc gggccattag tttttttgt tttgtttgt 660
tttgtttttt tggtttgttg ttgttgagac aaagtttcac tctgtcacc aggctggagt 720
gcagtggcgc gatctcagct tattgcaacc tccacctcct gggttcaagc aattctcatg 780
tctcagctc ccaagtagct gggattacaa gtgtgtgcca ccaagcctgg ctaatttttg 840
tatttttagc agaaacagcg tttctccatg ttggccaggc tgggtctcaa ctcctgacct 900
cagggtgatc gccaccttg gcctcccaaa gtgctgggat tacaggcatg accaccgcgc 960
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203

<210> 238
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-187-65 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-187-65.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-187-65.mis2, potential complement

<220>
 <221> primer_bind
 <222> 437..456
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 839..859
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-187-65 potential probe

<400> 238
 cctatatatttt tattttattta tttattttatt tttctgagat ggagtctcac tctgtcacct 60
 aggctggagt gcagtgggtgc aatcttggct cactgcaacc tccgcctccc aggttcaagg 120
 gattcttgtg cctcagcctc ccgagtaaat gggattacaa gcacccgcca ctgcatctgg 180
 ctaattttttg tatttttagt agagacaagg tttcaccacg ttggccaggc tgggtctcgaa 240
 ctcttaacct caaatgatct gccggcctca gcttcccaaa gtgctgggat tacagggtgtg 300
 agccaccgtg cccggccggc atcctatatt tttatatctt aactctggca accttaaata 360
 taagtgacaa atgaaaccaa aaataatggg caaaggtcta aacacatcag tgatcataaa 420
 aaggaattga gaacattgtc agaacactgt cctgccttaa acactcttct ggaaagtcc 480
 acaggttaag tgtgtcgtgt ygtcaggacc tgagatctct tctgccaatt aagctcccac 540
 accatagaat aaggaggaaa atttgcacat ctgctttatg aagccagcgt agcactgacc 600
 ccaaacttgg caaagaaaaac cgcagactaa ttgtgtttat gatgcaaagc aaaatcctaa 660
 caaaattgga gaatatataa ttaaaaaaga gaatccagta gtacattaaa aagaacaaca 720
 tgacttacct accctagtgg agccaacgct aatattgcaa ggaagatctt ctgagtatgt 780
 ccctgaccgt gactcttagc tcttaccttt caccagagga gaaaaaaatc actccatcga 840
 gactgaagac gcatttgaca atatttaaca cccattcttt tttttttttt ttttttaaaga 900
 caggtctcac tctgttgcgc atgctggagt ggagtgggtgc gatcacagct cactgcagcc 960
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<210> 239
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-187-66 : polymorphic base A or G

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<220>
<221> misc_binding
<222> 481..500
<223> 12-187-66.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-187-66.mis2, potential complement

<220>
<221> primer_bind
<222> 436..455
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 838..858
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-187-66 potential probe

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<400> 239
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attcttgtgc ctcagcctcc cgagtaaagtg ggattacaag caccgcgcac tgcattctggc    180
taatttttgt atttttagta gagacaaggt ttcaccacgt tggccaggct ggtctcgaac    240
tcctaacctc aaatgatctg ccggcctcag cttcccaaag tgctgggatt acaggtgtga    300
gccaccgtgc ccggccgggca tcctatatTT ttatatTTta actctggcaa ccttaaatat    360
aagtgcacaaa tgaaacccaaa aataatgggc aaaggtctaa acacatcagt gatcataaaa    420
aggaattgag aacattgtca gaacactgtc ctgccttaaa cactcttctg gaaagttcca    480
caggttaagt gtgtcgtggt rtcaggacct gagatctctt ctgccaatta agctcccaca    540
ccatagaata aggaggaaaa tttgcacatc tgctttatga agccagcgta gcactgaccc    600
caaacttggc aaagaaaacc gcagactaat tgtgtttatg atgcaaagca aaatcctaac    660
aaaattggag aatatataat taaaaaagag aatccagtag tacattaaaa agaacaacat    720
gacttaoccta ccctagtgga gccaacgcta atattgcaag gaagatcttc tcagtatgtc    780
cctgaccgtg actcttagct cttacctttc accagaggag aaaaaaatca ctccatcgag    840
actgaagacg catttgacaa tatttaacac ccattctttt tttttttttt ttttaaagac    900
aggtctcact ctgttgccca tgctggagtg gagtgggtgcg atcacagctc actgcagcct    960
tgacctccta ggctcaagag atcctcctgc ctcagctttt g                                1001

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<210> 240
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-189-348 : polymorphic base G or A

<220>
<221> misc_binding
<222> 502..520
<223> 12-189-348.mis1, complement

<220>
<221> misc_binding
<222> 481..500

```

205

```

<223> 12-189-348.mis2, potential

<220>
<221> primer_bind
<222> 832..849
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 384..402
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-189-348 potential probe

<220>
<221> misc_feature
<222> 69,615
<223> n=a, g, c or t

<400> 240
cgaggcaggt ggatcaagtg aggtcagaag tttgagacca gcctagccaa catggtgaaa      60
ccctgtctnc taccaaaaaat ataaaaaatt agctgggtgt ggtggtgcgt gcctgtaatc      120
ccagctaatt gggaggctga ggcagaagaa tcgcttgaac ccgggaggca gaggttgcaa      180
tgagccgata tcgtgccgct gcactccagc ctgggcaaca aagtgagact ccctctcaaa      240
aaaaaaaaaa aaggactagg acaaaaatac ctactttcaa ggagttcaca gtctacagga      300
ataaacagga catgtaaatg aacaaaatag gtcccatcc tttatgaacc tactttaaaa      360
aacaaaaaac agggcaagta tatgtacagg atacaatgga agcagaaaga tccccaattc      420
tgccttactt tgggcaacaa agtaggaggt acacctcgaa ggtatgagag taaacacagg      480
ttcaactgaa gaactctaata racttggcta gaatacagta tggctagaat acagaaatgt      540
caaatgagg acttgtcggc aagggccaga agaccagtca agccctgggc ttcattgtgac      600
acaggacggt gaatnaaaaag ccgtgcagtc ctataacctg acttgcagtt cccaaagact      660
aacctgcgct gctgtactga agatacagaa tgggagggtc agggatgagg aaaacagaat      720
gggcatctaa ttccctgtaa tgtctttgct ctcccttaat ctaagcttta tgttcaaaat      780
aaaagtacca ctctcactcc acaactcccc cagtatctga agaccaccat ggcgattccc      840
taaattggcc ctcttccaa gtcagcacca cacattcccc atccactcct ccagatttca      900
gtaccctgtg tccactggca tcaaagtatg acaggcacct cggaagtggg cacagatata      960
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<210> 241
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-192-63 : polymorphic base C or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-192-63.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-192-63.mis2, potential complement

<220>
<221> primer_bind

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206

<222> 544..563
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 75..94
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-192-63 potential probe

<400> 241
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 gctggggtac cgggtcactg ttgaagacct ggaccgggag aaggaggcgg ccttccagcg 120
 catcaacagt gactgcagg ttgaggacaa ggccatctcg gactgcagac cctcacggcc 180
 ttcccacact ttgtcctcac ttgcaacagg ggcttctggt ctgcctgccg tttctaaagc 240
 acccagtatg gatgcacagc aggagacaca caagtcccaa gactgcctgg gcctactgga 300
 ccccttagca tctgctgcag ggggtccctc tacagctccc atgtctggga agaagcacag 360
 accaccaggc cccctgttct cctcctcaga tccccttctt gccacctctt ctgattccca 420
 ggactcagcc caggtcacct cgctgattcc tgcccccttc ccagctgcaa gcatggatgc 480
 gggcatgaga agaacaaggc stggcacttc tgctcctgca gctgccgcag cagccccctc 540
 ccgctccaca ttgaacccca cgttggggtc actactggag tggatggagg cccttcacat 600
 ttctgggcct cagccacagc tgcagcaggt gcccagaggt cagaaccaga gatcccagac 660
 ctccctggacc agctcgtgcc ccaaataaaa tgccatctcg agccccctaca gctctacggg 720
 aggcctcccg gaacaaaagc ggaagagggg ccagcctcat cccactgcca gctgaccctc 780
 agttcctcaa acacagttag tgaggacgga cctcaggctg tctcttcggg tcacacccag 840
 tgtgaaaaga cggcagatac agcaccaggg cagacactcg cctccagggg tggctcccc 900
 agatcccagg cctctaggcc ccgtatatgc aagtttcccc tgctgccacg caggcgaggg 960
 gagcctttga tgctgccacc tcccttagag atgggggtacc g 1001

<210> 242
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 502
 <223> 12-192-64 : polymorphic base T or C

<220>
 <221> misc_binding
 <222> 482..501
 <223> 12-192-64.mis1, potential

<220>
 <221> misc_binding
 <222> 503..522
 <223> 12-192-64.mis2, potential complement

<220>
 <221> primer_bind
 <222> 545..564
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 76..95
 <223> downstream amplification primer

<220>

207

<221> misc_binding

<222> 490..514

<223> 12-192-64 potential probe

<400> 242

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acaagtttcc cctgctgcca cgcaggcgag gggagccttt gatgctgcca cctcccttag      60
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gcatcaacag tgcactgcag gttgaggaca aggccatctc ggactgcaga ccctcacggc      180
cttcccacac tttgtcctca cttgcaacag gggcttctgg tctgcctgcc gtttctaaag      240
caccacagat ggatgcacag caggagacac acaagtccca agactgcctg ggcctactgg      300
accccttagc atctgctgca ggggtcccct ctacagctcc catgtctggg aagaagcaca      360
gaccaccagg cccctgttcc tctcctcag atccccctcc tgccacctct tctgattccc      420
aggactcagc ccaggtcacc tcgctgattc ctgccccctt cccagctgca agcatggatg      480
cgggcatgag aagaacaagg cytggcactt ctgctcctgc agctgccgca gcagccccctc      540
cccgctccac attgaacccc acgttggggg cactactgga gtggatggag gcccttcaca      600
tttctggggc tcagccacag ctgcagcagg tgcccagagg tcagaaccag agatcccaga      660
cctcctggac cagctcgtgc cccaaatgaa atgccatctc gagccccctac agctctacgg      720
gaggcctccc ggaacaaaag cgggaagagg gccagcctca tccactgcc agctgaccct      780
cagttcctca aacacagtga gtgaggacgg acctcagget gtctcttcgg gtcacaccca      840
gtgtgaaaag acggcagata cagcaccagg gcagacactc gcctccaggg gtgggtcccc      900
cagatccccc gcctctaggc cccgtatatg caagtttccc ctgctgccac gcaggcgagg      960
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<210> 243

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-192-268 : polymorphic base C or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-192-268.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-192-268.mis2, potential complement

<220>

<221> primer_bind

<222> 749..768

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 280..299

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-192-268 potential probe

<400> 243

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tgccggggct aaagcgagg agggggccag cctcatccca ctgccagctg accctcagtt      60
cctcaaagac agtgagttag gacaggcctc aggctgtctc ttcagggtcac acccagtgtg      120
aaaaggcagc agatatagca ccagggcaga cactcaccct caggaatgac tcctccacat      180
ccgaggcctc tagggccagt acacacaagt ttcccctgct gccacgcagg cgaggggagc      240

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208

ctttgatgct	gccacctccc	ttagagctgg	ggtaccgggt	cactggtgaa	gacctggacc	300
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tctcggactg	cagaccctca	cggccttccc	acactttgtc	ctcacttgca	acaggggctt	420
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cccaagactg	cctgggccta	stggaccctt	tagcatctgc	tgcaggggtc	ccctctacag	540
ctcccatgtc	tgggaagaag	cacagaccac	caggccccct	gttctcctcc	tcagatcccc	600
ttcctgccac	ctcttctgat	tcccaggact	cagcccaggt	cacctcgctg	attcctgccc	660
ccttcccagc	tgaagcatg	gatgcgggca	tgagaagaac	aaggcatggc	acttctgctc	720
ctgcagctgc	cgcagcagcc	cctccccgct	ccacattgaa	ccccacgttg	gggtcactac	780
tggagtggat	ggaggccctt	cacatttctg	ggcctcagcc	acagctgcag	caggtgcccc	840
gaggtcagaa	ccagagatcc	cagacctcct	ggaccagctc	gtgccccaaa	tgaaatgcc	900
tctcgagccc	ctacagctct	acgggaggcc	tcccggaa	aaagcggaag	agggggccagc	960
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<210> 244

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-192-334 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-192-334.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-192-334.mis2, potential complement

<220>

<221> primer_bind

<222> 815..834

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 346..365

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-192-334 potential probe

<400> 244

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gaggcttgcc	ggggctaaaag	cggaggaggg	ggccagcctc	atcccactgc	cagctgaccc	120
tcagttcctc	aaagacagtg	agtgaggaca	ggcctcaggc	tgtctcttca	ggtcacaccc	180
agtgtgaaaa	ggcagcagat	atagcaccag	ggcagacact	caccctcagg	aatgactcct	240
ccacatccga	ggcctctagg	cccagtacac	acaagtttcc	cctgctgcca	cgcaggcgag	300
gggagccttt	gatgttgcca	cctcccttag	agctggggta	ccgggtcact	ggtgaagacc	360
tggaccggga	gaaggaggcg	gccttccagc	gcatcaacag	tgactgcag	ggtgaggaca	420
aggccatctc	ggactgcaga	ccctcacggc	cttcccacac	tttgtcctca	cttgcaacag	480
gggcttctgg	tctgcctgcc	rtttctaaaag	caccagtag	ggatgcacag	caggagacac	540
acaagtccca	agactgcctg	ggcctactgg	accccttagc	atctgctgca	ggggctcccct	600
ctacagctcc	catgtctggg	aagaagcaca	gaccaccagg	ccccctgttc	tcctcctcag	660
atcccccttc	tgccacctct	tctgattccc	aggactcagc	ccaggtcacc	tcgctgattc	720
ctgccccctt	cccagctgca	agcatggatg	cgggcatgag	aagaacaagg	catggcactt	780

209

```

ctgctcctgc agctgccgca gcagccccctc cccgctccac attgaacccc acgttgggggt      840
cactactgga gtggatggag gcccttcaca tttctggggc tcagccacag ctgcagcagg      900
tgcccagagg tcagaaccag agatcccaga cctcctggac cagctcgtgc cccaaatgaa      960
atgccatctc gagccccctac agctctacgg gaggcctccc g                               1001

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<210> 245
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-192-352 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-192-352.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-192-352.mis2, potential complement

<220>
 <221> primer_bind
 <222> 833..852
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 364..383
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-192-352 potential probe

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<400> 245
ataacccgac atcccagacc tcctggacga gctcctgcac caaccgaaat gccatctcca      60
gtcctctacag ctccacggga ggcttgccgg ggctaaagcg gaggaggggg ccagcctcat      120
cccactgcc a gctgacctc agttcctcaa agacagttag tgaggacagg cctcaggctg      180
tctcttcagg tcacacccag tgtgaaaagg cagcagatat agcaccaggg cagacactca      240
ccctcaggaa tgactcctcc acatccgagg cctctaggcc cagtacacac aagtttcccc      300
tgctgccacg caggcgaggg gagcctttga tgctgccacc tcccttagag ctggggtagc      360
gggtcactgt tgaagacctg gaccgggaga aggaggcggc cttccagcgc atcaacagtg      420
cactgcaggt tgaggacaag gccatctcgg actgcagacc ctcacggcct tcccacactt      480
tgtcctcact tgcaacaggg rcttctggtc tgccctgccgt ttctaaagca cccagtatgg      540
atgcacagca ggagacacac aagtcccaag actgcctggg cctactggac cccttagcat      600
ctgctgcagg ggtcccctct acagctccca tgtctgggaa gaagcacaga ccaccaggcc      660
ccctgttctc ctccctcagat ccccttcctg ccacctcttc tgattcccag gactcagccc      720
aggtcacctc gctgattcct gcccccttcc cagctgcaag catggatgcg ggcatgagaa      780
gaacaaggca tggcacttct gctcctgcag ctgccgcagc agccccctcc cgctccacat      840
tgaaccccac gttgggggtc ctactggagt ggatggaggc ccttcacatt tctgggcctc      900
agccacagct gcagcagggt cccagagggtc agaaccagag atcccagacc tcctggacca      960
gctcgtgccc caaatgaaat gccatctcga gcccctacag c                               1001

```

<210> 246
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-194-135 : polymorphic base G or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-194-135.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-194-135.mis2, potential complement

<220>
 <221> primer_bind
 <222> 363..381
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 878..893
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-194-135 potential probe

<220>
 <221> misc_feature
 <222> 223,412,431,439..440,565..566,894
 <223> n=a, g, c or t

<400> 246
 gcgggtgat cacctgaggt taggagttcg ataccagcct ggccaacatg gtgaaacccc 60
 gtctctacaa aaaatataaa aattagtcgg gcgtgggtggc acacgcttgt gatcccagcg 120
 gctcgggagg ccgagacagg agaattgctt aggaggcaga ggggtgcagtg aaccgaggtc 180
 tcgccactgc actccagcct gggcgacaga gtgagactct gtntcaaaa aaaaaaaaaa 240
 acagctatta caatatacat gtatgttgta aaataaccaa accaacatag aagggtatat 300
 agtgaaagga gaagtattgt tgtgggtaaa attgtttcaa taaatggcta atccagtatt 360
 tttttcctcc aaaaaaacac cttttcccct ttgatttagt gtataaccaca cnagagtcgc 420
 ttagccgatt ncagtgacnn ttttttgata gctggagaat gcttcctaata ggttgcagggt 480
 gtgtaggggt tttcttgaca ktttcagtaa gaaagtgaat gttgtgccat aggaaagctt 540
 tatcacagggt gcacgttggt agccnnaact aaataacgtg agtgtcaagt acagtatcta 600
 gtgagtgagg aataactgta ataattacaa ttacagttgt agttaaagtg aagtttgtat 660
 caaaatttct gtttcaaagg tgaactttta ggaggtgtat ctgcggtgtt tcttcctcag 720
 atgtgatttc tctgaagcag tggttctcta taactgactt gacacacagt gcacttgata 780
 tttcgaatga cttaagtgat agtatcaaaa ttactatcat atacatattt aaatcacatg 840
 actaacctgt gtgtggtatt atgcaaactg ctcagctcag taagggaaca gaanataaga 900
 aaaaaaggac aatattggga gtcttttata caattcaatt tattcaattg aaggactatc 960
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<210> 247
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501

211

<223> 12-194-325 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-194-325.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-194-325.mis2, potential complement

<220>

<221> primer_bind

<222> 171..189

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 686..707

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-194-325 potential probe

<220>

<221> misc_feature

<222> 31,220,239,247..248,373..374,702

<223> n=a, g, c or t

<400> 247

tccagcctgg	gcgacagagt	gagactctgt	nctcaaaaaa	aaaaaaaaac	agctattaca	60
atatacatgt	atgttgtaaa	ataaccaaac	caacatagaa	gggtatatag	tgaaaggaga	120
agtattgttg	tgggtaaaaat	tgtttcaata	aatggctaata	ccagtatttt	tttcttccaa	180
aaaaacacct	tttccccttt	gatttagtgt	ataccacacn	agagtcgctt	agccgattnc	240
agtgacnntt	ttttgatagc	tggagaatgc	ttcctaattg	ttgcaggtgt	gtaggggttt	300
tcttgacatt	ttcagtaaga	aagtgaatgt	tgtgccatag	gaaagcttta	tcacaggtgc	360
acgttggtag	ccnnaactaa	ataacgtgag	tgtcaagtac	agtatctagt	gagtgagagaa	420
taactgtaat	aattacaatt	acagttgtag	ttaaagtga	gtttgtatca	aaatttctgt	480
ttcaaagggtg	aacttttagg	rggtgtatct	gcggtgtttc	ttcctcagat	gtgatttctc	540
tgaagcagtg	gttctctata	actgacttga	cacacagtgc	atctgatatt	tcgaatgact	600
taagtgatag	tatcaaaatt	actatcatat	acatatatta	atcacatgac	taacctgtgt	660
gtggtattat	gcaaactgct	cagctcagta	agggaaacaga	anataagaaa	aaaaggacaa	720
tattgggagt	cttttataca	attcaattta	ttcaattgaa	ggactatctt	ttctttaaaa	780
aagttctgct	ttcttggtgt	taaaataaag	catcttttat	gaaatgatgg	tgatagtaaa	840
tggtgatata	tggtaaacgt	aaatagtaaa	tgcaagggtg	gttattgtga	tttttaaaaa	900
taaagagagc	cgagaatctc	ttgttttctc	gctgctgtta	gggagttcag	gaaaaagttc	960
ctggggcttt	tgctgttaag	aagattcaaa	tatagagtat	t		1001

<210> 248

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-194-337 : polymorphic base A or G

<220>

<221> misc_binding

212

```

<222> 481..500
<223> 12-194-337.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-194-337.mis2, potential complement

<220>
<221> primer_bind
<222> 159..177
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 674..695
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-194-337 potential probe

<220>
<221> misc_feature
<222> 19,208,227,235..236,361..362,690
<223> n=a, g, c or t

<400> 248
gacagagtga gactctgtnc tcaaaaaaaaa aaaaaaacag ctattacaat atacatgtat      60
gttgtaaaat aaccaaacca acatagaagg gtatatagtg aaaggagaag tattgttgtg      120
ggtaaaattg tttcaataaa tggctaatacc agtatttttt tcttccaaaa aaacaccttt      180
tcccctttga tttagtgtat accacacnag agtcgcttag ccgattncag tgacnntttt      240
ttgatagctg gagaatgctt cctaatagggt gcagggtgtgt agggggttttc ttgacatttt      300
cagtaagaaa gtgaatgttg tgccatagga aagctttatc acagggtgcac gttggtagcc      360
nnaactaaat aacgtgagtg tcaagtacag tatctagtga gtggagaata actgtaataa      420
ttacaattac agttgtagtt aaagtgaagt ttgtatcaaa atttctgttt caaagggtgaa      480
cttttaggag gtgtatctgc rgtgtttctt cctcagatgt gatttctctg aagcagtggt      540
tctctataac tgacttgaca cacagtgcac ctgatatttc gaatgactta agtgatagta      600
tcaaaattac tatcatatac atattttaa cecatgacta acctgtgtgt ggtattatgc      660
aaactgctca gctcagtaag ggaacagaan ataagaaaaa aaggacaata ttgggagtc      720
ttatataaat tcaatttatt caattgaagg actatctttt ctttaaaaaa gttctgcttt      780
cttggtgtta aaataaagca tcttttatga aatgatgggtg atagtaaagt gtgatatatg      840
gtaaacgtaa atagtaaagt caagggtagt tattgtgatt tttaaaaata aagagagccg      900
agaatctctt gttttcctgc tgctgttagg gagttcagga aaaagttcct ggggcttttg      960
ctgttaagaa gattcaaata tagagtattt ctaagagta a                                1001

<210> 249
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-194-479 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-194-479.mis1, potential

<220>

```

213

```

<221> misc_binding
<222> 502..521
<223> 12-194-479.mis2, potential complement

<220>
<221> primer_bind
<222> 17..35
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 532..553
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-194-479 potential probe

<220>
<221> misc_feature
<222> 66,85,93..94,219..220,548
<223> n=a, g, c or t

<400> 249
gctaattccag tatTTTTtttc ctccaaaaaa acaccttttc ccttttgatt tagtgatac      60
cacacnagag tcgcttagcc gattncagtg acnntttttt gatagctgga gaatgcttcc      120
taatggttgc aggtgtgtag gggttttctt gacattttca gtaagaaagt gaatgttggt      180
ccataggaaa gctttatcac aggtgcacgt tggtagccnn aactaaataa cgtgagtgtc      240
aagtacagta tctagtgagt ggagaataac tgtaataatt acaattacag ttgtagttaa      300
agtgaagttt gtatcaaaat ttctgtttca aagggtgaact tttaggaggt gtatctgcgg      360
tgtttcttcc tcagatgtga tttctctgaa gcagtggttc tctataactg acttgacaca      420
cagtgcattc gatatttcga atgacttaag tgatagtatc aaaattacta tcatatacat      480
atttaaatac catgactaac ytgtgtgtgg tattatgcaa actgctcagc tcagtaaggg      540
aacagaanat aagaaaaaaa ggacaatatt gggagtcttt tatacaattc aatttattca      600
attgaaggac tatcttttct ttaaaaaagt tctgctttct tggtgttaaa ataaagcatc      660
ttttatgaaa tgatggtgat agtaaatggt gatatatggt aaacgtaaat agtaaatgca      720
agggtagtta ttgtgatttt taaaaataaa gagagccgag aatctcttgt tttcctgctg      780
ctgttaggga gttcaggaaa aagtccctgg ggcttttgct gttagaaga ttcaaatata      840
gagtatttct taagagtaaa tatgagttaa ttttgagatc attggtcaca gtctactgag      900
aaatccactg agaaagctgt taaatttgca tggcattaaa gatgttccta ttctgatcat      960
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<210> 250
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-442-133 : polymorphic base G or C

<220>
<221> misc_binding
<222> 482..500
<223> 10-442-133.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-442-133.mis2, potential complement

```

214

<220>
 <221> primer_bind
 <222> 369..386
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 777..794
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-442-133 potential probe

<400> 250
 ggcagagttg ggaaatgcag cctgcacagg tgtgttcagg tggccggtga tatgtcaccc 60
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 cagaggccag gagctcggaa gccccagggt cccagtggcc gccctgactg cctggcctct 180
 ccccgcaaaa ctccaggcac aatgacctcc cctggcagct gctggatatg ttcaacaacc 240
 ggctgcagga cgaggggcc aacctgacca ccttgccggg cacacacacc aacatcccca 300
 agctgagggc cggctttgtg ggaggccagg taccgcctgc cctgccttgt gcttgccctg 360
 tgtggggtca tcccgtctcc tacctcaggc ctggctacag tgggaccatc cctgtggtgt 420
 tctccagggt tccctcgggt cccaggccga gggagggtt cccagcgggt gggaaaccag 480
 actcccacag gcatgcgggg sgtgggctga gacctggctg catcagctcc tggcaccccc 540
 tgcggcccac agttctggtc cgtgtacacg ccctgcgaca cccagaacaa agacgccgtg 600
 cggaggacgc tggagcagat ggacgtggtc caccgcattg gccggatgta cccggagacc 660
 ttctgtatg tcaccagcag tgcagggtgg gtctcgacct gggctcctcca ggtcctgcgt 720
 cttctcaccc agccctcatc ctgagcagca ggtgccggtc aggacacctc accctccaga 780
 taccaggtgc cactccctgc gcacctgac tctccccgca ggcattcggc aggccctccg 840
 ggaagggaaag gtggccagcc tgatcggcgt ggagggcggc cactccattg acagcagttt 900
 gggcgtcctg cgggcactct atcagctggg catgcggtac ctgaccctca cccacagctg 960
 caacacgccc tgggtgcgtga ctccccatgg gagggccccc g 1001

<210> 251
 <211> 984
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 484
 <223> 10-444-248 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 464..483
 <223> 10-444-248.mis1, potential

<220>
 <221> misc_binding
 <222> 485..503
 <223> 10-444-248.mis2, complement

<220>
 <221> primer_bind
 <222> 237..253
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 567..586
 <223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 472..496
<223> 10-444-248 potential probe

<400> 251
gcattcggca ggccttccgg gaagggaagg tggccagcct gatcggcgtg gagggcggcc 60
actccattga cagcagtttg ggcgtcctgc gggcactcta tcagctgggc atgcggtacc 120
tgaccctcac ccacagctgc aacacgccct ggtgcgtgac tcccatggg agggccccgg 180
gctgtggtca ggaggaggg ggcagacact ccctgccacc ctccagagcc catccccctc 240
gcctgtgagt cccaggccgg gcctcgctg ctgggctgat gggaggccga gaccaccgct 300
cacctcttgg gcacctgcct ttgcttctc cagggctgac aactggctgg tggacacggg 360
agacagcgag cccagagcc aaggcttgtc accctttggg caggtgagtg gggaggagc 420
ggccagtac ccccgaggag aaggcagagg ccctggaggg tgaccagaac aatgcatctc 480
ctcrcgtggg acctcagtgt ccttgtctgt aaaatggagc tggcagccat cccccaggg 540
tgggtgtga gccctgagtg gcccgggact tccagccacg aaggatgatg actcacatct 600
ggtccagccc gtccacctcc gcagccccga ccctgggggc tgtgaggggtg gacggagccc 660
tgtcttccca gcgtgtggtg aaggagctga accgtctggg ggtcctcatc gacttggtc 720
acgtgtctgt ggcaccatg aaggccaccc tgcaactgtc cagagccccg gtcatttca 780
gccactcctc ggcctacagc gtgtgcgcaa gccggcgcaa cgtgcctgac gacgtcctga 840
ggctggtggt gagggccgag ggggcgacct ccaccccgcc tccctgggca ggccctccca 900
gctctcagct tcacctgtc ttccttcttg tgcagaaaca gacagacagc ctggtgatgg 960
tgaacttcta caacaattac attt 984

<210> 252
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-445-281 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 10-445-281.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-445-281.mis2, potential complement

<220>
<221> primer_bind
<222> 221..238
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 624..641
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-445-281 potential probe

<220>
<221> misc_feature
<222> 926,936,957,960,972

216

<223> n=a, g, c or t

<400> 252

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cgggagacag cgagccccag agccaaggct tgtcaccctt tgggcagggtg agtgggggtgg      60
gagcggccag tcacccccga ggagaaggca gaggcccttg aggggtgacca gaacaatgca      120
tctcctcgcg tgggacctca gtgtccttgt ctgtaaaatg gagctggcag ccatcccccc      180
agggtgggtg ctgagccctg agtggccccg gacttcacgc cacgaaggat gatgactcac      240
atctggtcca gcccgtcac ctccgcagcc ccgaccctgg gggctgtgag ggtggacgga      300
gccctgtctt cccagcgtgt ggtgaaggag ctgaaccgtc tgggggtcct catcgacttg      360
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ttcagccact cctcggccta cagcgtgtgc gcaagccggc gcaacgtgcc tgacgacgtc      480
ctgaggctgg tggtgagggc ygagggggcg acctccaccc cgcctccctg ggcaggccct      540
cccagctctc agcttcaccc tgtcttcctt cttgtgcaga aacagacaga cagcctggtg      600
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gccggtagggt ggggtgtgag cgcccaaggg ggccgaaggg ggagggcctc actcgggacc      720
catacctgct gctccctgga cagaccatct ggatcacatc aaggagggtg caggagccag      780
agccgtgggt tttgggtggg actttgatgg tgttccaagg taaggggctg agagctctgt      840
cctgtggatg agccgggagg ttcattggcct cgtcagaggg atgagggtggc tggaggaggg      900
acctgtgtcc tagtgtgggg gccangttc tcctgncctc aacacagggt ccttganggn      960
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```

<210> 253

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-668-362 : polymorphic base T or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-668-362.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-668-362.mis2, potential complement

<220>

<221> primer_bind

<222> 844..861

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 390..410

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-668-362 potential probe

<400> 253

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cccagctgct gtgacacca aggggagggc cggcgctccc gaagccagggt cagccgtgca      120
cccggcagag ccccgcatat tggccccagc agagcttggg gtgggggggag ctcgggtgtca      180
ccaacaggcc cttgaggaca ctcgtgtgga gaatccctgg gacacgtgga ggacccccaa      240
gtcctgagcc ccgtactccg tactgcaggg agcaggccag gagccacggg ccttgggggca      300
cagggtcctt ctcagggaca ggttcaggca ctggctggaa caggctggac ccctctaccc      360

```

217

```

agcacatgtg ggcattgcgtc tgggttccga ggggtgggaa atgtggaaag gctcctgctg 420
gccggcttag gcctgctgcc cttggagcct tccatataca gagagtccca cctccagcaa 480
gggttggcct ggactctcca wccccctgct gtgcccagga ctccccagg gacaaggcaa 540
ccagaggccc agaccctcc ccagcaaaga gaagcaccac gggagctgtc tccaagagc 600
ccttgacctg gggcccagct ggcctagggc cgggcccccg ggctgttgta gagcagagtg 660
tccatctgtg cacgctgtag ccacaagcgc cgctgggctg cgccaagcag cacacgcagc 720
gagtggcctg gacggcaggc gggcagggct gcacagtggg cagcatgcag ctggcgacag 780
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gggggctccg agacagacct ataggctgag gctggtaccc cctctgcccc aatacgctc 900
gggctggccg ctgcagagct ttcaggggtg gccagggtccc caggcctact cagctcacgg 960
cgcagagaga ggaaggagaa ggcggaaggt tcagggtcca g 1001

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<210> 254

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-670-48 : polymorphic base G or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-670-48.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-670-48.mis2, potential complement

<220>

<221> primer_bind

<222> 454..474

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 883..901

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-670-48 potential probe

<220>

<221> misc_feature

<222> 49,105,142,317

<223> n=a, g, c or t

<400> 254

```

cttttctgga cattccatgg aaagggaact gcaacatgag tggctcttnc ctctggcttg 60
tctcactcag tgtccacact ttgggactcc ttcacgggtgt ggcangggag tcagcagcct 120
gctcctcact gtcgctcagc cngtcaactgc atggagagcg tgcacacttc attttatctg 180
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ttccgttact ggcagangtc ctgcccactc ccatgcttca cagctccctc cagccccctgg 360
tgaatttgca ccattgaatg agtcctgcag aggcctgggca ggcgaagcct tcctgggaaa 420
ggtttccttg ctaatatgaa gcaaggagca atgcctttgc agtagatgca gtcctgcctg 480
cgtgtggggg gctgtacact satcgggggc tgtggacact gagagtgggc aagaagagac 540
acgcaaagtc tttgatgtca ctggtgtgct aacaagccaa cctggaagct ccacctctga 600

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218

```

cccttcattc gtgagacatt aaatccctgt gttaaagctg cgttttagtga gcttttctgt 660
aactttcagc taaaagcacc gtgacagaca ggtagcattt tccaaactgc caccgaagg 720
tgatgctatt cctgcagggt tccatcctcc ggtggggggg tgcgccctcc tgtgaggggt 780
tccaccctcc agtgggagggt tccaaagttg ggaattcaaa tccaagtctt tcttccaagt 840
ccaaggccca gagcctccta ctttcagccc ttgatcctac aagcgtgtca gtgtgaagca 900
gtccaggccc agtcctctct cctagcaggc cagtcatccc cctgacattc tttcttctct 960
gacccgagtg gttctctctt tattattttt ttttttttct g 1001

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<210> 255

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-670-91 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-670-91.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-670-91.mis2, potential complement

<220>

<221> primer_bind

<222> 411..431

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 840..858

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-670-91 potential probe

<220>

<221> misc_feature

<222> 6,62,99,274

<223> n=a, g, c or t

<400> 255

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tcttttncctc tggcttgtct cactcagtgt cccacctttg ggactccttc acggtgtggc 60
angggagtca gcagcctgct cctcactgtc gctcagcng tcaactgcatg gagagcgtgc 120
acacttcatt ttatctgtct aaactctgtt ctcactcttg ctctgtctgt ttcccttcat 180
gtccaccttc cccccacc ctctggtgtg acagacactg ctggggccct tccaacaggc 240
ggctctcctt cccccacttc cgttactggc agangtcttg cccactccca tgcttcacag 300
ctccctccag cccctggtga atttgcacca ttgaatgagt cctgcagagg ctgggcaggc 360
gaagccttcc tgggaaagggt ttccttgcta atatgaagca aggagcaatg cctttgcagt 420
agatgcagtc ctgcctgcgt gtggggggct gtacactcat cgggggctgt ggacactgag 480
agtggtaag aagagacacg yaaagtcttt gatgtcactg ttgtgctaac aagccaacct 540
ggaagctcca cctctgaccc ttcattcgtg agacattaaa tccctgtgtt aaagctgcgt 600
ttagttagct tttctgtaac tttcagctaa aagcaccgtg acagacagggt agcattttcc 660
aaactgccac ccaagggtga tgctattcct gcagggttcc atcctccggt gggggggttc 720
gccctcctgt gaggggttcc accctccagt gggaggttcc aaagttggga attcaaatec 780
aagtctttct tccaagtcca aggccagag cctcctactt tcagcccttg atcctacaag 840

```

219

```

cgtgtcagtg tgaagcagtc caggcccagc tcctctgcct agcaggccag tcatccccct    900
gacattcttt cttgtctgac ccgagtgggt ctctccttat ttttttttt tttttctgag    960
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<210> 256

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-670-157 : polymorphic base C or T.

<220>

<221> misc_binding

<222> 482..500

<223> 12-670-157.mis1

<220>

<221> misc_binding

<222> 502..521

<223> 12-670-157.mis2, potential complement

<220>

<221> primer_bind

<222> 345..365

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 774..792

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-670-157 potential probe

<220>

<221> misc_feature

<222> 33,208

<223> n=a, g, c or t

<400> 256

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gtcagcagcc tgctcctcac tgtcgctcag ccngtcactg catggagagc gtgcacactt    60
cattttatct gctgaaactc tgttctcact cttgctctgc tgttttccct tcatgtccac    120
cttctcctcc caccctctgg tgtgacagac actgctgggg cccttccaac aggcgggtcct    180
ccttccccca cttccgttac tggcagangt cctgcccact cccatgcttc acagctccct    240
ccagcccttg gtgaatttgc accattgaat gagtcttgca gaggctgggc aggcgaagcc    300
ttcctgggaa aggtttcctt gctaatatga agcaaggagc aatgcctttg cagtagatgc    360
agtctgcctt gcgtgtgggg ggctgtacac tcatcggggg ctgtggacac tgagagtggg    420
caagaagaga cagcaaaagt ctttgatgac actgttgtgc taacaagcca acctggaagc    480
tccacctctg acccttcatt ygtgagacat taaatccctg tgttaaagct gcgttttagt    540
agcttttctg taactttcag ctaaaagcac cgtgacagac aggtagcatt ttccaaactg    600
ccacccaagg gtgatgctat tcctgcaggg ttccatcctc cgggtgggggg ttgcgccttc    660
ctgtgagggg ttccaccctc cagtgggagg ttccaaagt gggaattcaa atccaagtct    720
ttcttccaag tccaaggccc agagcctcct actttcagcc cttgatccta caagcgtgtc    780
agtgtgaagc agtccaggcc cagctcctct gcctagcagg ccagtcattc ccctgacatt    840
ctttcttgct tgaccgaggt ggttctctcc ttattatttt tttttttttc tgagacagag    900
tctcactctg tagcccaggc tggagtgcag tgggtcgatc tcgctcaccg ctacttctgc    960
ctcccgggtc ccggttcaag gttcgagcaa ttctcctgcc t                                1001

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220

<210> 257
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-671-148 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-671-148.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-671-148.mis2, potential complement

<220>
 <221> primer_bind
 <222> 354..372
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 784..804
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-671-148 potential probe

<220>
 <221> misc_feature
 <222> 31,33,37,88,270,348,764
 <223> n=a, g, c or t

<400> 257
 agcggcctcc ctcagctggt gtcggagtgc ncngccntgg aggagtcat ccacgagggg 60
 tagaccctgg cgggtcaggg tgggggtncct ctgtgcgaag agcagggacc tcatccctca 120
 acctaaacgg tggttgctcag tagcagctgg ggagggtagc gtgtgggtcc gtcacagcca 180
 tgcccttcggg cagccctgt gggctccact gtgcagagt cctgctgcca catgtcccgt 240
 ggcccttcgc ttagctcagc ctctcccagn acagcaggag ctgggggctg tcccctgagc 300
 agcatctgcc tggggagggg ataaggatcc agtgccatcc ctggctcnta ccgtccaagg 360
 acgagcacat agtgggtggg aaaggcctcc tctagcccag ccgcccctgac agccccacct 420
 gccaccctc agcaccaggg tcctgaactg ggagggcaga cactaccttc tggagggccg 480
 ggggtgtcct tctgttcgtt yagatgacac cggctgcccc tgccatccat gcaggtacct 540
 gatcggagag gagggtact gcctcacatc actgcagagt gccctgagct acgtggagct 600
 gctgccccgg ggaggcctgg ccaagtagta cagctagagc ccaggggtccc tgcagggcct 660
 ggccctgcct ccagggctg tctctcctac acctggagcc atgggatcta ctgaggacca 720
 tcctggagcc tcacgtgct ctgcacatgg tgggggcttg tccnactgtg gtgtgctctc 780
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 ccgacagaat ggggtcgaat cagctccagg aggaaccagg ccctgctctc ctgtgtaggc 900
 ctcagagagg ccaagaaggg aagctttggg cttcgggtgg tgcaggctca gcgatgaaca 960
 tctggctggg gcagctcctg gggagcatca ggggaagagg g 1001

<210> 258
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

221

<220>
 <221> allele
 <222> 253
 <223> 12-679-245 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 233..252
 <223> 12-679-245.mis1, potential

<220>
 <221> misc_binding
 <222> 254..273
 <223> 12-679-245.mis2, potential complement

<220>
 <221> primer_bind
 <222> 9..29
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 439..458
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 241..265
 <223> 12-679-245 potential probe

<220>
 <221> misc_feature
 <222> 257..258,678,798
 <223> n=a, g, c or t

<400> 258
 tgcccactta cttcctttct gggtaaggct caaaggactc gtccgaagac tgggcatttt 60
 gcttcttgct attttcatct tcaactcaaga cgtctctagg aattaagaga gaatcttcag 120
 caaagccctg ggcctgggca gtgacagacc caacacgacc tcctgcctaa agataccaaa 180
 tggaccccca tgtcccatcat ttgagttctt ctgaaaatgt cttaaatcta aaatcccca 240
 atttccaatc ccrtttnncg aacacaaaagg gccagccagg ctcacaagcc agcaatcccc 300
 acaagccatg tgctctgggc accaggacac tggacttgga aacagccctt tccacagcgg 360
 cccagaaggg gtggaggcgc tcaaaggtag cttcctgcta agcagacttt gagaaatcga 420
 ccacctcacc ccataactgc gaacctatg caactgatgg gtttgccatg agtcacttct 480
 aagttcacaa aagtggctgg gtgcagaggc taactcctgt aatcccagca cttcgggagg 540
 ctgacgtagg tggatcgcat gaggtcagga gttcaagacc agcctggcca ataccgtgaa 600
 accccgtctc tactaaaaat acaaaaattg gccgggtgcg gtggctcaca cctgtaatcc 660
 cagcactttg ggaggcanga ggcgggcgga tcacgaggtc aggagatcaa gaccatcccc 720
 gctaacaaaag tgaaaccccg tctctactaa aaatacaaaa aattagccgg gcgtggtggc 780
 ggggtgcctgt agtcccangc gactcagaag ctgaggcccg agaattggcgt gaacccggga 840
 ggcagagctt gcagtaggcc gagattgtgc cactgcactc cagcctgggc aacacagcga 900
 gactccgtct caaataaaaa aaaaataaat aaatacaaaa cttagctggg tgtggtggcg 960
 ggcgcctgta atcccagcta ctcgggaggc tgaggcggga g 1001

<210> 259
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 379

222

<223> 12-679-371 : polymorphic base A or G

<220>

<221> misc_binding

<222> 359..378

<223> 12-679-371.mis1, potential

<220>

<221> misc_binding

<222> 380..399

<223> 12-679-371.mis2, potential complement

<220>

<221> primer_bind

<222> 9..29

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 439..458

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 367..391

<223> 12-679-371 potential probe

<220>

<221> misc_feature

<222> 257..258,678,798

<223> n=a, g, c or t

<400> 259

tgcccaactta	cttcctttct	gggtaaggct	caaaggactc	gtccgaagac	tgggcatttt	60
gcttcttgtc	attttcatct	tcactcaaga	cgtctctagg	aattaagaga	gaatcttcag	120
caaagccctg	ggcctgggca	gtgacagacc	caacacgacc	tcctgcctaa	agataccaaa	180
tggacccccca	tgtcccacat	ttgagttctt	ctgaaaatgt	cttaaatcta	aaatccccaa	240
atttccaatc	ccatttnncc	aacacaaaag	gccagccagg	ctcacaagcc	agcaatcccc	300
acaagccatg	tgctctgggc	accaggacac	tggacttgga	aacagccctt	tccacagcgg	360
cccagaaggg	gtggaggcgc	tcaaaggtag	cttcctgcta	agcagacttt	gagaaatcga	420
ccacctcacc	ccataactgc	gaacctatg	caactgatgg	gtttgccatg	agtcacttct	480
aagttcacaa	aagtggctgg	gtgcagaggc	taactcctgt	aatcccagca	cttcgggagg	540
ctgacgtagg	tggatcgcat	gaggtcagga	gttcaagacc	agcctggcca	ataccgtgaa	600
accccgctctc	tactaaaaat	acaaaaattg	gccgggtgcg	gtggctcaca	cctgtaatcc	660
cagcactttg	ggaggcanga	ggcgggcgga	tcacgagggtc	aggagatcaa	gaccatcccc	720
gctaacaaaag	tgaaaccccg	tctctactaa	aaatacaaaa	aattagccgg	gcgtggtggc	780
gggtgcctgt	agtcaccangc	gactcagaag	ctgaggccgg	agaatggcgt	gaaccgggga	840
ggcagagctt	gcagtaggcc	gagattgtgc	cactgcactc	cagcctgggc	aacacagcga	900
gactccgtct	caaataaaaa	aaaaataaat	aaatacaaaa	cttagctggg	tgtggtggcg	960
ggcgccctgta	atcccagcta	ctcgggaggc	tgaggcgggg	g		1001

<210> 260

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 434

<223> 12-679-426 : polymorphic base C or T

<220>

<221> misc_binding

223

<222> 414..433
 <223> 12-679-426.mis1, potential

 <220>
 <221> misc_binding
 <222> 435..454
 <223> 12-679-426.mis2, potential complement

 <220>
 <221> primer_bind
 <222> 9..29
 <223> upstream amplification primer

 <220>
 <221> primer_bind
 <222> 439..458
 <223> downstream amplification primer, complement

 <220>
 <221> misc_binding
 <222> 422..446
 <223> 12-679-426 potential probe

 <220>
 <221> misc_feature
 <222> 257..258,678,798
 <223> n=a, g, c or t

<400> 260
 tgcccactta ctctctttct gggtaaggct caaaggactc gtccgaagac tgggcatttt 60
 gcttcttgct attttcatct tcaactcaaga cgtctctagg aattaagaga gaatcttcag 120
 caaagccctg ggctctgggca gtgacagacc caacacgacc tcctgcctaa agataccaaa 180
 tggacccccca tgtcccacat ttgagttctt ctgaaaatgt cttaaatcta aaatccccaa 240
 atttccaatc ccatttnncg aacacaaagg gccagccagg ctcacaagcc agcaatcccc 300
 acaagccatg tgctctgggc accaggacac tggacttggg aacagccctt tccacagcgg 360
 cccagaaggg gtggaggcgc tcaaaggtag ctctctgcta agcagacttt gagaaatcga 420
 ccacctcacc ccayaactgc gaaccttatg caactgatgg gtttgccatg agtcacttct 480
 aagttcacaa aagtggctgg gtgcagaggg taactcctgt aatcccagca cttcgggagg 540
 ctgacgtagg tggatcgcat gaggtcagga gttcaagacc agcctggcca ataccgtgaa 600
 acccgtctc tactaaaaat acaaaaattg gccgggtgcg gtggctcaca cctgtaatcc 660
 cagcactttg ggaggcanga ggcgggcgga tcacgaggtc aggagatcaa gaccatccc 720
 gctaacaaag tgaacccccg tctctactaa aaatacaaaa aattagccgg gcgtggtggc 780
 ggggtgcctgt agtcccangc gactcagaag ctgaggccgg agaatggcgt gaacccggga 840
 ggagagctt gcagtaggcc gagattgtgc cactgcactc cagcctgggc aacacagcga 900
 gactccgtct caaataaaaa aaaaataaat aaatacaaaa cttagctggg tgtggtggcg 960
 ggcgccgtga atcccagcta ctcgggaggc tgaggcggga g 1001

<210> 261
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

 <220>
 <221> allele
 <222> 503
 <223> 12-680-331 : polymorphic base C or T

 <220>
 <221> misc_binding
 <222> 483..502
 <223> 12-680-331.mis1, potential

 <220>

224

<221> misc_binding
 <222> 504..523
 <223> 12-680-331.mis2, potential complement

<220>
 <221> primer_bind
 <222> 173..192
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 645..665
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 491..515
 <223> 12-680-331 potential probe

<400> 261
 ggtaagagga tcctctaggt gggggggggg gggtcccccag gtgagggggac ctccaggttaa 60
 gaggatcctc taggtggggg agtccccccag gtgaagggcc ctccaggttaa gagggtcctc 120
 caggtgagag ggtcctccag cggagggggg cccccaggta agagggtcct ccagttggga 180
 gtccttcagg tgggggtggtc ctccaggtga gagagtcttc caggtgagag ggtcctccag 240
 gtgagaggtg aaggtgaagg tcctccaggt gagggtcagg tcaacttggtc cagggatgtg 300
 gcttcagcaa gcatttggtt gcctcctctg tgttcaggac atgggggactc cgggagactg 360
 aaggaagcaa gtggcaatgt ccatgccgtc aagttctgtc acagaaataa gcaggagtga 420
 gtgaaagaca ggagagaagc tctgtgaggg gtggcattca agcttagctt ctgggcagga 480
 agaggcagct atgtcagcat tcyctaacaa ggtttggtcaa agtagatacc tccccctact 540
 catggaagac ctgacttccc aggctggttag aagcttctct cacaggcacc tgcctctcca 600
 atctctttca cagcccagcc ctggaaggtg gaaaaagaaa agttgacatg gaatgttttag 660
 gaagcaccat tgggtccaggt ccaggatcgg ggcagccagc atgtcctcta atctggcttc 720
 actgttgaaa tccagtcgag caagcagggc ccaaaccact gcgagaccag ctcggtcggg 780
 cccaaaccac cgcccactgc gggaccagct cggtcggggc caaaccaccg cccactgcgg 840
 gaccagctcg gtcgggcca aaccactgcc cactgcggga ccagctcggg cggtggagacc 900
 ctaaccacagc ggcgctagag gaattaaaga aacacacaca gaaatatagg gtgtggagtg 960
 ggaaatcagg ggtctcacag ccttcgaagc tgaaagcctc g 1001

<210> 262
 <211> 384
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 154
 <223> 10-151-154 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 134..153
 <223> 10-151-154.mis1, potential

<220>
 <221> misc_binding
 <222> 155..173
 <223> 10-151-154.mis2, complement

<220>
 <221> primer_bind
 <222> 1..18
 <223> upstream amplification primer

225

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<220>
<221> primer_bind
<222> 367..384
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 142..166
<223> 10-151-154 potential probe

<220>
<221> misc_feature
<222> 346..347
<223> n=a, g, c or t

<400> 262
actcaamacc caaggagccc attctctccc ttggctttct ctcagggtcaa ggtgttgaaa      60
tgcattctcag aggtgcaggc caacaatgtg gtcctgggcc agtacgtggg gaaccccgat      120
ggagagggcg aggccaccaa aggggtacctg gacracccca cggtgccccg cgggtccacc      180
accgccactt ttgcagccgt cgtcctctat gtggagaatg agaggtggga tggtaggtga      240
tgccttcgag gccagcaag gcagaactgg gcatgccctg tgtgcgggca ctggagctcc      300
cactgagaca ctacgcact ggtccacacc ctgagagagc tggtgnnag gctgcccttt      360
ccgccacgta ggggtgccct tcat                                           384

<210> 263
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 205
<223> 10-138-206 : polymorphic base C or T

<220>
<221> misc_binding
<222> 186..204
<223> 10-138-206.mis1

<220>
<221> misc_binding
<222> 206..225
<223> 10-138-206.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 193..217
<223> 10-138-206 potential probe

<220>
<221> misc_feature
<222> 243
<223> n=a, g, c or t

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226

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<400> 263
atgatgmcca agaagccggg catgttcttc aacccccgagg agtcggagct ggacctgact    60
acggcaacag atacaagggtg ccctacagag aaggagcagt gtggaggggtg ggcggcctgg    120
gcccggggga ctccacatgg tggcaggcag tggcatcagc aagacactct ctccctcaca    180
gaacgtgaag ctccctgacg cctaygagcg cctcatcctg gacgtcttct gcgggagcca    240
gangcacttc gtgcgcaggt gaggcccagc tgccggcccc tgcatacctg tgggctatgg    300
ggtggccttt gccctccctc cctgtgtgcc accggcctcc caagccatac tatgtcccct    360
cagcgacgag ctccgtgagg cctggcgat tttcacccca ctgctgcacc agattgagct    420
ggagag                                           426

<210> 264
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 351
<223> 10-138-352 : polymorphic base C or T

<220>
<221> misc_binding
<222> 332..350
<223> 10-138-352.mis1

<220>
<221> misc_binding
<222> 352..371
<223> 10-138-352.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 339..363
<223> 10-138-352 potential probe

<220>
<221> misc_feature
<222> 243
<223> n=a, g, c or t

<400> 264
atgatgmcca agaagccggg catgttcttc aacccccgagg agtcggagct ggacctgact    60
acggcaacag atacaagggtg ccctacagag aaggagcagt gtggaggggtg ggcggcctgg    120
gcccggggga ctccacatgg tggcaggcag tggcatcagc aagacactct ctccctcaca    180
gaacgtgaag ctccctgacg cctacgagcg cctcatcctg gacgtcttct gcgggagcca    240
gangcacttc gtgcgcaggt gaggcccagc tgccggcccc tgcatacctg tgggctatgg    300
ggtggccttt gccctccctc cctgtgtgcc accggcctcc caagccatac yatgtcccct    360
cagcgacgag ctccgtgagg cctggcgat tttcacccca ctgctgcacc agattgagct    420
ggagag                                           426

<210> 265
<211> 1001

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227

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-586-414 : polymorphic base A or G

<220>
<221> misc_binding
<222> 482..500
<223> 12-586-414.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-586-414.mis2, potential complement

<220>
<221> primer_bind
<222> 88..107
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 552..572
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-586-414 potential probe

<400> 265
gtggtcagct atcccaaggc tcttggtgt tgacatttta tggtcagctt gcacttctct 60
ttctctctct tagtgctgc aacttctcac ccacactttc aacagagaat tcagccaggt 120
gcacggcagc gtcagtgc gtaagggtgag cacattgc gtaattttta gccagtatgt 180
tgataactga tttctccaca gcagcccaga ttacctatc ctgggttttg ctgcttttaa 240
gcaactgtc atgggcatag cattgtattt gaaaatttat gacatactgc tctgggtatc 300
attctaattt ttcagagtcc gaacactgac ttctgaagat aaaagtactc ctttgtgtct 360
cttagagtga ttatcagatg ggaaacattt tggctttttc atgactcctt tggaggagaa 420
tattctatgg ggaggtggta tgttattctt tgccagggtg caaggaaacc ctgaggttcc 480
tgggtggcata aagttttatt racttcaaca aagagtgaag taaacacttc agagaatttc 540
tgtgttatc actcaattct agtcagcttg accttaaacc ctcccggctc attcctgcct 600
tgggggtctt gcacacctac tatttctttg cctggaattg ctttctcca ggtattgcc 660
tggttggctc cttacctct ttcatctttc tactccatta tcacctctg tgagtcgact 720
ctgttaacac ctgataataa atctgacagc tgtctgaaac tttctaccta cccctctttc 780
ctgctttatt ttttgcata gcactaatta ctacctgatg ctttttaaag tgtttgttga 840
gtggtttatt gtctgtctta agctccaggg aggcagatcc tctgccatat tattagaaca 900
atgcctagta catggaaggc gcaccactgt aataccactt atattaattc aggggctggg 960
tgtgggtggtg catacctgta atcccagcac tttgggaggg c 1001

<210> 266
<211> 999
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-587-379 : polymorphic base C or A

<220>

228

<221> misc_binding
 <222> 479..498
 <223> 12-587-379.mis1, potential

<220>
 <221> misc_binding
 <222> 500..519
 <223> 12-587-379.mis2, potential complement

<220>
 <221> primer_bind
 <222> 857..877
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 478..498
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 487..511
 <223> 12-587-379 potential probe

<400> 266
 cagcactttt ctagctctcc cggtcccat ctccattgct ctgtactctt ttcttttttc 60
 ttgtgctgag aatctcgta gtagcatgtg gcctaacaaa aggaaaaaat gtttttaaac 120
 acacacacac acacacacac atacacagac aaaaacacaa aaactctgag 180
 gggatctggt gaatctcaa attattgtgg gtgtactttg gcttcctttt gtatgatagg 240
 tccccatcat gaccacctct gatgtctgtg ctgctgtcac caggcacctt tgtttttcaa 300
 gacaacatac ttttttttcc ttttctctgt ttgtgatatc actttaattt ttcttgggtg 360
 gcttagagac taaggaggga gacatctggc ctttttagaa cctgagagga aaaaaagagt 420
 ctttttttcc cctctgtctc tttttgcat ggctaattcc tgcatttcca ttcagggaaa 480
 aggtggtagt gtagcatagma ctgcaacagt tatattctga gtcaaagttg gggcttttta 540
 cggcataatt atggaatttt tatttactgg tagagaggag acgagaggct ttttcagtgg 600
 gcctgggaca gtggctgctc ttgactttgt gtgaaggga atgccaagga tgcttctggt 660
 ggacttcagg ggacccagg gtttgccgt gggccgtgat ggcagcaggc ggtgggatgc 720
 ttgtagctcc tcacagcagg attcctgcc actgtttttt ctctgttggg agggaagctc 780
 ttttctagga gtgtctcagt tctgcttttg gcattagtga tgggtggtgg acagttggaa 840
 ttagtgccat gtcatacaca aatgttcac aaggcgggag tgtttctact tctggtgata 900
 aacttgatgg tcattgttat gattaagata atgccgggca ggccgggcac agtggctcac 960
 gcctgtaatc caagcacttg gggaggccga ggcgggcag 999

<210> 267
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-588-103 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-588-103.mis1, potential complement

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-588-103.mis2

229

<220>
 <221> primer_bind
 <222> 585..603
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 60..77
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-588-103 potential probe

<400> 267
 gcttaatgaa ttcattgtttt gttttcaaat gtgtccgtgc tctgtttttt ttatcctttc 60
 ttttaggtcg tatttcggaat aagcctgagg tggatgaagc tgcagttgat gccatcctct 120
 ccctaaatat tatttctgcc aagtacctga agtcttccca caactctagc aggtgggaca 180
 cccagagcag tgtgaagaag tccacacttg caggcgtaa ttggtacacc gttaggtgcc 240
 ttattcatta atgactccca gttcggacaa agaaattaac tcccttctcc cttctagctt 300
 caaaaatctc tttatttctt cacctgcctg ctgtactctc caaaaagaaa gaaagaaagt 360
 attgcagata tttgtatgtg atcagttact cttagagaat ggaagtgatc ctgtcccatg 420
 tgaagtttga atagatgtaa caagtataa atgaaaattg gagaaagaaa acagtatatt 480
 cccaaggtat ttaaaagtac raattaatta ttgccaagat taaatttttt cctgtgaaat 540
 ggttgctgtg gagagaaagg tttctctcac tccccaagta tcatggaaat gtgccctctg 600
 agataaaatg aagcctcttg tgtaagtctt ttgtgtctgc tgactatagg ctccattatc 660
 cttagtattt gtttttcatt tatgcacaaa agcgataaat aatatgaact cttatgacca 720
 agattggctg ccataaataa tagattttac tttgtttttt attttaaatg tttcacttaa 780
 aattatcttt tataatcagg tgataacaga cagttcgtaa agtacatagc cattctgctt 840
 tcctttgtaa gactagaact aaaccagctg ggatcctctt acctcaccca ggaaggaggat 900
 tctcattgtc tcagaggctc cgtctctata tcctaggggc tgggaaacag gagcggctgc 960
 ctcttctaag gtgggctgag cacactgcct tcccaccaca g 1001

<210> 268
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-589-152 : polymorphic base T or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-589-152.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-589-152.mis2, potential complement

<220>
 <221> primer_bind
 <222> 636..654
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 190..210
 <223> downstream amplification primer

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<220>
<221> misc_binding
<222> 489..513
<223> 12-589-152 potential probe

<220>
<221> misc_feature
<222> 393,614,617,695,819,849
<223> n=a, g, c or t

<400> 268
ggctggggtgt ggtagctcac gcctgtaatc ccagcacttt gggaggctga ggtgggtgaa    60
tcacctgaga tcaggagttt gagaccagcc tggccaacat ggtgaaaccc cacctcaaaa    120
aaaaaaaaaa agacatcaaa ggcattgaggt gtaggcacat agtgacagaga ggactccagg    180
caggggacat gtgcgatggc tctttaatgg cccaggcctt gaaatgggca agtctagctg    240
gggtgcccac aatagaggag ggtgatctgt gtatgtgttg actttgaaag tgaaattatc    300
catttgatac cttacgccaa attccttctc ttttaaatc tggtgcagta gttgtgtgtt    360
gagggctctg tttagaactt tttagaactt ttncattctt acgttttttt acaccagagc    420
ttcaactctc tgtttcttag catttctctc tctcctgctt tggagcagac tgaaagggaa    480
gtggcattat ttcattctga ktaatgttca tttgcagtta tttttgttat atgtttcatt    540
tgtatttcat ttatgctcta gttatgttaa catttggttt tctgtgatgt attatgtctg    600
ttttcataat ttncantta ctttgagttg aaatcccaaa taccagctct atcctcctcc    660
tctctttgtt ttaaaataga ttccagagca ggaanaagca tcagataaac atgtatgtca    720
cttggttttg tttgatttat tgatacaagt gtctgtcttt gtcttttctc ttatgttcga    780
agatcagcat ataccaaatg ggaagactgg aatcatagnt aggaactaga ttctatttcc    840
ctttcactna attggaatga acactctagc tttgtgacca ccagttttta ttgctttttt    900
aaaaaagtag tagctacaca ataaagaaga aaatacaaat gtgataggac tttgctagtt    960
tgcttgaaat ataaagtgtt agagctataa tttagctttc a                          1001

<210> 269
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-592-118 : polymorphic base A or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-592-118.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-592-118.mis2, potential complement

<220>
<221> primer_bind
<222> 384..402
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 830..849
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513

```


231

<223> 12-592-118 potential probe

<400> 269

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ctcaaaacca gcctgggcaa cttagtgage ccccatctct acaaaaaata aaaacaatta    60
actgggcatg gtggtacaca cctgtagcct cagctactca ggaagctgag atgggaggat    120
cccttgagcc caggagtttg agactgcagt gagctatgat ggtgccactg gcgcctgggt    180
aacaaagcaa gaccctgtct caaaaaaaaaa aaaaaaaaaa aaaaggagct gggcatagtg    240
gcatgtgcct gtaaatgaaa ggcattcattt catgcaagct cctctgagcc caggagtcc    300
agcctagccc aggcaacagg gcaagaccac gtctcaaaaa aaaaaaaagt actctttcca    360
cctaaaatat attcaggtca tttgagttca gtttgagttc agctacgaga attatttagt    420
tgagtgagtg tcagagctgg gattttcaaa tctgccctta ctggtatgtt gctttacaca    480
ccctcttacg taaatcaaac waggattcca ccctgggagg tttgcataga gggctgttct    540
tgtagaactt gtgctcatgc tttgatttgg gatttgggga gttagggcaa gccagaaagt    600
ttttctgggt gataataatg tgggttgact ttcttaagca ttttaagcca agcacttgag    660
tttctaacaa ctaaaaagct aagtcagcct gacacagctc tagcgcgccc tggcttgatt    720
ctgttcattc ccagggggag acttgccctt gttccagtc tgctctccca agccagctta    780
ctgtagtttt ccagcaattc tgagaagcag tattttttac tgctgattag aaccttaaca    840
tggaatgga aagtttgtgt agcatgtaac attattagaa gggaaaacat gactatatga    900
ttagatacat attgatttta tgcaatatgt ttgcataaaa tctcttcagt agtaacttgg    960
ttaaattatt cacattgact cagcataatt tctcccttgc t                                1001

```

<210> 270

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-593-174 : polymorphic base T or C

<220>

<221> misc_binding

<222> 502..520

<223> 12-593-174.mis1, complement

<220>

<221> misc_binding

<222> 481..500

<223> 12-593-174.mis2, potential

<220>

<221> primer_bind

<222> 658..675

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 138..158

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-593-174 potential probe

<220>

<221> misc_feature

<222> 22,187,214,652,684

<223> n=a, g, c or t

<400> 270

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agggtcaaagt ataaggattc tncaaaaatg cagagtaatt atgaaaattc tgtttaaaaa    60

```

232

```

gcttcagaat agaatgttta tatagcattg atttggagct aagggtata ttctggtaac 120
ataacaaggt gctatctagt gaatgtgtga ttgtgtagtc atggagctga tgtccctgcc 180
atagaantta cagaattatc taaaaaggga aatnctataa taatggcctt caatgctccc 240
acacttggac tagccattgc cataggcaga aaggcaatct catctttact gtgtgtgcaa 300
acagtacttt aatgtaatgt gtgcttaata taagctttct ttaaaaaaaa aaaaggtggc 360
tcctgttttt gaatagctat ttttaagata gatatagtta ggaatctaaa tgtgttctat 420
atagttaata tccattatga ggtggctctg aaaaatcaac ctagtataag ttggatggct 480
ttgtctttct gcttctgtta yaaccattt ttctagaaaa gcttccactt ctacttaaag 540
ataagaggca aatcattttc ctgttccctt atgcacatag atgttcactt accaaatatt 600
tatagagtgg cccagccctc tgcagacagt ggtgagcaaa accagacatg gnttcctgcc 660
ctcatagact tatagtctga tggnatgaca cagacataaa ttaaataatt gcacaaataa 720
atgtaaatga tagcagtgat gaaatagttg tgtgtgttgt cggagatcac ataacgttgg 780
gggacctgtt atgagaaagt ggtgtttgaa ataagacctg aagatgtgaa atcaaaggcg 840
tgaggctggg tgtggtagct cagcctgta atcccagcac tttgggaggc tgagggtgggt 900
gaatcacctg agatcaggag tttgagacca gctgggcaa catggtgaaa cccacctca 960
aaaaaaaaa aaaagacatc aaaggcatga ggtgtaggca t 1001

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<210> 271

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-596-124 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-596-124.mis1, potential

<220>

<221> misc_binding

<222> 502..520

<223> 12-596-124.mis2, complement

<220>

<221> primer_bind

<222> 378..397

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 805..825

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-596-124 potential probe

<400> 271

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gacagaccag gtcacatggc ttccgagatc atcagagaag ataagtctgt ctctttcagc 60
tgccagtaag ttttccagga tgagagggga aaaagaaagc ctccagtgc ttcagtgtgt 120
ttgccagtgt tcttgggatt gttttacacc atcctttact tcccttgctc agacctctct 180
gtttcaccat tgctcaggca ttcaggaaaag tatctgctca ctcccacttg gtgagtcctc 240
ggccttgagg ttgctgactc tcaggcggtta ggcagctgga tgacttcccg cttcacgcag 300
caaaggccag gggcttgccg gcctctgcag agttgtgtgt agggagactt gtgtcatcat 360
ccacaacctt gttttctcact tcctgggttg gctcatctct gaagaacagg tctcccagct 420
tcgctcctta tcactgcatt gtgaagagga ggaaaagtga atcacggaga gagaaggaag 480
aggatagaat cacaggctgc rtctgcacct gaaaagtgc cgcgggaaac tctatggcgg 540
attttttttt taactttctt cttcctgtta aaacataggt cactaactgt gatgttattt 600

```

233

```

gttttctaag tggatatgtga gatttttctaa tgtagttaga agtttcattg tctgatggac 660
acaatatgcc cttccggttc tattcaaacc agcaggatct gtcggtgctt agagatggct 720
gcctggactg gaatcaaate taatttcagg gaaatgaaga tggaatttga aggtcacttt 780
taaaattaag tcattgatgc tgctgttaca gagtgtgaca gaggatccat gtctgtgaca 840
caggacggtg ggaagcctga gagagagtga aattatgtga tacactgaaa tgacttttgt 900
ttttcttcta actcatacaa aactggtttg gaaagtcctt gctttggaag cgtcagacat 960
tagaacaggc caaactggac tgtctgttca tagcgtgcct g 1001

```

<210> 272

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-602-196 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-602-196.mis1, potential

<220>

<221> misc_binding

<222> 502..520

<223> 12-602-196.mis2, complement

<220>

<221> primer_bind

<222> 307..325

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 704..724

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-602-196 potential probe

<400> 272

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ggccagcctg ggtttctcca gttgggtctc ataatgcac tgcaccctgg cgcagcatgt 60
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aggtcatttg cctgttttcat cgaatctaag gacttggcct aagtgtggcg tattttgatg 180
gtcctcagca cgattatttt ctttttgtga gaaactaact tttgtcatat tgctgttttt 240
agctcagtgg tctctaagaa aggatacctt catttcaagg agcctcttta cagtaactgg 300
gctaaacatt ttgttgctgt ccgtcggcct tatgtcttca tctataacag tgacaaagac 360
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caggccatgg tgaagggtccg tcctgcccctg ccttggtttc ttattgccac gtgtgcccct 480
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gtctctgtag taactttctt gtctacctgc atttttcttt cagacaccaa acacctttgc 660
tgtctgcaca aagcacctgt gggtcctttt gcaggccctc aatgacaaag acatgaacga 720
ctggttgat gccttcaacc cacttctagc tggcacaata cggtagaag ttttgttgtt 780
gttgttggtt tttttgagac ggagtctcac tttttctccc tgaagtgcag tggcttggtc 840
ttggctcact gcaacctccg cccctggtt caagcgattc tcctgactca gcctccccag 900
tagctgagac tacaggcacg tgccaccatt gcctggctaa ttttcgtatt tttttagtag 960
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<210> 273

234

<211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-602-350 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-602-350.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-602-350.mis2, potential complement

<220>
 <221> primer_bind
 <222> 153..171
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 550..570
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-602-350 potential probe

<400> 273
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 tcaaggagcc tctttacagt aactgggcta aacattttgt tgcgtccgt cggccttatg 180
 tcttcatcta taacagtgcg aaagaccctg tggagcgtgg aatcattaac ctgtccacag 240
 cacaggtgga gtacagtgcg gaccagcagg ccatggtgaa ggtccgtcct gccctgcctt 300
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 tgaaatttcc ctattctctc tggttttgaa cttcctttgt gaagtgcctat atgccttggg 420
 aatatggcaa ggcagtcctc attgctgtct ctgtagtaac tttcttgtct acctgcattt 480
 ttctttcaga caccaaacac mtttgcgtgc tgcacaaagc accgtggggg ccttttgcag 540
 gccctcaatg acaaagacat gaacgactgg ttgtatgcct tcaaccact tctagctggc 600
 acaatacggg aagaagtttt gttgtgtgtg ttgtgtttt tgagacggag tctcactttt 660
 tctccctgaa gtgcagtggc ttggtcttgg ctcactgcaa cctccgcccc ctgggttcaa 720
 cgattctcct gactcagcct cccagtagc tgagactaca ggcacgtgcc accattgcct 780
 ggctaatttt cgtatttttt gttagagacgg ggttttacca caatggccag gctgggtctca 840
 aactcctgac ctcaagtaat ccaccacct cagcctccca aagtgcctggg attacagggc 900
 tgagccactg caccagcct agaagttgtt ctgtgttttc tttctctctt tggccttttg 960
 cttcaggaat atcaggataa ataggaaagg aagaattttt c 1001

<210> 274
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-603-191 : polymorphic base T or C

235

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<220>
<221> misc_binding
<222> 502..520
<223> 12-603-191.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-603-191.mis2, potential

<220>
<221> primer_bind
<222> 668..688
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 240..260
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-603-191 potential probe

<220>
<221> misc_feature
<222> 339
<223> n=a, g, c or t

<400> 274
tctatgtttt tgcaggctct ttcttgataa ggatattcct aggtattgtc tgtttgcttt      60
tttgcacgta ggattctagt ttatcagaat gctttctgtc ttatgttgct ttgccatttt      120
aattttgtag tccctcctccc atgtaaacct actgtaccta ggatagagta gacctgttc      180
tgtaccctaa gaagcgtata gcttcttaaa tgatttttag agtttcaaat tattttttca      240
ttccatttgc taaacttgtc agttttatc ttagactctt tcaagtttct ctcttctaca      300
ttacaaagta gaatgtttct cccttcattt catacagana tctcagggtt tgttttctgt      360
tttcctcttt atctgtcttc tctccgtcaa aagcatgaag ggtttattgc ttataaaaac      420
ctgagtccat tgcagtcttg caaaactggt cactttcttc tctgttttgt cctgtgtggt      480
aatagagaca aatttggtta yttggatagc tgagtctatg agaaatattt tatatatatt      540
ttttaacatt tatctttctc ctgtcagggc tgcttgtttt atctgtttat tttcttcttt      600
tggaatagga aaaatcctgg tttggtatta aaggaagttt tttaaaaaat ctgtctcatt      660
tagggaagaa aattgaagga agtgatacat gacaatataa cctaaaatgt taaaaaaaat      720
acaacataaa cgggctgggc tcagtggctc acacctgtaa tcccagcact ttgggaggcc      780
aaggcggttg gatcacgagg tcaggagttc aagaccagcc tggccaagat ggtgaaaccc      840
catctttact aaaaatacaa aaattagcct ggcgatgtgg tgggcgcctg taatcccagc      900
tactcaggag gctgaggcag aggatcgctt gaaccggga ggcggagggt gcagtgagcc      960
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<210> 275
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-783-73 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-783-73.mis1, potential

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<220>
<221> misc_binding
<222> 502..521
<223> 12-783-73.mis2, potential complement

<220>
<221> primer_bind
<222> 429..446
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 858..878
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-783-73 potential probe

<220>
<221> misc_feature
<222> 202,209,236,281,447,461,627,992,995
<223> n=a, g, c or t

<400> 275
ctagtctgtgt cttaccatct agaattttcta gtttcagtta tttccaatgg gatgtgattt      60
acagactcta gcaaggcata cagtatagct ttccagattt tttgttgttt tcctcctagt      120
tttttattca tgtcatcctc acttactttg actattgttt gtttctactgg attgctgtta      180
attgttcttt ctaaaacatt anccttagnt tttctttcac agaaacagtg ctatttcttt      240
ttgtgttcat tttttattgg tatatataat acttaacgtg nttcactcag caaacacacg      300
agtgtctttac tatatgccaa gcatgattct aaatgctggg gatatactag tgaagaaagc      360
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agttagcgat gactgtgaga acgaagnagt aaactgggac naagatccgg tgattgcaga      480
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gaggagacaa cacttctggt ggccagaaat tcagtataac cagggttcaga acaaacacaa      600
ctgactctgg gttagcataa aactcancca gcaggagcag aagtccccag gcagacgcga      660
gcagagcctg ctggcaaccg tgagcattgg tcagcgtgga cattggacaa ggggcttctt      720
tgctcagccc tcattcctct aacatgggtc tctcctgtgt tctgcatgta ggcctttgag      780
gattggaata agacagagct agactcattc ctgattgaaa tcacagccaa tattctcaag      840
ttccaagaca ccgatggcaa acacctgctg ccaaagatca gggacagcgc ggggcagaag      900
ggcacaggga agtggaccgc catctccgcc ctggaatacg gcgtaccctg caccctcatt      960
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<210> 276
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-783-421 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-783-421.mis1, potential

<220>
<221> misc_binding
<222> 502..521

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237

<223> 12-783-421.mis2, potential complement

<220>

<221> primer_bind

<222> 81..98

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 510..530

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-783-421 potential probe

<220>

<221> misc_feature

<222> 99,113,279,644,647

<223> n=a, g, c or t

<400> 276

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ggtgattgca gaaggcttct gaggaggcga cactgcacag agacctagt gaagtgagga      180
gcccttgctt ctgaggagac aacacttctg gtggccagaa attcagtata accaggttca      240
gaacaaacac aactgactct gggtttagcat aaaactcanc cagcaggagc agaagtcccc     300
aggcagacgc gagcagagcc tgctggcaac cgtgagcatt ggtcagcgtg gacattggac     360
aaggggcttc cttgctcagc cctcattcct ctaacatggt tctctcctgt gttctgcatg     420
taggcctttg aggattggaa taagacagag ctagactcat tcctgattga aatcacagcc     480
aatattctca agttccaaga yaccgatggc aaacacctgc tgccaaagat cagggacagc     540
gcggggcaga agggcacagg gaagtggacc gccatctccg ccctggaata cggcgtaccc     600
gtcaccttca ttggtaatgt tatgcttttc acatgggccc tttngtncac tattctgac     660
ttgatgtctg gaggacagat acagactggg ctttagagaa tctcttcagc cctctttagc     720
tttcagagtg ctttttgctc tttcttgctg tgaagaaact gacagtgtga gagaggctga     780
cgctgctttt gattctcttc cttgtagttc ttatctcatt cgtacaaact gtgaggtaaa     840
ttcagaagtg actgtccttc ctatccagtt ttatctttgg aatatttttag cattagtgat     900
gtaattgtag tcagtgatct aagattttat ttatgaggca ggtaacttga gtaaaatttt     960
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<210> 277

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-785-200 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-785-200.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-785-200.mis2, potential complement

<220>

<221> primer_bind

238

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<222> 302..322
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 791..811
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-785-200 potential probe

<400> 277
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ctaatacaggc aactgatacg ttttatggaa aacatctatt tggtaactg atgtctgaag      180
tgacaataat agtgagttga cctttgtcct acaatctcct aaaaagagca gcatctctac      240
ctgggtgttag ctctggggaa aagggcatgt tgcttctgtt gaaagcagcc tcaaaggcgt      300
cctgtgtttt tatagtcgct cctctggcct gtgccgggaa ggtatggctg cagagcactg      360
tgaatagatt cacctgtcgt cagggaaacc caggaatgct gcggtgccag caatacagga      420
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tggaagacaa caagttcata ytaccagtct gtctgtcccc ccagttgaaa atagtttctt      540
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aaatctttgt gttgggtcct ctttaactgt gcagttcttt ttatttcaga ctaataatag      660
ggagagagag agagagaacg ataacatctc actatctgtg aaaataacta aatatagccc      720
attgttttaa caaatcttcc cagagtatct tctgtgtgtc gagacctgtg ggaaaacgct      780
tgctgtctgg gggagagagg catataaata cattattaca gtgaaatcat tgctattaag      840
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gcctggaaga ggtgacattt gaatccacaa cagactctta tgtaactatg ccatccacag      960
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<210> 278
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-785-393 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-785-393.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-785-393.mis2, potential complement

<220>
<221> primer_bind
<222> 109..129
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 598..618
<223> downstream amplification primer, complement

<220>

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239

<221> misc_binding
 <222> 489..513
 <223> 12-785-393 potential probe

<400> 278
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 agtcgctcct ctggcctgtg ccgggaaggt atggctgcag agcactgtga atgagttcac 180
 ctgtcgtcag ggaacccag gaatgctgcg gtgccagcaa tacaggaatc agggatttgg 240
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 gttcatatta ccagtctgtc tgtcccccca gttgaaaata gtttcttttt ctccattttt 360
 tcttgatgga aggggtgtcc ttctgatgga tttttctatc tggcagtaaa tctttgtgtt 420
 ggttcctctt taactgtgca gttcttttta ttccagacta ataataggga gagagagaga 480
 gagaacgata acatctcact rtctgtgaaa ataactaaat atagccatt gttttaacaa 540
 atctttccag agtatcttct gtgtgtcgag acctgtggga aaacgcttgc tgtctggggg 600
 agagaggcat ataaatacat tattacagtg aaatcattgc tattaaggaa aaaaacatta 660
 ctagtaatgt gggaacacaa agctgccagg gtaagtcagg aaagactgcc tggaagaggt 720
 gacatttgaa tccacaacag actcttatgt aactatgccca tccacaggct ctgcactaa 780
 ctgtggaagc ttgagtctgc taaattttgt ctgtacaaaa tgacattgtt tttattttta 840
 gtaaaaagct tttacaaagg aagaggagtt aattgaatgt acttcttcac tctctctaaa 900
 gcattcttgc atatacctcc atatagctaa gtgatcaggg tcagttaatt tttcagtcac 960
 ttttgaaata aaatctaaaa tgccctctgt gcaatatgga a 1001

<210> 279
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-787-103 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-787-103.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-787-103.mis2, potential complement

<220>
 <221> primer_bind
 <222> 583..602
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 74..94
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-787-103 potential probe

<400> 279
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 atcatgggta aaaaccatgt tttccgcttt aaccacccgg aacaagcacg agctgagcga 120
 gagaagactc cttctgtgta gacccctctt gagcctgtgg actggacatt tgcccagagg 180
 gagcttctgg aaaaacaagg aattgatatg aaacaagaga tggagaaaag gtaatgcaca 240

240

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gttacgcagc ccataatgact gtttcttctt ttaaacaatgt aataactaata gcattcttga 300
atTTTTTTTT tttttttttac ttctaggcta caggaaatgg agatcttata caaaaaggag 360
aaggaagaag cagatcttct tttggagcag cagagactgg taggagtcct gaatctgcta 420
aactgttggg aaaagggcag cttgttccca tactttccct gttccacaga gcagtactca 480
cccaaattgc ttctgtctca rtgataccaa gcactattct ttaatttcct taatggagaa 540
tgaacttaaa tctcccggtg gccttagcct gaaaaaatag tccacagagg tactcttttg 600
ggctttttat gtcttaaagc caaatcttaa cttctgttac aaccaaatac tttttaagga 660
aataagactt ttctggtagc ctttgccctc tgatagtggg tttggaattt gcttcagtgg 720
tggttcttta aatgataatt actctgaata ttgaatttgg tgagagtttg ccttggtttt 780
gtttctgata acttgatagt actaattctc tgctcttggg ctgactttgg gattgttctt 840
acgctgggca gacttttttt ttttaagtta aactgtgtct aaaagtgttg ctgcacagtt 900
gcatgtgtta ctcttttcct tatccctgc atggagtctg aattctcaat caggttctca 960
gtggcatgtg tggtagcggg gggagcaaag gctgcatacc c 1001

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<210> 280

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-790-396 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-790-396.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-790-396.mis2, potential complement

<220>

<221> primer_bind

<222> 876..896

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 423..443

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-790-396 potential probe

<400> 280

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aaagtttttt ttgtttgtta gtttttgttt ttgagtcttg ctatgtggcc caagctggag 120
tgcaagtggc agattgtagc tcgctgcagc ctcagacacc tgggctcgtg tgattctcct 180
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ggcctcaagt gatactcccc acttgccctc ctaaagtgtt gggattacag gtgtgagctg 360
cctcccgagg cctgtatttt tttatgtatg agtaggtttc attacttttag tctggaactc 420
tctacccttc ttccatgaaa gacacttgat gtaatggaat aaacactata cagtctcata 480
agttgggttt aagtcctctc rctgttatth ccattgtgat cttgggcaaa tcacttaaat 540
tcacttgagc ctttttcttc atctttaata ggtactataa agctttatac aaatgtatta 600
ttatcaaggc tcataaaatg taaacactca ggatatttga tttagagata atagtatgtt 660
acttatgaga agtagaacat atgagaaatg acaagaacaa attttctttt tggatctaga 720
tatgcagatc gtgcaaaaca aattaaatgc aatgctgtta tcaatgagga cccaatgcc 780

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241

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aaactgggttc gtgaattaaa ggaggaggtg acacgggtga aggaccttct tcgtgctcag      840
ggcctggggag atattattga tagtaagtga attaaggatc gttacaaaat ctaatccttt      900
cttcttcagg gttcttattc agcgttctta tatttaaaat aaacttcaag ttaaggagca      960
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<210> 281

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-791-211 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-791-211.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-791-211.mis2, potential complement

<220>

<221> primer_bind

<222> 291..311

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 671..690

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-791-211 potential probe

<400> 281

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tacattggaa tcttttagtt tgtaaattgca gaaatgattc tgaacctgta ggataccact      60
attaaagaca gacatgtttt agaactgccca tctagaacag ttgtaacctg tgtttgtatt      120
atagcgtgtc ttgggtcttg cgctttaatg ctgtcccttc ttacaacgat attccttcct      180
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ctatctccca gatctgaaag attttcagaa caataagcat agatacttgc tagcctctga      300
gaatcaacgc cctggccatt tttccacagc atccatgggg tccctcactt catcccatc      360
ttcctgctca ctcagtagtc aggtgggctt gacgtctgtg accagtattc aagagaggat      420
catgtctaca cctggaggag aggaagctat tgaacgttta aaggtaagta atagttcaga      480
ctgaatacaa ggtattctat rtagctccac aaggaagaac taggagtaaa aatcactaag      540
atttcgactc agcatatgga gaactctttg actcttagaa gtgtcctgaa aattgaattt      600
tgtgctttgt aagttaattt cttttcatta gaatgcctga gtctgacatg gccaggcaga      660
gttgggagaa gtgcatgggc agttcatagg ctggcaaggc agagtaacag attaatagat      720
gtgtacgtta attctgggat agtacatcaa gttacagtgt aattgttttg ttagaaattt      780
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aaagatgaag tttgggccgg gtgcagtggc tcacgcctgt aatcccagca ctttgggagg      900
ccgaggcggg gtggatcacg aggtcaggag atcaagacca tcctggctaa cacggtgaga      960
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<210> 282

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-792-233 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-792-233.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-792-233.mis2, potential complement

<220>
 <221> primer_bind
 <222> 712..732
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 284..304
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-792-233 potential probe

<220>
 <221> misc_feature
 <222> 204,218,454,485..486,512,566,576,579,614
 <223> n=a, g, c or t

<400> 282
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 gaaaaatggg cataatttaa accattatta tattgttgag gtatccctag ctattattat 180
 agcaaatggg gaaaaaagtg ttnattcta ttgaagtnta tgtaatgac cgacattaat 240
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 gaattgttta ttacattgaa gtgacttgaa gtgncctttt gtgctttagg tgcaggttga 480
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 tgcctgggtg aaccttaatg aaggggcccgt ctaggcaca gtgcaaaaca agcatttgct 720
 ctgtactgtt agagccaaaa ttgtgatgag caatactgat aattgtccag tttatgtcat 780
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<210> 283
 <211> 989
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 505

243

<223> 12-793-383 : polymorphic base T or G

<220>

<221> misc_binding

<222> 485..504

<223> 12-793-383.mis1, potential

<220>

<221> misc_binding

<222> 506..525

<223> 12-793-383.mis2, potential complement

<220>

<221> primer_bind

<222> 866..884

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 365..385

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 493..517

<223> 12-793-383 potential probe

<220>

<221> misc_feature

<222> 505

<223> n=a, g, c or t

<400> 283

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caatagttga	tgaaatagtg	aaataaaagt	taactttggt	tgggcttgga	ataaaggaga	180
tgatacataa	taaactattc	tttggttagc	attagtaatg	cttgtagaca	ctcaaacaag	240
gaaggcgaag	tcctgatgat	gatttattgt	atcaatacct	cattttattt	ggttgtgggc	300
tcagtttgcc	tcactggaga	atccactaag	aaagatggat	tttaatggga	agaaaagaat	360
tattttctac	atcgttcctc	atctcttgag	tttgtcaaaa	agttttctaa	gaggcagtg	420
gaagagccag	agatgtccga	aattgcctga	cttcatgttt	tggagatttc	ctaagtcaca	480
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cagtttagcat	tcaaggaagc	cttaaagatt	gtgattatgt	ttttttttcc	tttgcgtgtg	600
ggcactatgc	tttattagaa	cacattattt	ttaatcatag	tattttttct	ttgcctctaa	660
gaaaatactt	tcttaatgct	cagaaaagtg	cttccaatta	atgttttttt	ccccttaaaa	720
agagaagctt	tgagagatat	ttttgctttc	atagctagaa	cagttgaagt	cttcaactga	780
ggttttatag	cagattagac	atgggtaaat	gatgtctgta	atgggttgag	ttactgagat	840
gacaatctcc	tgtgccattt	ggtttgaatg	tacttgatag	gctgcttcaa	atcagtcact	900
tcaatgcatt	ttgtgtaaac	ccagttgtcc	ttttttattc	ctcttttagac	ataaatgtgc	960
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<210> 284

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-803-125 : polymorphic base T or A

<220>

<221> misc_binding

244

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<222> 481..500
<223> 12-803-125.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-803-125.mis2, potential complement

<220>
<221> primer_bind
<222> 605..625
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 169..189
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-803-125 potential probe

<400> 284
caggagaatc ccttgaaccc aggaggcgga ggttacagtg agctaagatt gcgccaatgc      60
cctccagcct gggcaacaga gtgagactcc atctcaaaaa aaaaacaaaa acaaaaataa      120
tgtgtctgtt tcttccttca gaacatgtaa gtggaaaagt agtgaagtgc tgcaacacct      180
agcaaaagga gaaggagtga gaaatctttc cattaaatgt tgtaggctgc agggtaactt      240
ttactgttgg taaaattgac ttgaaattt tactaaagac cttagtgaag aggagtggta      300
agactccatt cacacatttt ctcacaatag gcgtcagtga ccatgttgct ttgcagggct      360
cttttcagag ccagagtgaag aaatagggag ctccttgga atgagaagta aaactccac      420
ttactgagtc cttaatataa aatgttcttt ttctttgggg atcttaagtc ttaactattt      480
gcttattaaa gccttagctc wtacacttga gattaccctt tcctttgacc ttcctcttga      540
tgtaaaggag aaatttctcc ctaactgcca agtgggacca attgaaaata atgtcacatg      600
ttaggagtc aagacattaac cagactcttc aagattcagg taaccagtg tcttccaaat      660
aatttctagg gaataacact gtcattatct agggaaactc ccttccgact tccctatgtc      720
ccactaaagc aagacaaaaac tgtattactt caatcagaaa acaaatttct ctgttttaat      780
tcttccttac gccaaaataa agaactcttc tgttttccct agttttattc tagaaagaaa      840
acagcttctc tagtggtttg tggtgtcttg agtttttaat gcagtgtggg agttcactga      900
agcataagca ccttagttct gctcttattt tgtgaatggg gagaatttct ttcgggcaga      960
cctgcatttt aatgctgcac gcagataaca tctttcatcc g                                1001

<210> 285
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-805-115 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-805-115.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-805-115.mis2, potential complement

<220>

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245

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<221> primer_bind
<222> 596..615
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 135..155
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-805-115 potential probe

<220>
<221> misc_feature
<222> 313,721
<223> n=a, g, c or t

<400> 285
gagccaccgc gcccggttc tgtatgtgat ttctttttca ctctaattca ctttactaat      60
ttgttcataag gtgagctaca tggaaattta ctgtgaaaga gtacgagatt tgctgaatcc      120
aaaaaacaag ggtaatttgc gtgtgctgta acaccactt cttggaccct atgtggagga      180
tctgtccaag ttggcagtta ctctctacac agacattgct gacctcatgg atgctgggaa      240
caaagccagg tatggttagga aatagagtaa tgactgaggt ctttggcacc ttttgaggtc      300
cttttttccc agnttaaggg tttgaggcca catttatagc tatgaaagtt gctttaattg      360
tggagtcctc tgatcctttg actgtgctgt aacagtgagg gcttcagagt gttaagtatc      420
ttctcatcta aacagtacat tgctgaaaca tgttagagct ctcatagagt ttactctta      480
ggttttgata aagtcatggt raaatgttag ttatcatgta tatatgcggc tgtggtagta      540
attgattctg gaataaatga gcaccaataa agaataaaaa ttaaatgctt cattggtttc      600
taaaagggata gctggagtat gaaaaatgat tctgatgggg tgcctttgga attggagagt      660
aacttgatgg gctcacaaat aaggcagtat tgagagcaat tgtgtaagtg acaatcttgc      720
naatctgtga ataagtttaa gactattgct tgtgattggt atgcttataa tgtggagcct      780
gctgtccatt tcaactctca tctaagaatt cccttgtcac gtggtcacct ttatgtttat      840
ttaggacagt ggcagctaca aacatgaatg aaacaagtag ccgttccac gctgtgttta      900
cgattgtttt caccagaag aaacacgata atgagaccaa cctttccact gagaaggtag      960
gagagtttca gtctctaggc ttgagttgtg aaggatggag a                                1001

<210> 286
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-808-52 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-808-52.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-808-52.mis2, potential complement

<220>
<221> primer_bind
<222> 450..469
<223> upstream amplification primer

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246

<220>
 <221> primer_bind
 <222> 894..914
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-808-52 potential probe

<400> 286
 ccttgtgata caccgcctc agcctccaa agtgctagga ttacaggctt gagccaccgt 60
 gcccaaccta taattatattt tttagatgg agtttgactc ttgtcaccca tgctgggtgtg 120
 caatggcacc atctcagctc actgcaacct ctgcctcccc agttcaaaca attctcttttc 180
 ctacgcctcc caggtagttg caattacagg tgcccgccac cacacctggc taatttttaa 240
 aaatattttt agtagagacg gggtttcagc acattggcca gactgggtctc aaactcctga 300
 cctcagggtga tccgcccacc tcggcctccc aaagtgtgtg gattacaggc gtgagccacc 360
 gtgcctggcc atgttgggtt tttttgggtg ggggaagggt aatggggatt tgaaaagttg 420
 aacatgtcaa tttaatttaa caagccctca tcacgagcag agcatgagca ggggccactg 480
 tcctgggtgt ttggggagaa rcagaagaag ggagggagga gcagccctca ggttaaaagc 540
 aatgatttgt tccaaccaat atttgagtac ccacctgtg cctggtgtgc tgctgggtgc 600
 agtaattcag cagccaacaa agcaagccca tgcacttgtg ccctccatt ccagtgggga 660
 agacaatgtt taaacaaatt tacaacatcg gtcctaagta ttttggagga aagcagctaa 720
 ataaaaggat gaaagaggga tgggaacgag ggatgttttag atggcatagt cagggaaggc 780
 ctctcttcgg agatcacatt tgagcagact ctagaatgaa aggatagggt aagccatgca 840
 aaccctctgg caaagaggtc tccaagtaga gaaatgaagc ccttgaggca gcagtgtcct 900
 cagtaggttc cagaaatagc aaggctcgtg gtacagagtc agggactggg agcgcaatag 960
 aagacatcag aaagtagcca gggaccagga tatttagggc t 1001

<210> 287
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-808-75 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-808-75.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-808-75.mis2, potential complement

<220>
 <221> primer_bind
 <222> 427..446
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 871..891
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-808-75 potential probe


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<400> 287
ctcccaaagt gctaggatta caggcttgag ccaccgtgcc caacctataa ttattttttt    60
gagatggagt ttgactcttg tcacccatgc tgggtgtgcaa tggcaccatc tcagctcact    120
gcaacctctg cctccccagt tcaaacaatt ctctttcctc agcctcccag gtagttgcaa    180
ttacagggtgc cggccaccac acctggctaa tttttaaaaa tatttttagt agagacgggg    240
tttcagcaca ttggccagac tgggtctcaa ctcttgacct cagggtgatcc gcccacctcg    300
gcctcccaaa gtgctgggat tacaggcgtg agccaccgtg cctggccatg ttgggttttt    360
ttgggtgggg aagggtaaat ggggatttga aaagtgaac atgtcaattt aatttaacaa    420
gccctcatca cgagcagagc atgagcaggg gccactgtcc tgggtgtttg gggagaaaca    480
gaagaaggga gggaggagca scctcaggt taaaagcaat gatttgttcc aaccaatatt    540
tgagtacca ccctgtgcct ggtgtgctgc tgggtgcagt aattcagcag ccaacaaagc    600
aagcccatgc acttggtgcc tccattcca gtggggaaga caatgtttaa acaaatttac    660
aacatcggtc ctaagtattt tggaggaaag cagctaaata aaaggatgaa agagggatgg    720
gaacgaggga tgtttagatg gcatagtcag ggaaggcctc tcttcggaga tcacatttga    780
gcagactcta gaatgaaagg atagggttaag ccatgcaaac cctgggcaa agaggtctcc    840
aagtagagaa atgaagccct tgaggcagca gtgtcctcag taggttccag aaatagcaag    900
gtcgttggtg cagagtcagg gactgggagc gcaatagaag acatcagaaa gtagccaggg    960
accaggatat ttagggctta ggtgaggact tggattttca t                                1001

<210> 288
<211> 987
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-809-119 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-809-119.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-809-119.mis2, potential complement

<220>
<221> primer_bind
<222> 383..402
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 888..908
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-809-119 potential probe

<220>
<221> misc_feature
<222> 511
<223> n=a, g, c or t

<400> 288
gtggagtgta gttcaaagaa gtatttttat atgtggactt gacctttggt cttttattct    60
cattttccac ttaagaaaat cttggctgtg tgaatgaaag agtgatactt ttaaggttat    120

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248

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agaaagtgaa atgtaatcat gccagataat tttatataga tttttttatg tatggctgac 180
ctggatgact ctaacagtg c atgtgtttgt gagtgtgtgt gtgtgcatgt gcgtgtattt 240
aatgagaaaa gtaaacttgt gtataggagg cttaaaaaat gtgtaggga ttttaggtga 300
ctgttctgat tccagacact tttattatgg aagcaatcaa gtaagtatag gaagaaatat 360
taataaaaagg ttattttattt ctctttttac tctttacagc ccgaagatcc ctgttttgca 420
tctcaaaacc gtgtgtacaa tgacattggc aaggaaatgc tcttacacgc ctttgaggga 480
tataatgtct gtatttttgc statgggcag nactggtgct ggaaaatctt atacaatgat 540
gggtaaaaca gaagaaagcc aggctggcat cattccacag gtgaaaaaca aaacaaaaca 600
aaaatcttct cttcattatt agtggttagtc ttaaattgct ttaacagtta tttttatttg 660
gcgaacattt atgcggggat tgttttatgt caggcacaaa gatgaacaac ccattatttt 720
ccctcagagg agctcacaat tgaatgggaa ggattgacat gtacacatgt ctgtcattaa 780
aggtgggaaa gtcagtgttt tgtaatgatt ttgccatata tccaatgcca tattattttg 840
tcatttgaaa agtgttacca gcttggttaa gctctgttct aagtcctgga gatgggggga 900
tattgttgat ctgatttttt ttcaaattcc atgcatagat tacctctgaa gaatgtgatt 960
atttttgggt tttttgatag ccttatt 987

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<210> 289

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-810-77 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-810-77.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-810-77.mis2, potential complement

<220>

<221> primer_bind

<222> 558..577

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 126..146

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-810-77 potential probe

<400> 289

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ctggtctcaa acttctgact acaggtgatc tgctgcctc ggccctccaa agtgcctggga 60
ttacaagcat gagccacat gccaggtctt cctgtcaaat aagggtttta acatgcagct 120
gtagccacag ctctcgtgtt tattagtctg gcatcacagt cagtactgtg agtgccgttg 180
cttaggctta gcctataaat atccacaaat atccattaca gaagcaggca agggcaaatg 240
ctgtgctaag cagcccaagg gccacatttg gaaccacatt aggaagcatg ctatgttcag 300
tacagtaaaa ccttggtgat tcaatggctt caacaaatgt tctgtgtagt aagtgttttt 360
catggaaata tttctgactt gtctctggtga tttctgtgtt tccttaactg aatcatcatc 420
aagaagagat taaattgttt agctatatga acataattta ttaaccagtg ctatacaaat 480
aactagagat gcagacagat rtgacgtgag accaaagagt gaatgacacc tgagcctggc 540
attcctcgga gcttaaagaa gagttcctgg tgccctctg ttttttgga tttttttttt 600
ttcaaagaaa gggaggagga ttaaagattt atctcctcaa cccctcattt ctgaaccatg 660

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249

aatccacatt	tcaagttcat	cttacattag	gcccctagag	tggggtatgg	gaagccctgg	720
acaccagcat	gcctgcctgc	cagcagaatg	agttgatgct	cctgagactg	aatgctgttt	780
tgcacttgge	ttccctatatt	atactaagtt	tgctactcag	gcttgaacag	aatatccttc	840
actttttctt	aacttagggg	gaactgtttc	atagaacatt	tacttgaaag	cctattgatc	900
ctgtttttatt	tgaagaaaga	acagtggagtc	agcaaatagc	tctagacctg	tctcagtgag	960
tagtgtgggc	tcacttagct	tctctgggtct	gttggaaacac	a		1001

<210> 290

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-265-178 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 10-265-178.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-265-178.mis2, potential complement

<220>

<221> primer_bind

<222> 324..341

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 662..681

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-265-178 potential probe

<400> 290

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cagagctcct	tcctgcggg	cccgccccc	tgccctctcg	gccgcgcagg	catggggcgg	120
ggcgggtccc	ttcgagggc	agggaggagg	cgcgggccagg	cctcgccgag	tctgcaggga	180
cacctgcggg	acgcgtgcca	gcgggagccg	ggcgcgaggg	cggggctggg	ggccgcctgc	240
ccggccgagg	ctctgcagcg	tgcgcgcccg	gcttctgggg	gcccgcggga	ggcgcgagg	300
aaagtgcaga	ctcccagtca	cggccaaatg	tgggaaggacc	ggacccctgg	gttgcagcgc	360
gtcgagcggg	gctgactctt	tcctttgttc	tgtttctgcc	tctctagagc	tgacatcgcg	420
ctgatcggat	tggccgtcat	gggccagaac	ttaattctga	acatgaatga	ccacggcttt	480
gtggtaagcg	gcgtgggcgc	rttgtcttct	ctctgggtcc	cgggcgcttt	agccgaggcc	540
ggcgataagg	ttgggagctt	acgggtctcc	tggccgtgct	ttgctaattg	gctctgttgc	600
tgctcgtggc	atthttgtat	ggaaaggaga	agcaccctgt	aggcgtgggc	gggcccgtcc	660
cgaacttagt	cctgcggagt	gtgcctgtgg	gtccgtgagg	ttcacagccc	gaatgaacga	720
attagtgtct	taagttagaga	agaagggtgc	gggaggagaa	cccttgctgg	ctgtgtagag	780
ctctaacttg	attgcctgat	gagatctggg	gagagtgaag	atgtttcttc	taaatgttaa	840
agtggccttag	acgccaggat	gatcaataac	aacagataga	gcctgttgaa	ccggccagtt	900
cctggatttg	atthttgagtc	ctaacacggt	gggtgtggat	tctacctgac	acaccggggg	960
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<210> 291

<211> 1001

250

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-266-203 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-266-203.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-266-203.mis2, potential complement

<220>
<221> primer_bind
<222> 301..320
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 701..720
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-266-203 potential probe

<400> 291
cagcccgaat gaacgaatta gtgtcttaag tagagaagaa ggggtgcggga ggagaaccct 60
tgctggctgt gtagagctct aacttgattg cctgatgaga tctggggaga gtgaaaatgt 120
ttcttctaaa tgtaaagtg gcttagacgc caggatgatc aataacaaca gatagagcct 180
gttgaaccgg ccagttcctg gatttgattt tgagtcctaa cacgttgggt gtggattcta 240
cctgacacac cgggggtagt tggccttcgc ctcggttgtc cgccgttttc atcctactga 300
ggtgacataa ctttacagtg agcctccac agctggggga agaaaaggca aaggcaggtc 360
tgacctcccc agaacttggg ttgaatggaa aggtcattgt tactttggcc acagtctgaa 420
agtcttggtg gtcttggtgc tctactcag gacttttgtc cttctaggtc tgtgctttta 480
ataggactgt ctccaaagt gaygatttct tggccaatga ggcaaaggga accaaagtgg 540
tgggtgcccc gtccctgaaa gagatgggtc ccaagctgaa gaagccccgg cggatcatcc 600
tcctggtgaa ggctgggcaa gctgtggatg atttcatcga gaaattggtg aggccagctg 660
tgctctcagc tgctaccacg atagcagctg tttttgggtt cttcctttag ttctccttct 720
tttaactcta gagatttttt tttttcaatt tctgctaagc tctgaccaa tgattgctta 780
actgttgagc tgttggttaa cttgataagc gcttatgaag taactttgtc ctttgggtgt 840
agtaattctg agaatactaa cagacatttc aataaacatt aaggcggggc acagtggctc 900
aggcctgtaa tcccagcact ttttgggagg ctggttcaga tggatcggtt gagcccagga 960
gttcgagacc agcctgggca acatggcgaa accctgtctc t 1001

<210> 292
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-403-312 : polymorphic base C or T

<220>

251

<221> misc_binding
 <222> 481..500
 <223> 10-403-312.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-403-312.mis2, potential complement

<220>
 <221> primer_bind
 <222> 190..208
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 593..611
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-403-312 potential probe

<400> 292
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 ctacgtgccc aggcctctct cctctcatc agatcacatg accttctctg agcgggtgaa 180
 gaacatgctc attgcctttt cacagaactt tctgtgcgac gtggtttatt ccccgatgc 240
 aacccttgcc tcagaattcc ttcagagaga ggtgactgtc caggacctat tgagctctgc 300
 atctgtctgg ctgttttaga gtgactttgt gaaggattac cctaggcccc tcatgccccaa 360
 tatggttttt gttggtggaa tcaactgcct tcacccaaat ccactatccc aggtgtgtat 420
 tggagtggga cttttacatg cgtatattct ttcagatgta ttactttgga tcgattaact 480
 agccccagat atatgctgag yaagcattct gagataattt aaaatgccct cttttgttaa 540
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 ctgagatttc gggaaagcat tccttggaaca ttttactctg tgtgctccag tggatagtaa 660
 tcaattagaa acaacaagct gttaaagcc ataggcacag aatgctgggt ttggggcacc 720
 ctgcagaaaa ctgagttgaa gcctgcacct tgccctggat tcagtcaggc aggcaatgtt 780
 caggactgat gaaatcatc tttgatgat atagatcctg gaaatgaaag ttgcctttgt 840
 gaccctggtt aaagctccag tttctaaata ttctgataag aagctaaatc ctgcagtcgg 900
 ttctcttcta atgagtgaat caccagacag tcaggttctg acatgataca gaaaggttgt 960
 aggtttcatt ctcaagctat taggtttatt tttcccctac a 1001

<210> 293
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-405-54 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-405-54.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-405-54.mis2, potential complement

252

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<220>
<221> primer_bind
<222> 448..465
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 848..867
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-405-54 potential probe

<400> 293
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ttgtcattgt tttcaatttg actctcaaat actctattaa actatgatcc accacactca      120
gaagtatcat tttctctaag agactcaaaa gtgtattagg gagaatttat ttaaaaaataa      180
aataaatggg atattgtttc ttcattattaa atagaagtat ttctccaaaa agctgttggt      240
tagaacactg aatttatgtc ttacatttct gctcttatag ttctgcatcc acttgtttca      300
ttaagcaaac tttcccttaa agtgcaggaa agtgaaaaaa tcctaagtgc acagcttgat      360
aaattatcac aaattcacgt agtgcataca cccttgtaac taaacctcca aaacaagatg      420
ccggaagttg ccagtcctca gaagccttca cagttactga tcctcccact ctgttaaaga      480
ctgttccttc agaggacccc ygttttctag ttagtatagc agatttggtt tctaatacata      540
ttatgttctt tctttacgtt ctgctctttt tgccccctcc aggtcctgtg gcggtacact      600
ggaacccgac catcgaatct tgcgaacaac acgatacttg ttaagtgggt accccaaaac      660
gatctgcttg gtatgttggg cggattggat gtataggtca aaccaggggc aaattaagaa      720
aatggcttaa gcacagctat tctaaaggat tggtgagctt gaaaatatta tggccaacat      780
atcctacatt gctttttatc tagtggggta tctcaaccca cattttcttc tgcaaatttc      840
tgcaagggca tgtgagtaac actgagtcct tggagtgtt tcagaacctg gatgtgtcca      900
gctgtgaaac tcagagatgt aactgctgac atcctcccta ttttgcattc caggtcaccc      960
gatgacccgt gcctttatca cccatgctgg ttcccatggg g                               1001

<210> 294
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-408-356 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-408-356.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-408-356.mis2, potential complement

<220>
<221> primer_bind
<222> 146..165
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 546..565
<223> downstream amplification primer, complement

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<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-408-356 potential probe

```

<400> 294
agaacatcat ggcctctcc agccttcaca aggaccgccc ggtggagccg ctggacctgg      60
ccgtgttctg ggtggagttt gtgatgaggg acaagggcgc gccacacctg cgccccgcag     120
cccacgacct cacctggtag cagtaccatt ccttggacgt gattggtttc ctcttggccg     180
tcgtgctgac agtggccttc atcaccttta aatgttgctg ttatggctac cggaaatgct     240
tggggaaaaa agggcgagtt aagaaagccc acaaatccaa gacctattga gaagtgggtg     300
ggaaataagg taaaattttg aaccattccc tagtcatttc caaacttgaa aacagaatca     360
gtgttaaatt cattttattc ttattaagga aatactttgc ataaattaat cagccccaga     420
gtgctttaaa aaattctctt aaataaaaaa aatagactcg ctagtcagta aagatatttg     480
aatatgtatc gtgccccctc ygggtgtctt gatcaggatg acatgtgcca tttttcagag     540
gacgtgcaga caggctggca ttctagatta cttttcttac tctgaaacat ggcctgtttg     600
ggagtgcggg attcaaagggt ggtcccaccg ctgcccctac tgcaaattggc agttttaatc     660
ttatcttttg gcttctgcag atgggtgcaa ttgatcctta accaataatg gtcagtcctc     720
atctctgtcc tgcttcatag gtgccacctt gtgtgtttta agaagggaag ctttgtacct     780
ttagagtgtg ggtgaaatga atgaatggct tggagtgcac tgagaacagc atatgatttc     840
ttgctttggg gaaaaagaat gatgctatga aattgggtggg tgggtgtattt gagaagataa     900
tcattgctta tgtcaaatgg agctgaattt gataaaaacc caaaatacag ctatgaagtg     960
ctgggcaagt ttactttttt tctgatgttt cctacaacta a                                     1001

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<210> 295
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-409-148 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-409-148.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-409-148.mis2, potential complement

<220>
 <221> primer_bind
 <222> 354..372
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 779..798
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-409-148 potential probe

```

<400> 295
ctcacctggt accagtacca ttccctggac gtgattgggt tcctcttggc cgtcgtgctg      60
acagtggcct tcacacctt taaatgttgt gcttatggct accggaaatg cttggggaaa     120

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254

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aaagggcgag ttaagaaagc ccacaaatcc aagacccatt gagaagtggg tgggaaataa 180
ggtaaaatatt tgaaccattc cctagtcatt tccaaacttg aaaacagaat cagtgttaaa 240
ttcattttat tcttattaag gaaatacttt gcataaatta atcagcccca gagtgtctta 300
aaaaattctc ttaaataaaaa ataatagact cgctagtcag taaagatatt tgaatatgta 360
tcgtgcccc tccggtgtct ttgatcagga tgacatgtgc catttttcag aggacgtgca 420
gacaggctgg cattctagat tacttttctt actctgaaac atggcctgtt tgggagtgcg 480
ggattcaaaag gtggtcccac sgctgcccc actgcaaatg gcagttttaa tcttatcttt 540
tggcttctgc agatggttgc aattgatcct taaccaataa tggtcagtcc tcatctctgt 600
cctgcttcat aggtgccacc ttgtgtgttt aaagaaggga agctttgtac cttagagtg 660
taggtgaaat gaatgaatgg cttggagtgc actgagaaca gcatatgatt tcttgctttg 720
gggaaaaaga atgatgctat gaaattggtg ggtggtgtat ttgagaagat aatcattgct 780
tatgtcaaat ggagctgaat ttgataaaaa cccaaaatac agctatgaag tgctgggcaa 840
gtttactttt tttctgatgt ttcttacaac taaaaataaa ttaataaatt tatataaatt 900
ctatttaagt gttttcactg gtgtcgcatt tatttcttgt taagttgcat tttctaatta 960
caaaagtaat gcatgattat gacagaaagt ttggaaaata t 1001

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<210> 296

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-409-249 : polymorphic base G or C

<220>

<221> misc_binding

<222> 481..500

<223> 10-409-249.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-409-249.mis2, potential complement

<220>

<221> primer_bind

<222> 253..271

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 678..697

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-409-249 potential probe

<400> 296

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ccggaatgct ttggggaaaa aagggcgagt taagaaagcc cacaaatcca agacccattg 60
agaagtgggt gggaaataag gtaaaatatt gaaccattcc ctagtcattt ccaaacttga 120
aaacagaatc agtgtaaat tcattttatt cttattaagg aaatactttg cataaattaa 180
tcagccccag agtgctttta aaaattctct taaataaaaa taatagactc gctagtcagt 240
aaagatattt gaatatgtat cgtgccccct ccggtgtctt tgatcaggat gacatgtgcc 300
atttttcaga ggacgtgcag acaggctggc attctagatt acttttctta ctctgaaaca 360
tggcctgttt gggagtgcgg gattcaaagg tgggtcccacc gctgccccta ctgcaaatgg 420
cagttttaat cttatctttt ggcttctgca gatggttgca attgatcctt aaccaataat 480
ggtcagtcct catctctgtc stgcttcata ggtgccacct tgtgtgttta aagaaggga 540
gctttgtacc tttagagtgt aggtgaaatg aatgaatggc ttggagtgcg ctgagaacag 600
catatgattt cttgcttttg ggaaaaagaa tgatgctatg aaattggtgg gtggtgtatt 660

```


255

tgagaagata	atcattgctt	atgtcaaagt	gagctgaatt	tgataaaaac	ccaaaataca	720
gctatgaagt	gctgggcaag	tttacttttt	ttctgatgtt	tcctacaact	aaaaataaat	780
taataaaattt	atataaaattc	tatttaagt	ttttcactgg	tgctgcattt	atctcttggt	840
aagttgcatt	ttctaattac	aaaagtaagt	catgattatg	acagaaagtt	tggaaaatat	900
agagggttcac	acacacatgc	cttcattgcg	tgtgcatgca	taaattgcatg	agaaaagaaa	960
aataaccagt	aatcgcatcg	cccagaaata	accccgatga	c		1001

<210> 297

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-410-274 : polymorphic base A or C

<220>

<221> misc_binding

<222> 481..500

<223> 10-410-274.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-410-274.mis2, potential complement

<220>

<221> primer_bind

<222> 228..245

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 645..664

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-410-274 potential probe

<400> 297

tgcaaaggc	agttttaatc	ttatcttttg	gcttctgcag	atgggtgcaa	ttgatcctta	60
accaataatg	gtcagtcctc	atctctgtcc	tgcttcatag	gtgccacctt	gtgtgtttaa	120
agaagggaag	ctttgtacct	ttagagtgtg	ggtgaaatga	atgaatggct	tggagtgcac	180
tgagaacagc	atatgatttc	ttgctttggg	gaaaaagaat	gatgctatga	aattggtggg	240
tggtgtattt	gagaagataa	tcattgctta	tgtcaaatgg	agctgaattt	gataaaaacc	300
caaaatacag	ctatgaagt	ctgggcaagt	ttactttttt	tctgatgttt	cctacaacta	360
aaaataaatt	aataaattta	tataaattct	atttaagtgt	tttactgggt	gtcgcattta	420
tttcttggtt	agttgcattt	tctaattaca	aaagtaatgc	atgattatga	cagaaagttt	480
ggaaaatata	gagggttcaca	macacatgcc	ttcattgctg	gtgcatgcat	aaatgcatga	540
gaaaagaaaa	ataaccagta	atcgcatcgc	ccagaaataa	ccccagttac	aattgtggca	600
aatacacata	cttataaata	ttgcagatat	attaagtata	cctagtattt	gctaacactc	660
tttcttctac	tctgtcatga	agattctccc	aagggtgtttt	tgtataatat	ttaattcatt	720
ttcagtgccc	aagcagtatt	ctacttcatg	gatataccag	gatttattta	accataactt	780
ctggttggtt	tactctttat	tattttgttt	aattaaaaaa	aaaagacctc	ggctgggcac	840
agtggctcat	gcctgtaatc	ccagcacttt	gggaggccga	ggtgggtgga	tcacctaaga	900
tcgggagttt	gagaccagcc	tggccaacat	ggcaaaaccc	cgtctctact	aaaaatacag	960
aaaattagcc	gggtgtggtt	gccagcacct	gtaattccag	c		1001

<210> 298

<211> 1001

256

<212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-410-280 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-410-280.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-410-280.mis2, potential complement

<220>
 <221> primer_bind
 <222> 222..239
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 639..658
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-410-280 potential probe

<400> 298
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 aatggctcagt cctcatctct gtcctgcttc atagggtgcca ccttgtgtgt ttaaagaagg 120
 gaagctttgt accttagag ttaggtgaa atgaatgaat ggcttggagt gcactgagaa 180
 cagcatatga tttcttgctt tggggaaaaa gaatgatgct atgaaattgg tgggtggtgt 240
 atttgagaag ataatcattg cttatgtcaa atggagctga atttgataaa aacccaaaat 300
 acagctatga agtgctgggc aagtttactt tttttctgat gtttcctaca actaaaaata 360
 aattataaaa tttatataaa ttctatttaa gtgttttcac tgggtgctgca tttatttctt 420
 gttaagttgc attttctaata taaaaagta atgcatgatt atgacagaaa gtttggaaaa 480
 tatagaggtt cacacacaca ygccttcatt gcgtgtgcat gcataaatgc atgagaaaag 540
 aaaaataacc agtaatcgca tcgcccagaa ataaccccag ttacaattgt ggcaaataca 600
 catacttata aatattgcag atatattaag tatacctagt atttgctaac actctttctt 660
 ctactctgtc atgaagattc tcccaagggtg tttttgtata atatttaatt cattttcagt 720
 ggccaagcag tattctactt catggatata ccaggattta ttttaaccata acttctggtt 780
 ggattcactc ttattatttt gttaatttaa aaaaaaaaaga cctcggctgg gcacagtggc 840
 tcatgcctgt aatcccagca ctttgggagg ccgaggtggg tggatcacct aagatcggga 900
 gtttgagacc agcctggcca acatggcaaa accccgtctc tactaaaaat acagaaaatt 960
 agccgggtgt ggttgccagc acctgtaatt ccagctaatt g 1001

<210> 299
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-410-337 : polymorphic base A or G

<220>

257

<221> misc_binding
 <222> 481..500
 <223> 10-410-337.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 10-410-337.mis2, potential complement

<220>
 <221> primer_bind
 <222> 165..182
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 582..601
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 10-410-337 potential probe

<400> 299
 aataatgggc agtcctcatc tctgtcctgc ttcataaggc ccaccttggtg tgtttaaaga 60
 aggggaagctt tgtaccttta gagggttaggt gaaatgaatg aatggccttgg agtgactga 120
 gaacagcata tgatttcttg ctttggggaa aaagaatgat gctatgaaat tgggtgggtgg 180
 tgtatttgag aagataatca ttgcttatgt caaatggagc tgaatttgat aaaaacccaa 240
 aatacagcta tgaagtgcgtg ggcaagttaa ctttttttct gatgtttcct acaactaaaa 300
 ataaattaat aaatttatat aaattctatt taagtgtttt cactgggtgc gcatttattt 360
 cttgttaagt tgcattttct aattacaaaa gtaatgcagc attatgacag aaagtgttga 420
 aaatatagag gttcacacac acatgccttc attgcgtgtg catgcataaa tgcattgagaa 480
 aagaaaaata accagtaatc rcacgcacca gaaataaccc cagttacaat tgtggcaaat 540
 acacatactt ataaatattg cagatatatt aagtatacct agtatttgct aacactcttt 600
 cttctactct gtcattgaaga ttctcccaag gtgtttttgt ataataattt attcattttc 660
 agtggccaag cagtattcta cttcatggat ataccaggat ttatttaacc ataacttctg 720
 gttggattca ctcttattat tttgtttaat taaaaaaaaa agacctcggc tgggcacagt 780
 ggctcatgcc tgtaatccca gcactttggg aggccgaggt gggtggatca cctaagatcg 840
 ggagtttgag accagcctgg ccaacatggc aaaaccccgct ctctactaaa aatacagaaa 900
 attagccggg tgtggttgcc agcacctgta attccagcta attggggaggc tgaggcagga 960
 gaattgcttg aaccgggggtc aggggggttcg gaggtcggag g 1001

<210> 300
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-121-326 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-121-326.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-121-326.mis2, complement

258

<220>
 <221> primer_bind
 <222> 178..196
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 637..656
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-121-326 potential probe

<400> 300
 ttcttgatac cctcggacga ggcctaccgg ggtactccca gcacctcgta gtagtcact 60
 atgctggact gccaaagagc ctgcggggca ctggcacagc gagcggcaag gctgccagca 120
 cccgcgcaca ggtcagaggc ttggcgacct gggccgcctg gagggccgcc ctttatgacg 180
 cagccacatc tcattggccg aggcctgtga gcgcctcgca tcccaagatg cagtgtcct 240
 gggactggcc ctgctctctg tgaggctctg tgaggccctg tgatgctcca agaccaggcc 300
 ccgccactc cggcctccaa ccagccatgg tctccaaaaa ggatgggaaa aagaggttgg 360
 ggaaaagaga gggccttgac tttggctgcc tgaagaactg tttttcttaa agtaggcttt 420
 atatcagtct ttttcctcgg ccacaggagg gaagagggtg gtgggagtga gtttagtctg 480
 accggggctg aagacatcct rttgtttagg actgcggttc tccaacgttc cagccccggt 540
 gccatttgc ttttgttcat ctggattatg cctatcatat gtactgcatt agagattaaa 600
 acagaattaa aaagacatat tcattgggca atttaagaag aataaaccga tgacacacta 660
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 cactgtacac ttgtgggaga atgacaatga gaaaatcaag taacattatt acggaaatag 900
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<210> 301
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-122-341 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-122-341.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-122-341.mis2, potential complement

<220>
 <221> primer_bind
 <222> 162..180
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 595..612
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-122-341 potential probe

<400> 301
 gcttcggctt gccctcagtg ggatgcaccc actatccaac cagtcccaat gagatgaacc 60
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 aggtcacact agatttaata tggtttggt cttgtgtccc caccaaatct catcttgaat 480
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 aatctcatca tagtgagtga gttcttatga gatctgatgg ttttataagg ggcccttata 600
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 caattaaagc tctttccttt ataaattacc cagtcttggg tatgtcttta tagcagtgtg 780
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 tgaaaatgtg gaagtgactt ggaactgggt aacaggcaga ggctggaaca gtttgagag 900
 ctcaagagac aggaagatgt gggaaagttt ggaacttcct ggagacttgt tgaacggttt 960
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<210> 302
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-122-381 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-122-381.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-122-381.mis2, potential complement

<220>
 <221> primer_bind
 <222> 122..140
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 555..572
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-122-381 potential probe

<400> 302
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 cgtcgatcat gctgggagct gcagatcgga gctgttccta tttggccatt ggtgctgaag 120

260

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cttccgttct cctctccaac acctcctttt tttttccttt tctcttcag tttttcaatg 180
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cagaacaaat tgggaactgt ggcacagggt actcttgcta tgccccttaa gaattccaca 300
ttaacaaagc taattttcga gtgtggtaaa gaacaggcta gtgtatttag tagtgagtcc 360
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caccaaatct catcttgaat tgtaatcccc ataatcccca cgtgttgagg acaggacatg 480
gtgggagggt cccacctcct matctcatca tagtgagtga gttcttatga gatctgatgg 540
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cagccacatg gaactggagt caattaaagc tctttccttt ataaattacc cagtcttggg 720
tatgtcttta tagcagtgtg tgaatggact aatacagtaa attggtgtca tggagagtgg 780
ggtactgcta taaaactact tgaaaatgtg gaagtgactt ggaactgggt aacaggcaga 840
ggctggaaca gtttgagag ctcagaagac aggaagatgt gggaaagttt ggaacttcct 900
ggagacttgt tgaacggttt tgacaaaaat gctgataatg ttgtggacaa tgaagtccag 960
gctgagtctc agatagagat gaggaatctg ttgagaactg g 1001

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<210> 303

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-124-169 : polymorphic base G or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-124-169.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-124-169.mis2, potential complement

<220>

<221> primer_bind

<222> 334..352

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 830..848

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-124-169 potential probe

<400> 303

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caagctgatt caggtaaaagc ggtaacaagt ttgctgaggc ctgggaggag gagaaagatg 60
ggagcagatg gaaaggcatt tgggtgggctg ggcacatgag gaggtttagaa gccctaaaag 120
gacatgttct ccttctgtca gagaagactt gggagttaca aagtctatag ctgtgtccat 180
ccccagggga gaactgagag aaccttccat cccgagagcc aggtggccag gagggcagca 240
gggagtgaca ccccttctgc tagccgccag agccacagcc attcctcaga cccacagaac 300
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ccagattgag agctttgaca gccctctctt ggagaagggt tgtcttcata gggacaggag 600
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261

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gagatcagct ggacctgtgg ctgtttacag ggtcctggga ggagaggagc gtggtctgga 720
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tctggctagc aatcacatgt gtgtatttct ttgtaaacac aaaactatac cgcattgcta 840
caaaatttcta aaacattttt gaaagaaatc agtgagggtc tcaataaata gaaagcacc 900
catgttcagtg gattgaaaga tgctatagtt caaatggtga tactctccaa atttatcttc 960
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<210> 304

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-124-194 : polymorphic base C or T

<220>

<221> misc_binding

<222> 482..500

<223> 12-124-194.mis1

<220>

<221> misc_binding

<222> 502..521

<223> 12-124-194.mis2, potential complement

<220>

<221> primer_bind

<222> 309..327

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 805..823

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-124-194 potential probe

<400> 304

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caagtttgct gaggcctggg aggaggagaa agatgggagc agatggaaaag gcatttggtg 60
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gacttgggag ttacaaaagtc tatagctgtg tccatcccca ggggagaact gagagaacct 180
tccatcccca gagccaggtg gccaggaggg cagcaggagg tgacaccctt tctgctagcc 240
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aaatcagtgga gggcttcaat aaatagaaaag caccctcatgt tcatggattg aaagatgcta 900
tagttcaaat ggtgatactc tccaaattta tcttcagttt tagcatgaca cctatcacia 960
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<210> 305

<211> 1001

262

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-124-300 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-124-300.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-124-300.mis2, potential complement

<220>
<221> primer_bind
<222> 203..221
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 699..717
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-124-300 potential probe

<400> 305
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 cccttctgct agccgccaga gccacagcca ttctcagac ccacagaaca ttattagcac 180
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 aacatttttg aaagaaatca gtgaggggtc caataaatag aaagcaccac atgttcatgg 780
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 gacacctatc acaatccaag ctagtctctt tttttgatcc taaaattgat cctaaaattt 900
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<210> 306
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-124-58 : polymorphic base A or C

<220>

263

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<221> misc_binding
<222> 481..500
<223> 12-124-58.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-124-58.mis2, potential complement

<220>
<221> primer_bind
<222> 444..462
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 940..958
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-124-58 potential probe

<400> 306
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caggtaaacg ggtaacaagt ttgctgaggc ctgggaggag gagaaagatg ggagcagatg      180
gaaaggcatt tgggtgggctg ggcacatgag gagtttagaa gcccctaaag gacatgttct      240
ccttctgtca gagaagactt gggagttaca aagtctatag ctgtgtccat cccaggggga      300
gaactgagag aaccttccat cccgagagcc aggtggccag gagggcagca gggagtgaca      360
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gcaagtcagt actcaaggtc mcgtagcatt cccagagccc aggcaagaac aaggatgaag      540
gcctttggcc cttctacca acgtcttggt cctccccagt ttctgcgaaa ctccctcaag      600
aagaccggg ggtctagctg gagcctgcgc ttgagcaaag agctgaacaa ccagattgcg      660
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aggagtagac tccaggggtg atggagtgga gaggataaca ccgtgtgtgt gagatcagct      780
ggacctgtgg ctgtttacag ggtcctggga ggagaggagc gtggtctgga ttggtggttt      840
tagttttgtt ttggtttatt tttttgcttt gttttgttga tcctccagat tctggctagc      900
aatcacatgt gtgtatttct ttgtaaacac aaaactatac cgcattgcta caaaattcta      960
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<210> 307
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-126-222 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-126-222.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-126-222.mis2, potential complement

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264

<220>
 <221> primer_bind
 <222> 703..722
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 267..286
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-126-222 potential probe

<400> 307
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 ttatatcaga acggcctctg gggccatctg gagtgcaggg tgggctgtgc tcctggccct 180
 tcattacagg cagacatttg gagccaggcc aaatgcaaca gccaaagcacc atcctggtga 240
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 gagtccccag cccccagcct gctgctctga catgcacaga aaaattcctg tgtctatctg 600
 gaagatgagg gaacacttat gaaatcaagt tctgtcccca gagggcccct tgggagaggc 660
 tgcagtgacc tagtgccctg ggctgggtca gggagggaga ggggtgggatt gtggttggca 720
 gagctccagg ctttgtgggg cctgtggcct ctgtagcggg gagagccctt ttaagaaaa 780
 aagatacata gttatgaacc ccacattggc taggaaaaatg aatatttact ttgagaaaat 840
 caagtgtgc aaaatcataa attttgcaaa gcttgacaag taccgcaacc cttaaaatgt 900
 ctagaacgac gtagtgtttt tactgattga ccacttgaca cagcctgatg agacttaatt 960
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<210> 308
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-126-297 : polymorphic base T or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-126-297.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-126-297.mis2, potential complement

<220>
 <221> primer_bind
 <222> 778..797
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 342..361
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-126-297 potential probe

<400> 308
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 tctgtgtgag tccaggagtc cccagccccc agcctgctgc tctgacatgc acagaaaaat 660
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 ggattgtggg tggcagagct ccaggctttg tggggcctgt ggcttctgta gcggtgagag 840
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 caacccttaa aatgtctaga acgacgtagt gtttttactg a 1001

<210> 309
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-128-225 : polymorphic base T or G

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-128-225.mis1, complement

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-128-225.mis2, potential

<220>
 <221> primer_bind
 <222> 706..725
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 276..295
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-128-225 potential probe

<400> 309
 ccctgaaatg ggaccatgac agctgggtct gagagacagt ggtagaaaaca tccagattca 60
 gcacttactt gctggcttgg atgcaggggtc tagaacgaaa agagaagaaa agtcacttct 120

266

atacagaaac	atgtccagag	cgcttactgt	ctccaaaacc	atggactggc	acctgagtga	180
tagcatgatt	ccaaagccaa	aatcttgcct	gtaaggaata	tatatatata	tatatatata	240
tatatatgta	tatatgatat	agctatagtc	taatagcaag	gacagatatg	caaactgcta	300
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aaggagatga	aaggagctgg	kagtgtgtct	gatggtggcc	tactaactta	tgtcttcagc	540
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attcatgagc	atgaatgtgg	attgcccact	attcagatta	gtaagtattt	cttgggtcaag	960
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<210> 310

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-129-176 : polymorphic base G or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-129-176.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-129-176.mis2, potential complement

<220>

<221> primer_bind

<222> 326..344

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 779..797

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-129-176 potential probe

<400> 310

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aatgtgataa	tttttagtgg	tcctgtcttg	cgaatgatag	agaggtgacc	acaggagacc	180
taagcactcg	caggaagtag	aagtgttaaa	gaggttgact	cagttcagtg	gaagtagagc	240
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tttctcaggt	gaagctgaac	atatcaccaa	acccacccta	tcccactcca	agtttctata	600
gtgggatcta	cttctttacc	aacaatttca	aaggcagctt	tctttaatcc	agaatatttg	660

267

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gggttcattg atgtgggtact ctgggacctg aatattgttt cttattcctt ggtgtgccat 720
gtatttcattg agagaattca gcctttttat gtcatattca ctgaatgcat atgaacttcc 780
atgacttgat ccttttgtat ttttatttct gtacttcctt ttattaacat aggtattatt 840
gccaaacact ctaagcttca ttttttaaaa tcaaaccaca tgattttttt attggtgatt 900
ttctccctta tgcagtgtag ttattcaatt ataaaatatg tgtttattag atttgtaaca 960
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<210> 311

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-130-203 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-130-203.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-130-203.mis2, potential complement

<220>

<221> primer_bind

<222> 301..319

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 733..753

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-130-203 potential probe

<220>

<221> misc_feature

<222> 167

<223> n=a, g, c or t

<400> 311

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aatcgttcct tgaaacagaa catcttctga tgaaattttc tagaagaatg gcaattatga 60
acaatatgtc tttgatcata cataggtcct gtgtggagct actgcataat gaggccctga 120
tcaggcacct gcatgctact tcctttgatg tggttctaac agaccnctt tcacctctgc 180
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cgaggggact ttgtgatgga ytaccccagg ccgatcatgc ccaacatggt cttcattggg 540
ggcatcaact gtgccaacgg gaagccacta tctcaggtct gtattggtgc ctttatccaa 600
tcaatgttcc aggcataaca ctttttaaaa aatgtattta cttacaagtg cttccatata 660
tacttatctt tccaaagatt tcatttctgc ttctcattgt tgtaaatagc ttcagtgaga 720
taaactttta aagggtcaat ggtagtgcag ttcagggttt caatggccac tgagagggaag 780
gagaggcagg gacgaggatc tgtcaaaggc tgggcaagag tggtgtgact cacggagact 840
gttcggttgc aaaagcacca tcttcatggc tgtggatgtg cttcagctgg gcaggagcag 900

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268

ggacactaca ctgagaactg atccatccaa tcttgctggc aagattttca gtagaaagga 960
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<210> 312

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-130-260 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-130-260.misl, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-130-260.mis2, potential complement

<220>

<221> primer_bind

<222> 244..262

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 676..696

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-130-260 potential probe

<220>

<221> misc_feature

<222> 110

<223> n=a, g, c or t

<400> 312

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 tgcgcggcgg tgctggctaa gtacctgtcg attcctgctg tgtttttctt gaggaacatt 180
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 ttactaacga ccaattcaga ccacatgaca ttcttgcaaa gggcaagaa catgctctac 300
 cctctggccc tgctctacct ttgccatgct gtttctgctc cttatgcaag ccttgccctc 360
 gagctttttc agagagaggt gtcagtgggt gatcttgtca gccatgcatc tgtgtggctg 420
 ttccgagggg actttgtgat ggattacccc aggcgatca tgcccaacat ggtcttcatt 480
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 caatcaatgt tccaggcaaa acacttttta aaaaatgtat ttacttacia gtgcttccat 600
 atctacttat ctttcctaaag atttcatttc tgcttctcat tgttgtaata gtcttcagt 660
 agataaactt ttaaagggtc aatggtagtg cagttcaggg tttcaatggc cactgagagg 720
 aaggagaggc agggacgagg atctgtcaaa ggatgggcaa gagggtgtg actcacggag 780
 actgttcgtt tgtaaaagca ccattctcat ggctgtggat gtgcttcagc tgggcaggag 840
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 aaaagataga gaggtgacca caggagacct aagcactcag a 1001

<210> 313

269

<211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-131-112 : polymorphic base T or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-131-112.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-131-112.mis2, potential complement

<220>
 <221> primer_bind
 <222> 594..612
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 104..124
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-131-112 potential probe

<400> 313
 catcttgagc tcagcctccc tgcagctttt tttatattga cagccacttc agagagagtc 60
 ctcttttgagc tttacaagaa atatacctggt gtgaaaaacg accaaaacca gatagccagc 120
 ctccccactc cctgttttaa gaaagctggc ttagcaatgt tgtctgcatt ttggatgtgc 180
 tgtgtttacc atatgtggga agaaagagta ttaagagtta gcaaataagg tcacatccag 240
 cagagaccat atggttgggg actagggcaa tgggtgactcc tcagacctca gctgcagcct 300
 gataaacgtg gttaagagag aagtaggaga cagtgcacatg aaatgggggt tcacagcctt 360
 gtgttgggaa ttgaatgaga aacaagagct tgaacttgga tggtccccag agcgagcgca 420
 aggtcagatg agtttttcaa gataggagtg atcggctctt cccagggtgg ggcccataat 480
 gcaagacaat tatagattaa ygggtaataa gtaactggag gagggcactc tgtcttcaat 540
 tacatgttga tttgctaggt gtctcagtga caaggtaatt aagacgaagg aaacaattct 600
 aggaggcaca acgtgggggtg gacagtcagc tgcgggtggc ttctgctgag atggccacag 660
 gactccaggt tcccctgccg cagctggcca caggactgct gcttctcctc agtgtccagc 720
 cctgggctga gagtgggaag gtgctggtgg tgcccactga tggcagccac tggctcagca 780
 tgcgggaggc cttgcgggac ctccatgcga gagggcacca ggtgggtggc ctcaccctgg 840
 aggtgaatat gtacatcaaa gaagagaact ttttcaccct gacaacgtat gccatttcat 900
 ggaccagga cgaatttgat cgccttttgc tgggtcacac tcaatcgttc tttgaaacag 960
 aacatcttct gatgaaattt tctagaagaa tggcaattat g 1001

<210> 314
 <211> 755
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 255
 <223> 12-132-157 : polymorphic base C or T

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<220>
<221> misc_binding
<222> 235..254
<223> 12-132-157.mis1, potential

<220>
<221> misc_binding
<222> 256..275
<223> 12-132-157.mis2, potential complement

<220>
<221> primer_bind
<222> 99..117
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 557..577
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 243..267
<223> 12-132-157 potential probe

<400> 314
cagctccatg gccaggatgt ggatgtcagc gtggctggca agagcaggca aggtgggcaa      60
agttcctgtc cagctgattg gattgggcag gtgggctgtc tccttgtctg ggaatgcccc      120
cccctctcca cattcctccc accctcattc ccccttctcc tggaaacatc caagtccaaa      180
ttaatactat taatgcctac ctggatatta atgcctacct gatcatatct aggtcatggt      240
agaattgtgt aaacytcctt tggatagctc actcctcatg tcctgtcccc ccagcccaca      300
gccctgggtc agatcccac cttgggagct cctggcccag cctttcccat gcatgacctt      360
actgggcctc tgctctgcct ggcttctctg agccagctag agtaactata ggcattcccat      420
cctctgtaga ctaccctcac tgtggtccac tcagagtggg cactgttaac accaggctct      480
caaaacaact atgcccacct accatgcttg ctctgtccc cttccctcca actctggccc      540
caagggcatc gctgggtgat taggtgattg atggggctct ttaggatcca gggctagcaa      600
agggcagagc ctgctctctg actttgatct aaacaagctg gccagtcaat cctctgaggt      660
cttctctcatg cccctctcac tcttgactct ggttgagtc tctccaggtc ccctgcactg      720
gcatcttctc agcaggcctg gccgtgccct tgccc      755

<210> 315
<211> 991
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-132-437 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-132-437.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-132-437.mis2, potential complement

<220>
<221> primer_bind
<222> 68..86

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271

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 526..546

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-132-437 potential probe

<400> 315

tggtctggcaa	gagcaggcaa	ggtgggcaaa	gttcctgtcc	agctgattgg	attgggcagg	60
tgggctgtct	ccttgtctgg	gaatgcccac	ccctctccac	attcctccca	ccctcattcc	120
cccttctcct	ggaaacatcc	aagtccaaat	taatactatt	aatgcctacc	tggatattaa	180
tgcctacctg	atcatatcta	ggatcatgta	gaattgtgta	aacctccttt	ggatagctca	240
ctcctcatgt	cctgtccccc	cagcccacag	ccctgggtcca	gatcccatcc	ttgggagctc	300
ctggcccagc	ctttcccatg	catgacctta	ctgggcctct	gctctgcctg	gcttctctga	360
gccagctaga	gtaactatag	gcatcccatc	ctctgtagac	tacctcact	gtggtccact	420
cagagtgggc	actgttaaca	ccaggctctc	aaaacaacta	tgccaccta	ccatgcttgc	480
tcctgtcccc	ttccctccaa	mtctggcccc	aagggcatcg	ctggtgatgt	aggtgattga	540
tggggctcct	taggatccag	ggctagcaaa	gggcagagcc	tgctctctga	ctttgatcta	600
aacaagctgg	ccagtcaatc	ctctgaggtc	ttcctcatgc	ccctctcact	cttgactctg	660
gttgagtcct	ctccaggtcc	cctgcactgg	catcttctca	gcaggcctgg	ccgtgccctt	720
gtccatttgt	ttgtgcgctg	ttggtttgct	tttctctggc	tcattggctc	ccaaagcctg	780
tggagagagt	caggagtggg	tagaatggca	gtgtctaatt	acttttggct	caacagagga	840
tggggttcac	agtaggagac	aaaacactgt	catggaaagt	cttggtgtcc	actacaaaat	900
gcgcattggc	tgaaaagagc	atcttctaaa	cctcaaccca	ttagcacgat	tctccctctc	960
tcccaggata	agtgaatgt	aatgatgttc	t			991

<210> 316

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 666

<223> 12-133-153 : polymorphic base T or C

<220>

<221> misc_binding

<222> 646..665

<223> 12-133-153.mis1, potential

<220>

<221> misc_binding

<222> 667..686

<223> 12-133-153.mis2, potential complement

<220>

<221> primer_bind

<222> 800..818

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 250..270

<223> downstream amplification primer

<220>

<221> misc_binding

272

<222> 654..678

<223> 12-133-153 potential probe

<400> 316

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ggtctgggat ctaacgggtga tagttctagt gaaaccctcc cacccttcca ggagacccat    60
tcctataaga aatatgactg aagagcccag ctgtctcact ttgataacca attcttccat    120
ttgcatttcc attgatgtgt attgggccaa gaggagagct ttttcttggt gttaatatct    180
gtttaatcca gaagaagacc ctaaggaaag gtcagtattt aggtcccaga gtagctcttt    240
aaaatccttt aaaggaaaag agagtatggg atagtaaagg gccatgggat ggatctttga    300
ggatcaagga acttgggaca ggaggagaaa ggatctgaga gcctttcttc caccatctcg    360
acatctatgt tgggtgttct caatttttaa gaagctgtgg atgttgagag aacccttaa    420
aggagtattg agagatactg atatgaattt ctcattagcc attaattatc agtgtgtaga    480
agagagggcg agagggtctt attaaactaa ggatattatc tattgctgtg taacaaatta    540
tcataaactc agtggcttaa aagaacatcc attgattatc tcacgggtcc actggccagg    600
agtctaggca tggctttcct tggctcttgg tttaggggtc cagagactgc agtcctttct    660
ggagtycagc ttcctcttcc aagctcatgt gcttattgga gaattcagtt tcttatgggt    720
gtaggactga ggccctcagt tccttgctac gtggccctca ccacaggcag tttgcatcat    780
ggctgtttac ttttcaaggc cagtagaatg tttctgttca atctgataag agggaatctc    840
atgtggcata gtgtgatcat gggaaatgaca tcccaccatc tttgcatat gatgtaatcc    900
actcgagaga gggtcaccca tcacctttgc catattctgt tgattagaag gaagtcacag    960
gttccaccca cacaccctca aggggatggc tttatggaag g                                1001

```

<210> 317

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-133-318 : polymorphic base T or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-133-318.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-133-318.mis2, potential complement

<220>

<221> primer_bind

<222> 800..818

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 250..270

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-133-318 potential probe

<400> 317

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ggtctgggat ctaacgggtga tagttctagt gaaaccctcc cacccttcca ggagacccat    60
tcctataaga aatatgactg aagagcccag ctgtctcact ttgataacca attcttccat    120
ttgcatttcc attgatgtgt attgggccaa gaggagagct ttttcttggt gttaatatct    180
gtttaatcca gaagaagacc ctaaggaaag gtcagtattt aggtcccaga gtagctcttt    240
aaaatccttt aaaggaaaag agagtatggg atagtaaagg gccatgggat ggatctttga    300

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273

```

ggatcaagga acttgggaca ggaggagaaa ggatctgaga gcctttcttc caccatctcg 360
acatctatgt tgggtgttct caatttttaa gaagctgtgg atgttgagag aaccccttaa 420
aggagtatat agagatactg atatgaattt ctcattagcc attaattatc agtgtgtaga 480
agagagggcg agagggctct wttaaactaa ggatattatc tattgctgtg taacaaatta 540
tcataaactc agtggcttaa aagaacatcc attgattatc tcacgggtcc actggccagg 600
agtctaggca tggctttcct tggctctttg tttaggggtc cagagactgc agtcctttct 660
ggagttcagc ttcctcttcc aagctcatgt gcttattgga gaattcagtt tcttatggtt 720
gtaggactga ggccctcagt tccttgctac gtggccctca ccacaggcag tttgcatcat 780
ggctgtttac ttttcaaggc cagtagaatg tttctgttca atctgataag aggggaatctc 840
atgtggcata gtgtgatcat gggaatgaca tcccaccatc tttgccatat gatgtaatcc 900
actcgagaga gggtcaccca tcacctttgc catattctgt tgattagaag gaagtcacag 960
gttccaccca cacacctca aggggatggc tttatggaag g 1001

```

<210> 318

<211> 643

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 249

<223> 12-136-238 : polymorphic base A or G

<220>

<221> misc_binding

<222> 229..248

<223> 12-136-238.mis1, potential

<220>

<221> misc_binding

<222> 250..269

<223> 12-136-238.mis2, potential complement

<220>

<221> primer_bind

<222> 12..32

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 442..461

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 237..261

<223> 12-136-238 potential probe

<400> 318

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acacaggggtg agcaaaaggg agacttttta tccttttttg agaaagcaac cacaaaattt 60
tgaccttatg aagtatcttt gaaactttcc aaagctgatt agaatagcgt tgatgtattt 120
taatcagata cagaaagact ttacaaagta tgagctgcac acttgctgtc gtaatgctta 180
taagcactaa tttttttgta tacattcatg tacttgtaat tgcacaaaat gcgaaggaca 240
catttggcrg tgaggatgct gtgcacaatc aactccta atttttcagg aaaggataaa 300
cattccgcta aaaaatgagga aagacaagaa atgttcaaaa gcatgtcaaa agtgtccagc 360
tgttttcata gaatataggt gatttcctgg tgctagcaaa atccagaaga aacgttataa 420
taactagaaa tgtctataat tgtgaggaag cccaagtatg aagattcaca aaaatagaat 480
aagtggatga aattagttaa aacaaccttc ttagtaatga ggtactctga ttataaaagt 540
actttgactc tttagaatgt gtcactgaac accaagctga aaaaacaaat taacagtctg 600
tcactagagc atgatctccc acagacaata tgctcataaa tga 643

```

<210> 319

<211> 1001

274

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-138-141 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-138-141.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-138-141.mis2, potential complement

<220>
<221> primer_bind
<222> 623..641
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 186..204
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-138-141 potential probe

<400> 319
tgatgtgtgg tactgggata cagagatggg caagactgtg aggtgcttac tccctgagga 60
ccaattggga cctgagatgt tcataatddd taaaagttcc cttgtcttct gacacagtgg 120
gtttgggagc cattgtccta cagcacatga gctgagttgc aaagatgttg agccagtggg 180
catgggagag taaagataca ccagacacag tgtgcaggga tgtttggtta gtggggagat 240
gcctagctgg gttaaggggc tggggtagag gatgttgagg ggagtgatac aaagtgaac 300
caggggacct ggtgggcttg tacagacaag gtttgcatac cgtgggtacca gacaaggttt 360
tggactagac aagggttttg aacagagctg atccaaacct tgctgggcac caccgccaga 420
gtttctgatt cagtaagtct ggggtggagc ctgagaatca gcatttctaa caagttccca 480
ggatgatcca aggtgatct rgagagccta ctttgagaac tggttgattt tagactacc 540
ttttgtcttg gagtgggtag caaaggggtg ctatgagcag aggagcttat ttataaaaag 600
ttttattatt tttgttgat ttggatttgc atttgcgttt tccccctttt atttttagtt 660
gacacataac aattgtacat atttatagaa tacaaagtga tatttcaaaa catatataca 720
atgtgtaatg accgaatcag ggtaattagt atatccaaca ctgcaaacad ttatcatttc 780
tttgtgttgc aagcattcaa aactgtttct tctagttttt tgaaaatata caatcaatca 840
ttgttgacta tattcacaac ctacagtgtc atagaacaca agagcttatt ccttctctcc 900
agctgtaatt ttgtatcttt taatcaactt ctccctatcc tcccctgccc ttagctttcc 960
tataccctaa taccgaaatt ctactcttga cttctatgag c 1001

<210> 320
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-138-42 : polymorphic base T or G

<220>

275

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<221> misc_binding
<222> 481..500
<223> 12-138-42.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-138-42.mis2, potential complement

<220>
<221> primer_bind
<222> 524..542
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 87..105
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-138-42 potential probe

<400> 320
ccttgtcttc tgacacagtg ggtttgggag ccattgtcct acagcacatg agctgagttg      60
caaagatggt gagccagtgg gcatggggaga gtaaagatac accagacaca gtgtgcaggg      120
atgtttggct agtgggggaga tgcctagctg ggtaaagggg ctggggtaga ggatgttgga      180
gggagtgata caaagtgcaa ccagggggacc tgggtgggctt gtacagacaa ggtttgcatt      240
acgtggtacc agacaagggt ttggactaga caaggggttg gaacagagct gatccaaacc      300
ttgctgggca ccacccccag agtttctgat tcagtaagtc tggggtggag cctgagaatc      360
agcatttcta acaagttccc aggtgatgcc aaggctgata tggagagcct actttgagaa      420
ctgttggatt ttagactacc cttttgtctt ggagtgggta gcaaaggggt gctatgagca      480
gaggagctta tttataaaaa kttttattat tttgttggga tttggatttg catttgcgtt      540
ttcccccttt tatttttagt tgacacataa caattgtaca tatttataga atacaaagtg      600
atatttcaaa acatatatac aatgtgtaat gaccgaatca gggtaattag tatatccaac      660
actgcaaaca tttatcattt ctttgtgttg caagcattca aaactgtttc ttctagtttt      720
ttgaaaatat acaatcaatc attgttgact atattcacaa cctacagtgc tatagaacac      780
aagagcttat tccttctctc cagctgtaat tttgtatctt ttaatcaact tctccctatc      840
ctcccctgcc cttagctttc ctatacccta ataccgaaat tctactcttg acttctatga      900
gctcaccatt tttatagctc ccatatatga gtgagaacat gtgggtattta tctatctgtg      960
cctgactcat ttcacttgac ataatgtcct ccagttttat t                                1001

<210> 321
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-138-67 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-138-67.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-138-67.mis2, potential complement

```

276

<220>
 <221> primer_bind
 <222> 549..567
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 112..130
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-138-67 potential probe

<400> 321
 agatgttcat aattttttaa agttcccttg tcttctgaca cagtggggtt gggagccatt 60
 gtcctacagc acatgagctg agttgcaaag atgttgagcc agtgggcatg ggagagtaaa 120
 gatacaccag acacagtgtg cagggatgtt tggctagtgg ggagatgcct agctgggtta 180
 aggggctggg gtagaggatg ttggaggagg tgatacaaag tgcaaccagg ggacctgggtg 240
 ggcttgatga gacaagggtt gcatcacgtg gtaccagaca aggttttggg ctagacaagg 300
 gtttggaaca gagctgatcc aaaccttgct gggcaccacc cccagagttt ctgattcagt 360
 aagtctgggg tggagcctga gaatcagcat ttctaacaag tcccaggtg atgccaaggc 420
 tgatctggag agcctacttt gagaactgtt ggatttttaga ctaccctttt gtcttgaggt 480
 gggtagcaaa ggggtgctat ragcagagga gcttatttat aaaaagtttt attatttttg 540
 ttggatttgg atttgcattt gcgttttccc ccttttattt ttagttgaca cataacaatt 600
 gtacatattt atagaataca aagtgatatt tcaaaacata tatacaatgt gtaatgaccg 660
 aatcagggtg attagtatat ccaacactgc aaacatttat catttctttg tgttgcaagc 720
 attcaaaact gtttcttcta gttttttgaa aatatacaat caatcattgt tgactatatt 780
 cacaacctac agtgctatag aacacaagag cttattcctt ctctccagct gtaattttgt 840
 atcttttaat caacttctcc ctatcctccc ctgcccttag ctttcctata ccctaatacc 900
 gaaattctac tcttgacttc tatgagctca ccatttttat agctcccata tatgagtgag 960
 aacatgtggg atttatctat ctgtgcctga ctcatttcac t 1001

<210> 322
 <211> 663
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-139-380 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-139-380.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-139-380.mis2, complement

<220>
 <221> primer_bind
 <222> 122..139
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 602..620
 <223> downstream amplification primer, complement

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<220>
<221> misc_binding
<222> 489..513
<223> 12-139-380 potential probe

<220>
<221> misc_feature
<222> 655,658
<223> n=a, g, c or t

<400> 322
caagtctgac acctgtgtgg caggccagca ggctggagac tagcaggggc ggatgctgca      60
gccttgtggc tgaatatctt ctccctcaga gaaatcccag cgtttcactc ttaaggcggt      120
tcacccacct atgttattga ggataatctc ttttatggat tatgcacttt cgtcacacct      180
acaagctacc ttcacaacaa cacctagatt ggtgtttgac tgaatgacta ggtacagtcg      240
cctagccaag ttgacacaca aaactgaccg tcataccagg catgcacaac tggatcatct      300
gccccggggtg cccctctaga ggacttggga tcagagggag ggccctggat gagaaggggt      360
tgatgagtgt gggtttgtat gaggctggca gtgataggag ttgggcaaca gggatgctgg      420
ccccagcagg gactagcaga ctctcttgcc acatcagggt gggtgacact taaatgcccc      480
tgacaaagac tggatttggc rgtggagcca gttcagggct gagactgtca ggggacatct      540
ctggggaagc agggatggga tggcaccatg gcagagcctg actgttctcc ttagaagccc      600
agggcttggg ctaattctga gcccctttct ctcccacccc taccacagca gtttngcntg      660
agg                                                                                   663

<210> 323
<211> 951
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-140-134 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-140-134.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-140-134.mis2, complement

<220>
<221> primer_bind
<222> 368..386
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 868..888
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-140-134 potential probe

<220>
<221> misc_feature
<222> 923

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<223> n=a, g, c or t

<400> 323

ctgtagatca ttctggctaa ataatgggat tcacttttaa gtgaaggagg ccttgaatgc	60
cacactcagg ggcctagcgc agcacttccc aagccttgct gtggtttaga acaacctggg	120
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<210> 324

<211> 756

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-140-329 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-140-329.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-140-329.mis2, potential complement

<220>

<221> primer_bind

<222> 173..191

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 673..693

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-140-329 potential probe

<220>

<221> misc_feature

<222> 728

<223> n=a, g, c or t

<400> 324

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279

gatacctggaa	ctgtcagtca	ccaccaaacac	ccctgtcccc	caaatgcagc	tacacacccat	180
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gctgggcctg	ctctggaccc	ggtgagcatg	actaaagctg	tccttccacc	ctgcagctcg	660
ctcctacccc	aaggagctga	tgaagttctt	cttcagccag	atggagacaa	acaaggaggc	720
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<210> 325

<211> 700

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-140-385 : polymorphic base G or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-140-385.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-140-385.mis2, potential complement

<220>

<221> primer_bind

<222> 117..135

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 617..637

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-140-385 potential probe

<220>

<221> misc_feature

<222> 672

<223> n=a, g, c or t

<400> 325

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280

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<210> 326
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-141-159 : polymorphic base T or C

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-141-159.mis1, potential complement

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-141-159.mis2

<220>
 <221> primer_bind
 <222> 640..658
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 181..200
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-141-159 potential probe

<400> 326
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 aggcctcttc gcacctgagg tgagctgggt tcccaccctc accccatccc aaggggtagg 180
 gaaaagtcca agaccattcc tcggtgctcc ttcaggggtt gtgcctcctt tttcctctcc 240
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 caaaataaca gtgataacac tgaagagcat tgcaagcatc cttcaagatg agtcaggctc 480
 agtgagtgcg ttgaagggtc yagtcaacta tttgttgata ccaactggta aaaatgatct 540
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 cccctatagg ggaagattca ttacttaggc gcatagcaga actatctgtt actttaagct 720
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 ctgagtactg aagggaacac gagatacata agaccatgac ccagcctttt aaggacttag 840
 agataagaca gacacataca aacaggatta taggtcaaag ctgactaaca ggactgtgtt 900
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<210> 327
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>

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<221> allele
<222> 501
<223> 12-141-392 : polymorphic base C or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-141-392.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-141-392.mis2, potential complement

<220>
<221> primer_bind
<222> 873..891
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 414..433
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-141-392 potential probe

<400> 327
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cactctgctg cctcccctaa gatgccaaaa gccaaatggc ctaaaaaaga atgaaagaga 180
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gagttgaagg gctcagtcaa ctatttgttg ataccactgg taaaaaatga tctaaagccc 780
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<210> 328
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-142-315 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-142-315.mis1, potential

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282

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-142-315.mis2, potential complement

<220>
 <221> primer_bind
 <222> 187..205
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 637..657
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-142-315 potential probe

<400> 328
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 gggatgggag ttacttctgg ggtcctagtc actccggagc cgcctcact ctagtcccct 180
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 ggggtctcgc tggggcaggc ttcctgcagg aggactcaga gaggccgagg ggctttgcta 840
 ggtgggaagg cagggccccag cgaccctatc tcagagttag tgttgagcgc tctgaggggc 900
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<210> 329
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-142-321 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-142-321.mis1, potential

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-142-321.mis2, complement

<220>
 <221> primer_bind
 <222> 181..199
 <223> upstream amplification primer

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<220>
<221> primer_bind
<222> 631..651
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-142-321 potential probe

<400> 329
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ggagttactt ctggggtcct agtcactccg gagccgccct cactctagtc ccctttgtaa      180
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gcgagcgccc ctctctgag tgctcattct ctcatctgct ccttcattca ttcacacat      660
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tcgctggggc aggcttcctg caggaggact cagagaggcc gaggggcttt gctaggtggg      840
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<210> 330
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-143-453 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-143-453.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-143-453.mis2, complement

<220>
<221> primer_bind
<222> 50..68
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 533..552
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513

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284

<223> 12-143-453 potential probe

<400> 330

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gcagagctgt cttcagtcctc tggaggctgt ggagggaagc gagaagaggc tcgttctgca 660
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<210> 331

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-144-169 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-144-169.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-144-169.mis2, potential complement

<220>

<221> primer_bind

<222> 651..669

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 148..167

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-144-169 potential probe

<400> 331

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accgtgccct tctagctcac tttttaatgc ttttctgact cctggactat ttcttgggcc 120
ccagccagga cagagggcta agccagctct ggactgttag ggggttgagg tggagggcag 180
caggggtgtc ctctctgct tctctctgct cccccccagc cccaacttcc tgtaatcatc 240
cctcacaacc tcacagtgtt tgagttcatg ccatacatgg gcatcaccct ggctaccata 300
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285

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<210> 332

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-144-33 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-144-33.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-144-33.mis2, potential complement

<220>

<221> primer_bind

<222> 515..533

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 12..31

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-144-33 potential probe

<400> 332

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286

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<210> 333
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-146-174 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-146-174.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-146-174.mis2, potential complement

<220>
<221> primer_bind
<222> 655..674
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 271..291
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-146-174 potential probe

<400> 333
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caccagaaca aacttctaag tttatatagc ctctagttagc ataacctgag acccggaactt 420
ggcacttggt aagcacacaa tgaacagtca tagaaagctg gccgagggta gagttcagtg 480
tgaacaaagc aatttgggaa yatcaaagca agtttggaga acaacaagt atccagaatg 540
gctggagggt aagaggcaga gggagggggc aagcagaagg ggtggagagg aggaatgagc 600
ttagacaggg gggctggggg ctatcccaga gttttgagag caaggcagag gactctgaat 660
tttcttctgt gccaggaag ctgctgacca aggtccaga agtgttggtg ggggtggcgtt 720
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gacaggggccc ctgaaatggg accatgacag ctgggtctga gagacagtgg tagaaacatc 840
cagattcagc acttacttgc tggcttgat gcagggtcta gaacgaaaag agaagaggag 900
tcacttctat acagaaacat gtccagagt cttactgtct gcaaaaactgt ggactggcac 960
ctgagtgata gcatgattcc aaagccaaaa tcttgccctgt a 1001

<210> 334
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>

287

<221> allele
 <222> 501
 <223> 12-146-47 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-146-47.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-146-47.mis2, potential complement

<220>
 <221> primer_bind
 <222> 528..547
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 144..164
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-146-47 potential probe

<400> 334
 gtgattat t cactagaac tgctatatca tgaccatgaa ttttggggga atttttttga 60
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 attgtgaggg aatacactag taaaggtcac tcagttctaa ggggaaaaatg attaaccaaa 180
 gaacattcta agatttccta taggggtatta ggtctaattgg ggatgtgtta tgtcaccaga 240
 acaaacttct aagtttatat agcctctagt gacataacct gagaccgga cttggcactt 300
 ggtaagcaca caatgaacag tcatagaaag ctggccgagg gtagagttca gtgtgaacaa 360
 agcaatttgg gaacatcaaa gcaagtttgg agaacaacaa gtgatccaga atggctggag 420
 ggtaagaggg agagggaggg ggcaagcaga aggggtggag aggaggaatg agcttagaca 480
 ggggggctgg ggtctatccc rgagttttga gagcaaggca gaggactctg aattttcttc 540
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 gagcagctga ggcagtgatt cagaagggac agctgggggt tgggcaactg ggggacaggg 660
 gccctgaaat gggaccatga cagctgggtc tgagagacag tggtagaaac atccagattc 720
 agcacttact tgctggcttg gatgcagggt ctagaacgaa aagagaagag gagtcacttc 780
 tatacagaaa catgtccaga gtgcttactg tctgcaaaac tgtggactgg cacctgagtg 840
 atagcatgat tccaaagcca aaatcttgcc tgtaaggaat atatgtatag gatatagcta 900
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<210> 335
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-148-283 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-148-283.mis1, potential

288

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-148-283.mis2, potential complement

<220>
 <221> primer_bind
 <222> 765..783
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 375..395
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-148-283 potential probe

<400> 335
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 cccacaaatt gtgcagccca ttctgttctg gaggaaccat tcttatcaga acttggtgct 120
 ggattgactt ggagaagagc ctgaccataa tcttcaggat gaaataaagg cctggatgac 180
 tgaaataaag actggagcct tcggcattca gaagagggaat tcagactgtg caagatctga 240
 ggccaggctc cagctccccc agtcccttg tgagcaggag ctccctgaac ccaccatggg 300
 tctttgctag ggttgctctg cccatgtgtg ctttagatag cagcacctct tcttccatgg 360
 tgtatatgga gaatcctcaa caaagtcttc ccaagaatct gatcatcaca tcttgagctc 420
 agcctccctg cagctttttc tatattgaca gccacttcag agagagtcct ctctgaccc 480
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 cagagaaaagc tggcttagca atgttgtagt gtttttggat gcgctgctt actcatacat 600
 gagaagaaaag tttcaagggt tagcaaatag ggtcacatcc agcagagagc atatgactgg 660
 gggctagggc aatggtgact cctcagacct cagctgctgc ctgataaaca tgggttaacag 720
 agaagttaga gacagtgaac tgaaatgggt gttcacagcc ttgtgttggg aattggatga 780
 gaaacaagag cttgaacttg gatgttcccc agagtgaagc cagggtcaga cgtgtttttc 840
 aagatagtag tgatcgggtc tttccagggt ggggcccaca gtgaaaaaca gtgatagatt 900
 aatggttaat aattaactag aggagggcac tctgtcttcc aattacacgt tgatttgcta 960
 agtgggtcag tgacaaggta attaatgatga agaaagcaaa t 1001

<210> 336
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-148-311 : polymorphic base T or C

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-148-311.mis1, complement

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-148-311.mis2, potential

<220>
 <221> primer_bind
 <222> 793..811
 <223> upstream amplification primer, complement

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<220>
<221> primer_bind
<222> 403..423
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-148-311 potential probe

<400> 336
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ggaaccattc ttatcagaac ttgggtgctgg attgacttgg agaagagcct gaccataatc 180
ttcaggatga aataaaggcc tggatgactg aaataaagac tggagccttc ggcattcaga 240
agaggaattc agactgtgca agatctgagg ccaggctcca gctccccag tcccttggtg 300
agcaggagct ccctgaaccc accatgggtc ttgctaggg ttgtcttgcc catgtgtgct 360
ttagatagca gcacctcttc ttccatgggtg tatatggaga atcctcaaca aagtcttccc 420
aagaatctga tcatcacatc ttgagctcag cctccctgca gctttttcta tattgacagc 480
cacttcagag agagtcctct ytgatcctta caagaaatat cctggtgcga aaaacgacca 540
aaaccacata gccagcctcc acgctgttca gagaaagctg gcttagcaat gttgtatggt 600
ttttggatgc gctgctgtac tcatacatga gaagaaagtt tcaagggtta gcaaataagg 660
tcacatccag cagagagcat atgactgggg gctagggcaa tgggtgactcc tcagacctca 720
gctgctgect gataaacatg gttaacagag aagtaggaga cagtgcacatg aaatgggtgt 780
tcacagcctt gtgttgggaa ttggatgaga aacaagagct tgaacttggg tggtccccag 840
agtgagcaca gggctcagacg tggttttcaa gatagtcag atcggtcttt tccaggggtg 900
ggccacagt gaaaaacagt gatagattaa tgggttaataa ttaactagag gagggcactc 960
tgtcttccaa ttacacgttg atttgctaag tggctcagtg a 1001

<210> 337
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-149-320 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-149-320.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-149-320.mis2, potential complement

<220>
<221> primer_bind
<222> 800..820
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 368..387
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513

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290

<223> 12-149-320 potential probe

<400> 337

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cagcacctgt aattccagct aattgggagg ctgaggcagg agaattgctt gaaccggggt      60
caggggggttc ggagggtcgga gggtgcagtg agtccggatc atgccactgc attccagcct      120
gggtgacaca gccagactct gtctcaaaaa caacaacaac aacaaaaaca caacaacaac      180
aacaacaaaa atctcactgg acatcctagt agctaaggct tccacatat tcatgattac      240
ttctgttggga aagtgccttta caacaaattg ctagttgtct cagtctgggt tcccctgaga      300
tgaggattca agggccagga gtttatttag gaagtaaagg aaacactgat agaggagtgg      360
cagagtgaga aggggtgatg gtcattccaca gctggctctc ttgtggtcaa tcggagctta      420
atcctgctgg gtgactctgg gagccagtgg agaaaagaca ccccagactt atcccaatga      480
ggaacacggc tgttgggtgc ytgagtactt gcctctgcag ggattgaaac gtactccag      540
gtagtagtaa tttctctgcc cttccattag gccacaaagg gggctctgac agagagagct      600
gacgagaaaa aacacacgcc cttgtcactg aagaggtaca caggggatct gtgtggggca      660
ccacctgcac tgctaccctg gacaaatagc ttaagaaatc cccacactgc atcccaaac      720
ttactatcag cgtgtgaggg agacaggttc ccacaccctc attagcaca agtactatct      780
tgaaaaagaa agcctgtcag tttgatagga gaaaagcagg atcttgttta caatgtgctt      840
ttattattgt tattattaga gattgtattt cttttcaagc tgatgagccg tctgtgttta      900
ttttttggag gatacccttt gcccactttc ctattggagt gtattaccct gaggatttgg      960
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<210> 338

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-151-174 : polymorphic base G or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-151-174.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-151-174.mis2, potential complement

<220>

<221> primer_bind

<222> 328..345

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 827..845

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-151-174 potential probe

<400> 338

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gcctgtgtgt ctgacatgca cagaaaaatt cctgtgtcta tctggaagat gagggaacac      60
ttatgaaatc aagtctctgc ccagaggggc cccttgggag aggctgcagt gacctagtgc      120
cctgggctgg gtcaggagg gagaggggtgg gattgtggtt ggcagagctc caggctttgt      180
ggggcctgtg gcttctgtag cggtgagagc cttttttaag aaaaaagata catagttagt      240
aaccacacat tggctaggaa aatgaatatt tactttgaga aaatcaagtg ctgcaaaatc      300
ataaattttg caagcttga caagtaccgc aacccttaaa atgtctagaa cgacgtagt      360

```

291

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tttttactga ttgaccatct gacacagcct gatgagactt aattgtctac actttttggc 420
tccatgctgt ttgactgtct tgcctcagg atggctgtgg caggaggatg atggagtcag 480
ggtctggggc gcagggatgg kcgctctggtg caggagagaga agtgggctgg gcaggaggac 540
cctggtcctg ggcacctgga tggaggtggg gatgaaggct cagcaaaatg aggcaggggc 600
caagtccaac actcagtaac atgtgaggcc agaggctgtg tgggaaggctt cacctgggct 660
ctcatgacat tccctgcaag aggaggtgcc atcatcatct ccactgtgca gacaggaaac 720
atgagactga gaggcagagt accctgcctg gactgctcag ctagttagca ggaagctctg 780
atttgatccc cagggttcgt tacaggaaca actgggccc agttcagagc tgtgaactga 840
gcagagctga gtcagaggga gtcctgatcc agggcccaca gatccaggct gctcagcctc 900
caggggccc a gctgtgggca ggggaggctg atgcttgagc aggggacaga cagtggcacc 960
ctccccttcc ccaaattgggt gtttcagagc aggggtttgcc c 1001

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<210> 339

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-151-196 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-151-196.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-151-196.mis2, potential complement

<220>

<221> primer_bind

<222> 306..323

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 805..823

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-151-196 potential probe

<400> 339

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gaaaaattcc tgtgtctatc tggaagatga gggaacactt atgaaatcaa gttctgtccc 60
cagagggccc cttgggagag gctgcagtga cctagtggcc tgggctgggt caggagggga 120
gaggggtggga ttgtggttgg cagagctcca ggctttgtgg ggcctgtggc ttctgtagcg 180
gtgagagccc tttttaagaa aaaagataca tagttatgaa cccacattg gctaggaaaa 240
tgaatattta ctttgagaaa atcaagtgtc gcaaaatcat aaattttgca aagcttgaca 300
agtaccgcaa cccttaaaat gtctagaacg acgtagtgtt tttactgatt gaccatctga 360
cacagcctga tgagacttaa ttgtctacac tttttggctc catgctgttt gactgtcttg 420
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gtctggtgca gggagagaag ygggctgggc aggaggaccc tggctctggg cacctggatg 540
gaggtgggga tgaaggctca gcaaaatgag gcaggggcca agtccaacac tcagtaacat 600
gtgaggccag aggctgtgtg gaaggcttca cctgggctct catgacattc cctgcaagag 660
gaggtgccat catcatctcc actgtgcaga caggaaacat gagactgaga ggcagagtac 720
cctgcctgga ctgctcagct agtgagcagg aagctctgat ttgatcccca gggttcgtta 780
caggaacaac tgggccc aag ttcagagctg tgaactgagc agagctgagt cagagggagt 840
cctgatccag ggcccacaga tccaggctgc tcagcctcca ggggcccagc tgtgggcagg 900

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292

ggaggctgat gcttggacag gggacagaca gtggcaccct ccccttcccc aaatgggtgt 960
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<210> 340
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-151-270 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-151-270.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-151-270.mis2, potential complement

<220>
 <221> primer_bind
 <222> 232..249
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 731..749
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-151-270 potential probe

<400> 340
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 taagaaaaaa gatacatagt tatgaacccc acattggcta ggaaaatgaa tatttacttt 180
 gagaaaatca agtgctgcaa aatcataaat ttgcaaagc ttgacaagta ccgcaaccct 240
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 gtggcaggag gatgatggag tcagggtctg gggcgaggag atgggcgtct ggtgcaggga 420
 gagaagtggg ctgggcagga ggaccctggt cctgggcacc tggatggagg tggggatgaa 480
 ggctcagcaa aatgaggcag rggccaagtc caacactcag taacatgtga ggccagaggc 540
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 atctccactg tgcagacagg aaacatgaga ctgagaggca gagtaccctg cctggactgc 660
 tcagctagtg agcaggaagc tctgatttga tccccagggt tcgttacagg aacaactggg 720
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 cacagatcca ggctgctcag cctccagggg ccagctgtg ggcaggggag gctgatgctt 840
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 tgccctatca agttgtcctt tacactgccc ctgggcagcc ccaggtgtgc atgagagcac 960
 agaggtgtga gccccacggt ctctgtcccc tcagatccac c 1001

<210> 341
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>

293

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<221> allele
<222> 501
<223> 12-152-453 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-152-453.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-152-453.mis2, potential complement

<220>
<221> primer_bind
<222> 50..68
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 553..572
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-152-453 potential probe

<220>
<221> misc_feature
<222> 260
<223> n=a, g, c or t

<400> 341
gccacggctc tgggcaggag gcttagggaa ttgggggctc ccaagtgttt aaaggggatg      60
agtgggagcc ggggggatgt cagatatattt gacactgtgt caggaaccgc acatctgtgc      120
cctgcgaggg aggggcgtgg agcctggcac ccgtgggact catgggaatg aacactgccc      180
ttccgggttg aagggaccag gtgctgggtc ctcgaggct gcagtgaggc tgtggccttt      240
gcattagttt gttagggttn gctgtaacaa agaaccacac atgcgtagct tgaagcaaca      300
gagatgtatt ctctgtacgt cctggaggtc aggagtccaa actcagggtg tcggcagggc      360
tgtgtcctt ctgaaggctc taaggaagca agctctcttg cctcttccag cttctggtgg      420
ccccacatgt tctgtgactg tggcagcatc actccaattt ctcccttctt cattgcgtgg      480
cctttccctg tgtgtccctc ygtgtcctct tcttacaagg acacctaccc aaaatccagg      540
atgatctcac ttcgaaatcc tgaactaatt ccatacaaaa gacctattt ccaaataagg      600
tcacattatc agattctggg cgagcctgaa ttttggaagg acaccggtca actcaaggca      660
gccttggtag aggggtgaga tgtgtgagat ggagccgttg cagtgttccg cgtggagctg      720
tggtatggggc tgggtgccat gtaaagggat cactcatcta taaggagggt gtgggtctca      780
gctcttaaag caaggagtgg aaagggatgt gactgattta ggagccatct gtagatcatt      840
ctggctaaat aatgggattc acttttaagt gaaggaggcc ttgaatgccca cactcagggg      900
cctagcgtag cacttcccaa gccttgctgt gggttagaac aacctggggg ctgggtgaaa      960
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<210> 342
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-153-116 : polymorphic base C or T

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294

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-153-116.mis1

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-153-116.mis2, complement

<220>
 <221> primer_bind
 <222> 386..405
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 867..887
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-153-116 potential probe

<400> 342
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 cccttgacct cgtctctgtc cttgaaggag agggaccag acacccccga gtgctcagtt 180
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 ggcttggttc tgettccagc cctctggcg ccaagtgcac tcccctgttg ctgttggtag 360
 ccatggagac cttctgtgag acggtgcagt tttatctgaa gcacctggag gagagcgtgt 420
 acccctgtgat gactgaggag gagtttgccc tgaagggtgtt ccccatgtat cgctacttcg 480
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 ggtccacact tactcccagg accctagagg gcagtgcact gactcatggc agagccgggg 660
 aactcatgga tgctgaacag ctgggacctg ggagcctcat ccacgaggcc aggcttgatg 720
 aagggttggtg ataactctga gagcacttgt tacatgctgg gcactctacc agcgtcttac 780
 ccatgggagc tattttcaca cccactctgt gatataggac tagttgacaa atgaggaaac 840
 tcaggcacag aggggttaag tacctgctca aggtcatgtg gctgctaagt gggagggact 900
 caaaccggc cgctgtgca ggaaagacct tgctctgctt ctgaggcgcc ttctgtcctg 960
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<210> 343
 <211> 1000
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-154-480 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-154-480.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-154-480.mis2, potential complement

<220>
 <221> primer_bind
 <222> 23..43
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 522..540
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-154-480 potential probe

<400> 343
 ccattggagat gcagtgcagc atcttcaagt ctctaattct tacatctgtc tctttcactt 60
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 aaacccttaa tataatcaca tctataaagt ctcttccacc tgtaatggaa tatattccca 180
 gggttgcgca actacaatgt agatactttg tggggctgtg attctgccta ccacagacac 240
 taagcttaaa gtgaaaccca catcttattc aaaacttgga gggttttcctt catttgcca 300
 tttaaattta atttttgttt ctgtcctccg tagtcttcta ttctccaggc ttcagagctc 360
 tcagcttacc attcaattat ctcttttctc tccttatatt ccttttttca ttttttaaaa 420
 acaatacttt caaagagcaa aaattttaga atttgatgag gtttattcta gtgaagtgtt 480
 tatcgtttgt actttttgta ycctaaggaa gctttgttta cccaagata tagtttctac 540
 attctcttaa aaacactaaa gagttccagt ttatatgttt agctctgtga gattgggaga 600
 ggggagctag atcactcagg tcaggcttcc gggatgcctt tttctgtctc tggacgttgc 660
 tggggtgacc tcaactgacac ccattggcttc agctaccaca tatgctgatg gctccaagtc 720
 tatctgtgca gccagagccc ctctcatct ccagaccctg gaagctgatg ccttgggcag 780
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 ctgaggggccc ctatgtctct gaaggcacca ccatttcca agatacatgg gcctccgcag 900
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 ccactacatg gaaatagaac accactacat ggaaatagaa 1000

<210> 344
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-155-403 : polymorphic base A or C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-155-403.mis1, potential

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-155-403.mis2, potential complement

<220>
 <221> primer_bind
 <222> 99..116
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 628..647

296

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-155-403 potential probe

<220>

<221> misc_feature

<222> 49,58,62,639

<223> n=a, g, c or t

<400> 344

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tnctaataag	gacacaacaa	agagtgaag	cattgctatg	tctattctgc	ttgcccagaa	120
tcttggctct	aaaaaatgaa	gagtgtttgg	gtgtggggag	gagcttcagt	gtgcatgtgc	180
atgcaaagta	cctactctaa	ggagaagaat	gagaggggtac	cctaattacc	tgtaatatg	240
tcccatagga	cacccaaaact	ctagtttagct	gtttctctat	gatcctctaa	gcacatcccc	300
aagtatggct	ggccagtgat	gtgtatgggt	caaatgttgg	gatctgtgca	gttatcttgg	360
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gcacaatact	tgccccatag	tccatggtca	ataaatacaa	atttgagttg	tttttgctca	480
tctttccctt	ttgacttcaa	mtcagtcac	agaatttccc	caaatgcctt	tccccggat	540
cttggggccag	tggaatgagt	acaatttaac	ttaattgaat	ttgcttatct	atttggttct	600
ctgttgtgaa	caaaagtctt	ctgaaaagga	atttggaana	aagagacttt	gttctagtga	660
acagtttgca	aaccagggag	ttacagcctc	tggtacgcaa	tgaagggtgag	ttccacagaa	720
cacaaggcag	gcagggttca	cggcaaaaag	ttccttccca	ggttcccaat	caggtccatt	780
tatgcaaatg	aaggatggaa	acttgcttag	ttcttattgg	tcactgcagc	tgcatctctga	840
ttggttgatg	aagctgagcc	ctgagtggct	gaggtgggtg	agctttaatt	ggttggttca	900
ggtgagcgct	gaaaatctca	actataaaaa	ggtacaggtt	ttcaggatac	tcagagtaac	960
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<210> 345

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-156-91 : polymorphic base A or G

<220>

<221> misc_binding

<222> 482..500

<223> 12-156-91.mis1

<220>

<221> misc_binding

<222> 502..520

<223> 12-156-91.mis2, complement

<220>

<221> primer_bind

<222> 412..429

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 844..862

<223> downstream amplification primer, complement

<220>

<221> misc_binding

297

<222> 489..513

<223> 12-156-91 potential probe

<400> 345

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gtggtgcccc ttgatggcag ccactggctc agcatgcggg aggtcttgcg ggagctccat      180
gccagaggcc accaggcagt ggtcctcacc ccagaggatga atatgcacat caaagaagag      240
aactttttca ccctgacaac ctatgccatt tcgtggaccc aggatgaatt tgatcgccat      300
gtgctggggc aactcaact gtactttgaa acagaacatt ttctgaagaa atttttcaga      360
agtatggcaa tgttgaacaa tatgtctttg gtctatcata ggtcttgtgt ggagctacta      420
cataatgagg ccctgatcag gcacctgaat gctacttcct ttgatgtggt tttaacagac      480
cccgttaacc tctgcgcggc rgtgctggct aagtacctgt cgattcctac tgtgtttttt      540
ttgaggaaca ttccatgtga tttagacttt aagggcacac agtgtccaaa cccttcctcc      600
tatattccta gattactaac aaccaattca gaccacatga cattcatgca aagggtcaag      660
aacatgctct accctctggc cctgtcctac atttgccatg ctttttctgc tccttatgca      720
agccttgccct ctgagctttt tcagagagag gtgtcagtgg tggatattct cagtcatgca      780
tctgtgtggc tgttccgagg ggactttgtg atggactacc ccaggccaat catgcccac      840
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ggtgccttca tccaatcaat gttccaggca aaacactttt taaaaaatg tatttattta      960
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<210> 346

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-157-437 : polymorphic base A or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-157-437.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-157-437.mis2, potential complement

<220>

<221> primer_bind

<222> 67..87

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 513..533

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-157-437 potential probe

<400> 346

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tgaagagcat tgcaagcatc cttcaagatg agtcaggctc agtgagtggg ttgaagggct      180
cagtcaacta tttgttgata ccactgggtac aaaatgatct aaagcccaag acttaccttc      240
ctggagatgc caatccattg gtggggaggg ggaaggggga agaagttatg gatttataaa      300

```

298

```

attagatattt aaagagtttg ggtcatctct aagaatacct cccctatagg ggaagattca 360
ttacttaggc gcatagcaga actatctgtt actttaagct gcatcaaaca ggcagatttt 420
aaaataaatg tcatgaacat caactaagca caatgatatg ctgagtactg aagggaacaca 480
gagatacata agacctagtc mcagcctttt aaggacttag agataagaca gacacataca 540
aacaggatta taggtcaaag ctgactaaca ggactgtgtt tacaggtaaa cccacacaca 600
catcagcaaa aaaatatctg agaacaaaaa aaaaggggct actaacaaaa gcaactcagt 660
ttatacaaaa ggagctatca agaggcttgg tgcaaagttg gcatttggtt tttgacctgg 720
gcttaggcag aacgactgga cttggcgctt cctaggagag tgaatacaa gacactttgg 780
gggagcagga gtttaaagca ggatggtggc tctcaactct aggggcacaa tagaactcat 840
ggggaacttt taacagtatg gatatccagg tcccaccca gatcctgggg cttggacgtg 900
gtccctgggg gtccttaaaa aatcctcgag gtatctttaa tatgcatcaa gcttgagaat 960
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<210> 347

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-158-213 : polymorphic base T or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-158-213.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-158-213.mis2, potential complement

<220>

<221> primer_bind

<222> 691..710

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 230..247

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-158-213 potential probe

<400> 347

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ggaagctgat gccttgggca gctcctccta tttcccaggc accagggaatg tgagcttctc 180
cctccccaca gtcctgctgt cctcagggcc cctatgtctc tgaaggcacc accatcttcc 240
aagatacatc ggcctccgca ggggtctagga gtgccagaca cgtaaccaga aatcagatga 300
catcatatc taaataaaac accactacat ggaaatagaa caccactaca tggaaataga 360
acatgggagc ccttggaatg tggcaagagc accctcccag gcatgttcca ccctacccc 420
gggtcatca ggaggggttct taagatgcag acagtttttaa ggggggttga ggaatagttg 480
agaagctgag atgttgacc yacagctgag aatccctttc tagcactctg tgcctcaca 540
aatccccaga aatcgtcctc ccctggggag ttctcaagcc cttacagacc tgccctctct 600
gtgccatcct gcatatgcct cccttgagct ggggtgtccct ctgatggacg catccattca 660
ctgcctgtcc catgggttgt gtccaaaggt ggaatctgtt atcaatgtgg atttctaagt 720
ggagtaactt cctccataag ggaagcctca gcctcaccag caatggcaga catggccagg 780
catgtagaca cagaggtagt gagatggaaa gtgggcacag cccagagagc ctgcccacct 840

```

299

```

catcctgggg cgaccaggac aaggaagcat cagcaatctt gcgagcacat gtaggagtga    900
ctttctggag caggacgagc ctcatgggca tgagaccatt gtgagtgtctc aggggtctccc    960
cctagaaagg cacacattta attctccatt ttgaaatttg a                          1001

```

<210> 348

<211> 980

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 480

<223> 12-158-450 : polymorphic base T or G

<220>

<221> misc_binding

<222> 460..479

<223> 12-158-450.mis1, potential

<220>

<221> misc_binding

<222> 481..500

<223> 12-158-450.mis2, potential complement

<220>

<221> primer_bind

<222> 907..926

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 446..463

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 468..492

<223> 12-158-450 potential probe

<400> 348

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cgtttgtact ttttgtacct taaggaagct ttgtttacct caagatatag tttctacatt    120
ctcttaaaaa cactaaagag ttccagttta tatgttttagc tctgtgagat tgggagaggg    180
gagctagatc actcaggtca ggctttcggg atgccttttt ctgtctctgg acgttgctgg    240
ggtgacctca ctgacacca tggcttcagc taccacatat gctgatggct ccaagtctat    300
ctgtgcagcc cagaccctc ctcatctcca gacctggaa gctgatgcct tgggcagctc    360
ctcctatttc ccaggcacca ggaatgtgag cttctccctc cccacagtcc tgctgtcctc    420
agggccctta tgtctctgaa ggcaccacca tcttccaaga tacatgggcc tccgcagggk    480
ctaggagtgc cagacacgta accagaaatc agatgacatc actatctaaa taaaacacca    540
ctacatggaa atagaacacc actacatgga aatagaacat gggagcccct tgaatgtggc    600
aagagcacc ccccaggcat gttccaccct caccgccggc tcatcaggag ggttcttaag    660
atgcagacag ttttaagggg gttggaggaa tagttgagaa gctgagatgt tgcaccacac    720
gctgagaatc ctttcttagc actctgtgtc ctacaaaatc cccagaaatc gtctctccct    780
ggggagtctt caagccctta cagacctgcc ctctctgtgc catcctgcat atgcctccct    840
tgagctgggt gtccctctga tggacgcatc cattcaactgc ctgtcccatg ggttgtgtcc    900
aaaggtggaa tctgttatca atgtggattt ctaatggggag taacttcctc cataagggaa    960
gcctcagcct caccagcaat

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<210> 349

<211> 1001

<212> DNA

<213> Homo Sapiens

300

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<220>
<221> allele
<222> 501
<223> 12-161-157 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-161-157.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-161-157.mis2, potential complement

<220>
<221> primer_bind
<222> 345..363
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 729..749
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-161-157 potential probe

<400> 349
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actgaaaggg tttaaaggag agtctgagaa aaggaaatga atctgcattt attgagaaag      180
ttgatgagaa agtggaatta gaaattccta gaaaggtaag ttgttggtgtg aattatttcc      240
caaaatgggg aagtctctct acctgtttgg agacagaaag tggaatcaga ggagaagaag      300
atgatggaca gaaaggatca ttccctcttc cagatgcttt ccagtgtgtg atgtaagctg      360
aactaaaatc agctgtgttg aactccagcc agaaaaaatg tccggcattt tgtttttttg      420
gaccctaattg aaatggttac aggtctccag gtctcttggg gctcacaggg tcatgccttt      480
ccttgcccag tgtacttggt ragaaggtac aggtgtttcc atggagggtg ttcattttag      540
ggatttcaag agggtcattt ttgcaccaca ggaaatgccc ccttttacac tctgaaaacc      600
ttatcaaaac gttgtataaa agatgaatac ccacataaca ggctctagca ctgttctgtt      660
tttgagctga gacattttta aaggagattt ttcaattcta aaaattcttt aaataaaatg      720
ctcttgacag gacaacatag taggtcaaca ttgttcccat ctccacaaaa agtttttttt      780
ttaattagct aggtgtggta gcatttctgt agtcctagct actgggaatg ctgaggagga      840
aggatcactt gagcccagga attcgtggtt acagtaagct atgatcttgc ctaggtaaca      900
gctacagagc gagacctgtt ctttaaaaca aacaagcaaa cagacaatca agctttacac      960
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<210> 350
<211> 998
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 498
<223> 12-162-21 : polymorphic base A or G

<220>
<221> misc_binding
<222> 478..497
<223> 12-162-21.mis1, potential

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<220>
 <221> misc_binding
 <222> 499..518
 <223> 12-162-21.mis2, potential complement

<220>
 <221> primer_bind
 <222> 478..497
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 909..927
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 486..510
 <223> 12-162-21 potential probe

<400> 350
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 atacatgggc ctccccaggg tctaggagtc ctagacgtgg gagtagaaat tagatgacat 180
 tgggtgtctaa acaaaacacc actgcatgga gatagaacag gggagccccc tgaatgtggt 240
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 atgcatacag ttttaagggg gttggaggaa tagttcagag gctgagatgt tgcaccaca 360
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 ggagagtccc caaagccctt gcaggcctgc cttctctgtg ccttctgccc tgcgccctct 480
 ggtggacagc tccattcrct gcctgtccca tgggttctgt ccaaagggtg aatctattat 540
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 cagagagcct gccacatca tcttggggcg accaggacaa ggaggcgtca gcaatcttgc 720
 caagcacaag tatgagtac tttctggagc aggacgagtc tcatgggcgt gagaccattg 780
 tgagtgtcca ggtctctccc attagaaagg cacacgttta attctccatt ttgaaatttg 840
 aactagagcc cccacaaatt attctgttct ggaggaacca ttcttatcag aacttggtgc 900
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<210> 351
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 10-470-25 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 484..502
 <223> 10-470-25.mis1

<220>
 <221> misc_binding
 <222> 504..523
 <223> 10-470-25.mis2, potential complement

<220>
 <221> primer_bind
 <222> 479..498

302

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 880..899

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 10-470-25 potential probe

<220>

<221> misc_feature

<222> 271,364,831,842

<223> n=a, g, c or t

<400> 351

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agtaactttt cctcagtgct cagagtcagg gaagtcaacc actaatgact tcaaactaaa      180
ataattctgt agaaaacctg cctaaaataa gcatatgtga tttagcgagc aacaatatag      240
cattaaagcc aactgggtgcc actttaaaga ncctatatta gtacttataa tatgataagt      300
gaagagtttg ggtatctcct caaatactgt gtaataactc tatttcattt ctccctttca      360
caancgcaca cacatacaca cacacatatt tacacaaaga cccttaacag aggcaaccta      420
tctcatatta tacatatgtc aaaaaaaaac tgagtaattg agtcagttaa aaaacatcct      480
ttactccaat aattcctgat aawacttgat ttctctcttt ttataacaa ttctttcaca      540
gtgcttgctg tgctgataat ctattatgat agaacaaatt cttttttttc acaggaaatg      600
gaagagtttg tccagagctc tggagaaaat ggtgttgtgg tgttttctct ggggtcgatg      660
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caaaaaggta agataaaatg ttttaattgg gtaaaaaact actgaaaagag gctgttaaag      780
tttgtaaaga acccaaattg tagaaacttc ctgcctatat atttcagctg ntgggaaaag      840
cnctaattat ctcagatatt aattcaaaat caaaaatatg tatggaagat gataaactca      900
tacagaaggt gtttttcatt ggtaattaat ttggcattaa tattgtgatc aggaataaat      960
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<210> 352

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-471-84 : polymorphic base A or T

<220>

<221> misc_binding

<222> 484..502

<223> 10-471-84.mis1

<220>

<221> misc_binding

<222> 504..523

<223> 10-471-84.mis2, potential complement

<220>

<221> primer_bind

<222> 420..439

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 788..807
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-471-84 potential probe

<400> 352
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agtgggtgtga ttgtggetca ctgcaacttc cgcctcttgg gttcaagcga ttctcctgcc 180
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atcaaccagt gaagcccctt gawagagcag tcttctggat tgaatttgtc atgcgccata 540
aaggagccaa gcaccttcgg gttgcagccc acgacctcac ctggttccag taccactctt 600
tggatgtgac tgggttcctg ctggcctgtg tggcaactgt gatattcatc atcacaaaat 660
gtctgttttg tgtctggaag ttgtttagaa caggaaaaga ggggaaaaga gattaattac 720
gtctgaggct ggaagctggg aaaccaata aatgaactcc tttagtttat tacaacaaga 780
agacgttttg atacaagaga ttcctttctt cttgtgacaa aacatctttc aaaacttacc 840
ttgtcaagtc aaaatttgtt ttagtacctg tttaaccatt agaaatattt catgtcaagg 900
aggaaaacat tagggaaaac aaaaatgata taaagccata tgagggtata ttgaaatgta 960
ttgagcttat attgaaattt attgttccaa ttcacaggtt a 1001

<210> 353
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-471-85 : polymorphic base A or C

<220>
<221> misc_binding
<222> 483..502
<223> 10-471-85.mis1, potential

<220>
<221> misc_binding
<222> 505..523
<223> 10-471-85.mis2, complement

<220>
<221> primer_bind
<222> 420..439
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 788..807
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-471-85 potential probe

<400> 353

304

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atttactttg aatgatctgg cacttttaaa acctttcgtg gacttgatgt gctcaggcaa    60
attaacttac cttctctttt tttagagagg aagtctcact ctgtcaccag gctggagtg    120
agtgggtgga ttgtggctca ctgcaacttc cgcctcttgg gttcaagcga ttctcctgcc    180
tcagcctctc aagtagctgg gactacaggg acatgccacc acgcctgggt aatctttttt    240
tttttttttt ttttttttca tatttttact ggagacgggg tgacgggggt tcaccgtggt    300
agccaggatg gtcttgatct cctgacctcg tgatccgccc gcctcgacct cggaaagtgc    360
tgggattgca ggtgtgagcc tccgtgcttg gccaaattaa cttactttca atgttgatac    420
ttttctgctt atcgtttaga tataaagaga atgctatgaa attatcaaga attcatcatg    480
atcaaccagt gaagcccctt gamagagcag tcttctggat tgaatttgtc atgcgccata    540
aaggagccaa gcaccttcgg gttgcagccc acgacctcac ctggttccag taccactctt    600
tggatgtgac tgggttcctg ctggcctgtg tggcaactgt gatattcatc atcacaaaat    660
gtctgttttg tgtctggaag tttgttagaa caggaaagaa ggggaaaaga gattaattac    720
gtctgaggct ggaagctggg aaaccaata aatgaactcc tttagtttat tacaacaaga    780
agacgttggt atacaagaga ttcctttctt cttgtgacaa aacatctttc aaaacttacc    840
ttgtcaagtc aaaatttggt ttagtacctg ttaaccatt agaaatattt catgtcaagg    900
aggaaaacat tagggaaaac aaaaatgata taaagccata tgagggtata ttgaaatgta    960
ttgagcttat attgaaattt attgttccaa ttcacaggtt a                                1001

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<210> 354

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-472-202 : polymorphic base C or T

<220>

<221> misc_binding

<222> 484..502

<223> 10-472-202.mis1

<220>

<221> misc_binding

<222> 525..543

<223> 10-472-202.mis2, complement

<220>

<221> primer_bind

<222> 304..322

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 714..732

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 10-472-202 potential probe

<400> 354

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gatataaaga gaatgctatg aaattatcaa gaattcatca tgatcaacca gtgaagcccc    60
ttgaaagagc agtcttctgg attgaatttg tcatgcgcca taaaggagcc aagcaccttc    120
gggttgagc ccacgacctc acctgggtcc agtaccactc tttggatgtg actgggttcc    180
tgctggcctg tgtggcaact gtgatattca tcatcacaaa atgtctgttt tgtgtctgga    240
agtttgttag aacaggaaaag aaggggaaaa gagattaatt acgtctgagg ctggaagctg    300
ggaaacccaa taaatgaact cctttagttt attacaacaa gaagacgttg tgatacaaga    360
gattcctttc ttcctgtgac aaaacatctt tcaaaaactta ccttgtcaag tcaaaatttg    420
ttttagtacc tgtttaacca ttagaaatat ttcatgtcaa ggaggaaaac attagggaaa    480
acaaaaatga tataaagcca taygagggtta tattgaaatg tattgagctt atattgaaat    540

```

305

```

ttattgttcc aattcacagg ttacatgaaa aaaaatttac taagcttaac tacatgtcac    600
acattgtaca tggaaacaag aacattaaga agtccactga cagtatcagt actgttttgc    660
aaatactcag catacttttg atccatttca tgcaggattg tgttggttta actgttggtg    720
aggaagctaa taaataatta aattgtatag aaagtctctt cctcttgata ttttgagatg    780
attagtgtcg cttggctttt attgtgcatc gtgcttcaac gtcatttttt ttcctaaaag    840
gtatgataaa aatgcttacc attttagagc ttaagtcatt tcccagtgaa aagtatgtgg    900
aattagaaat atagcaactc ctacctggtt tctactacaa aatgaactaa ttttacaatg    960
cgtttggttt tttgagccaa ttctattttt ctgttcattt g                               1001

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<210> 355

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-473-333 : polymorphic base C or T

<220>

<221> misc_binding

<222> 483..502

<223> 10-473-333.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 10-473-333.mis2, potential complement

<220>

<221> primer_bind

<222> 171..189

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 582..600

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 10-473-333 potential probe

<220>

<221> misc_feature

<222> 887

<223> n=a, g, c or t

<400> 355

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gaagctggga aacccaataa atgaactcct ttagtttatt acaacaagaa gacgttgtga    60
tacaagagat tcctttcttc ttgtgacaaa acatctttca aaacttacct tgtcaagtca    120
aaatttgttt tagtacctgt ttaaccatta gaaatatttc atgtcaagga ggaaaacatt    180
agggaaaaca aaaatgatat aaagccatat gaggttatat tgaaatgtat tgagcttata    240
ttgaaattta ttgttccaat tcacagggtta catgaaaaaa aatttactaa gcttaactac    300
atgtcacaca ttgtacatgg aaacaagaac attaagaagt ccactgacag taccagtact    360
gttttgcaaa tactcagcat actttggatc catttcatgc aggatttgtt tgttttaact    420
gttggttgagg aagctaataa ataattaaat tgtatagaaa gtctcttcct cttgatattt    480
tgagatgatt agtgcctgctt ggyttttatt gtgcacgtg cttcaacgtc atttttttcc    540
ctaaaaggta tgataaaaat gcttaccatt ttagagctta agtcatttcc cagtgaaaag    600
tatgtggaat tagaaatata gcaactccta cctggtttct actacaaaat gaactaattt    660
tacaatgcgt ctgggttttt gagccaattc tatttttctg ttcatttgaa aatattcatc    720
tttttttatt ctttggtttt taggtatttc aatagctttt gggtgacaac tgggttttgg    780

```

306

```

ttacatggat aagctcttta gtggtgattt ttcagatttt ggtgcactca ttactcaaga   840
agtatacaact gtacccagtg tgtactgttt tatccctcac atccctncct acccttcctt   900
ctgagttcca agagtccatt atatcattct tatgcctcta tgccttaata gcttaggtcc   960
cccttataag tgagaacata cattgtttgg ttttatattt c                        1001

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<210> 356

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-494-284 : polymorphic base C or T

<220>

<221> misc_binding

<222> 483..502

<223> 10-494-284.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 10-494-284.mis2, potential complement

<220>

<221> primer_bind

<222> 220..238

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 624..641

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 10-494-284 potential probe

<400> 356

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ctggtgtgag atggtatctc tttgtggatt tgaccagtga tgtaaaccct tttttcatat   60
agtggtttgc cacatatagt tttcttttga aaagtgtaac aactttttta atacttgaac   120
ttttcattga ttatcttatt tgtctaagct actattttga aaaatcatga tttccttata   180
tacctaatta tgaaattaag gaaatgaaat atgagtattc tatttacatc agtctgagta   240
gttcttggtt cttaacatcc cttgttcttc tcattgttaa tctctttaga tttctaaccat   300
tctatgactt ttgagttcca ctcattggaat aagatatttt cttcactgta acagggttctg   360
tggagatttg atgggaataa accagatact ttaggactca atactcggct gtacaagtgg   420
ataccccgag atgatcttct tggtaagtct ctgaagaaca aatactgaat atattagtaa   480
cagattatta aagtgttaat agytatcatg aaacaagctt actgaacatt tgttatggaa   540
aaacttaaaa tgaaacttct ttatatttat tttccagtcc cgggggaaaa gaataaatga   600
taattgttgg cattttatga tatgcaccca cattctttac aatcagagtc agagtatctt   660
tatttcagggt gttattacct cccacagaat ttttctggca cttcctgggt tgtcttcctt   720
tctcatattt ctacaacttt acacctgttc tttcctcttc tgtagggtta tttcaaattg   780
cactaaaagt aacagctctt ctgctatcac cagggatgct gcattttctg taggattaaa   840
tcctaatctt taatcaaaaa gtgatgacac atttcataat gaaatgtgac ctgtctttcc   900
tcaattctag caccaccacc acctcactgc ctgctgcctt gcacacccta catatcacac   960
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<210> 357

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-637-219 : polymorphic base G or A

<220>
<221> misc_binding
<222> 500..519
<223> 12-637-219.mis1, potential complement

<220>
<221> misc_binding
<222> 480..498
<223> 12-637-219.mis2

<220>
<221> primer_bind
<222> 698..717
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 230..250
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-637-219 potential probe

<220>
<221> misc_feature
<222> 953
<223> n=a, g, c or t

<400> 357
ttttgtgtct ggaagtttgt tagaacagga aagaagggga aaagagatta attacgtctg 60
aggctggaag ctgggaaacc caataaatga actccttttag tttattacaa caagaagacg 120
ttgtgataca agagattcct ttcttcttgt gacaaaacat ctttcaaaac ttaccttgct 180
aagtcaaaat ttgttttagt acctgtttaa ccattagaaa tatttcatgt caaggaggaa 240
aacattaggg aaaacaaaaa tgatataaag ccatatgagg ttatatgaa atgtattgag 300
cttatattga aattttattgt tccaattcac aggttacatg aaaaaaaatt tactaagctt 360
aactacatgt cacacattgt acatggaaac aagaacatta agaagtccac tgacagtatc 420
agtactgttt tgcaataact cagcatactt tggatccatt tcatgcagga ttgtgttggt 480
ttaactgttg ttgaggaarc taataaataa ttaaattgta tagaaagtct cttcctcttg 540
atattttgag atgattagtg ctgcttggtt tttattgtgc atcgtgcttc aacgtcattt 600
tttttcctaa aagggtatgat aaaaatgctt accatttttag agcttaagtc atttcccagt 660
gaaaagtatg tggaattaga aatatagcaa ctctaccttg gtttctacta caaaatgaac 720
taattttaca atgcgttttg ttttttgagc caattctatt tttctgttca ttgaaaata 780
ttcatctttt ttattctttt gttttttagg tatttcaata gcttttgggt gacaactggg 840
ttttggttac atggataagc tcttttagtg tgatttttca gattttgggt cactcattac 900
tcaagaagta tacactgtac ccagtgtgta ctgttttatc cctcacatcc ctncctaccc 960
ttccctctga gttccaagag tccattatat cattcttatg c 1001

<210> 358
<211> 668
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499

308

<223> 12-639-95 : polymorphic base G or A

<220>

<221> misc_binding

<222> 500..519

<223> 12-639-95.mis1, potential complement

<220>

<221> misc_binding

<222> 480..498

<223> 12-639-95.mis2

<220>

<221> primer_bind

<222> 573..593

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 144..164

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-639-95 potential probe

<220>

<221> misc_feature

<222> 57,198,240,552,616,630

<223> n=a, g, c or t

<400> 358

aataaacaag	ggacctttgt	gtattttgtga	attacttttt	aatttcctat	ctgatanaag	60
ctttcttgta	atgacctcta	actttttgct	gaaacctgag	ttactttaac	actgatgtag	120
caaataaaag	ttaaacactg	taaattattg	ttcagtttgt	gaggattgct	tcggagtgtc	180
aaaatttagta	acttaaanat	aaaaatgtct	tggctatagc	agaacatatt	attcactgtn	240
tgtcaaactct	ttgtagcacg	ttgtctaagt	gttaataatc	agttgaccaa	attccgcaaa	300
atacaatttt	gagtttatcc	aatagctttt	tttgtattca	tgataccaac	agggttcctca	360
tttctaggcc	aaaaaaaaat	ccaaaattaa	caatactggg	aatattctga	atttgtgtca	420
aaaattgtca	cttgaaattt	ttcttggaag	tagtgcttga	taatttgtaa	ttctaataaa	480
gttatacata	aaaccctarc	agcatttatt	tatttcttat	aagtagctta	ttttatagac	540
ttgctatttt	gncaatcaaa	ggacaacagg	ctctaataata	ataacctacc	gacaaagtag	600
atacatttga	acttcntctc	ttattattcn	aaaacaaatg	aatacactgc	aattaaattt	660
ggagatga						668

<210> 359

<211> 814

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-639-241 : polymorphic base T or G

<220>

<221> misc_binding

<222> 479..498

<223> 12-639-241.mis1, potential

<220>

<221> misc_binding

309

<222> 500..519
 <223> 12-639-241.mis2, potential complement

<220>
 <221> primer_bind
 <222> 719..739
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 290..310
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 487..511
 <223> 12-639-241 potential probe

<220>
 <221> misc_feature
 <222> 38,95,116,203,344,386,698,762,776
 <223> n=a, g, c or t

<400> 359
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 gtaggaatat attttcttct atataaaata aacaaggac ctttgtgtat ttgtgaatta 180
 ctttttaatt toctatctga tanaagcttt cttgtaatga cctctaactt tttgctgaaa 240
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 gtttgtgagg attgcttcgg agtttcaaaa ttagtaactt aaanataaaa atgtcttggc 360
 tatagcagaa catattattc actgtntgtc aaatctttgt agcacgttgt ctaagtgtta 420
 ataatacagt gaccaaattc cgcaaaatac aattttgagt ttattcaata gctttttttg 480
 tattcatgat accaacagkt tcctcatttc tagggcaaaa aaaaatccaa aattaacaat 540
 actggtaata ttctgaattt gtgtcaaaaa ttgtcacttg aaatttttct tggaagtagt 600
 gcttgataat ttgtaattct aatgaagtta tacataaaac cctagcagca tttatttatt 660
 tcttataagt agcttatttt atagacttgc tattttgnca atcaaaggac aacaggctct 720
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<210> 360
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 499
 <223> 12-640-151 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 479..498
 <223> 12-640-151.misl, potential

<220>
 <221> misc_binding
 <222> 500..519
 <223> 12-640-151.mis2, potential complement

<220>
 <221> primer_bind
 <222> 629..649
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 156..176
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 487..511
 <223> 12-640-151 potential probe

<220>
 <221> misc_feature
 <222> 62
 <223> n=a, g, c or t

<400> 360
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 aatgagactc ccaagactga ttcataaaaa ttccaaatca caataactaga ctcaggaatg 180
 tcagtgtatc ttaaccacca gcttttattt tcattttttg aaaaactact ggaaaactct 240
 gacaaacttt aagtgaagca taaagcattg tagaggaaca taaatgtaga tataaaatta 300
 tcccaactgt gaatagcttt tcctcagtgc tcatatttag ggaagtagac cactaatggc 360
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 acaaaaatat aggattaaag cctagtgggtg ccacttttcc aagaacttat attagtaatt 480
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 ctgagtgtat gagtcagtta aaaaatatta tttactccaa taattcctca aaatacttga 720
 ttttctctct ttaatatattg gtaccagttc tttagtagtg cctgctgtgg tgatactctt 780
 ttgtgattaa acaatttttt tttcacagga aatggaggag tttgtacaga gctctggaga 840
 aaatgggtgt gtgggtgttt ctctgcggtc aatcataagt aacatgacag cagaaagggc 900
 caatgtaatt gcaacagccc tggccaagat cccacaaaag gtaagataaa gtaccttact 960
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<210> 361
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 499
 <223> 12-640-296 : polymorphic base T or G

<220>
 <221> misc_binding
 <222> 479..498
 <223> 12-640-296.mis1, potential

<220>
 <221> misc_binding
 <222> 500..519
 <223> 12-640-296.mis2, potential complement

<220>
 <221> primer_bind
 <222> 769..789
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 296..316

311

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-640-296 potential probe

<220>

<221> misc_feature

<222> 1..4,6..8,12..22,25..28,30,32..37,39,41..44,47..50,202

<223> n=a, g, c or t

<400> 361

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agagttcctc acatgcagtt agaaatagca catcaattta acagtgtgat ttcagggcaa      180
taggtgttcc acctaaacaa tnaacctgaa aggtacaatt attcaacaac taactataaa      240
ctctacaatt ccatgtgata aatgagactc ccaagactga ttcataaaaa ttccaaatca      300
caataactaga ctcaggaatg tcagtgattc ttaaccacca gcttttattt tcatTTTTTg      360
aaaaactact ggaaaactct gacaaaacttt aagtgaagca taaagcattg tagaggaaaca      420
taaatgtaga tataaaatta tcccaactgt gaatagcttt tcctcagtgc tcatatttag      480
ggaagttagac cactaatgkc ttcaaaactaa aagaattcta cagaaaacct gcctgaaata      540
aacacaagtg atttagtaga acaaaaatat aggattaaag cctagtgggtg ccacttttcc      600
aagaacttat attagtaatt atagtattat aagtgaagag tctgggtata ttttttcaca      660
ttatctccct gactacaatg taatagctcc atttcttttc tccattacac acatgcagac      720
acatacatat atatacacac atatttacac aaatatcctt aacagaggcc aactatctca      780
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taattcctca aaatacttga ttttctctct ttaatatTTg gtaccagttc tttagtagtg      900
cctgctgtgg tgatactctt ttgtgattaa acaatttttt tttcacagga aatggaggag      960
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<210> 362

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-640-325 : polymorphic base T or C

<220>

<221> misc_binding

<222> 500..518

<223> 12-640-325.mis1, complement

<220>

<221> misc_binding

<222> 479..498

<223> 12-640-325.mis2, potential

<220>

<221> primer_bind

<222> 797..817

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 324..344

<223> downstream amplification primer

<220>

<221> misc_binding

312

<222> 487..511

<223> 12-640-325 potential probe

<220>

<221> misc_feature

<222> 6,24..25,28..32,34..36,40..50,53..56,58,60..65,67,69..72,75..78

230

<223> n=a, g, c or t

<400> 362

tcgagncag	cacatcttca	ccannagnnn	nntnnngtgn	nnnnnnnnnn	ctnnnnanan	60
nnnnnnanann	nncnnnnnga	agaaaggcct	ggtggcctct	tctattcttg	tgccagtgc	120
gcctctgaga	cacaacaaag	tgatgatgag	agttccctcac	atgcagttag	aaatagcaca	180
tcaatttaac	agtgtgattt	cagggcaata	ggtgttccac	ctaaacaatn	aacctgaaag	240
gtacaattat	tcaacaacta	actataaact	ctacaattcc	atgtgataaa	tgagactccc	300
aagactgatt	cataaaaatt	ccaaatcaca	atactagact	caggaatgtc	agtgattcct	360
aaccaccagc	ttttattttc	attttttgaa	aaactactgg	aaaactctga	caaactttta	420
gtgaagcata	aagcattgta	gaggaacata	aatgtagata	taaaattatc	ccaactgtga	480
atagcttttc	ctcagtgcyc	atatttaggg	aagtagacca	ctaattggct	caaactaaaa	540
gaattctaca	gaaaacctgc	ctgaaataaa	cacaagtgat	ttagtagaac	aaaaatatag	600
gattaaagcc	tagtgggtgcc	acttttccaa	gaacttatat	tagtaattat	agtattataa	660
gtgaagagtc	tgggtatat	ttttcacatt	atctccctga	ctacaatgta	atagctccat	720
ttcttttctc	cattacacac	atgcagacac	atacatat	atacacacat	atttacacaa	780
atatecttaa	cagaggccaa	ctatctcaaa	tatcttcttg	caaagaaact	gagtgtattga	840
gtcagttaaa	aaatattatt	tactccaata	attcctcaaa	atacttgatt	ttctctcttt	900
aatatttgg	accagttctt	tagtagtgcc	tgctgtgggt	atactctttt	gtgattaaac	960
aatttttttt	tcacaggaaa	tggaggagtt	tgtacagagc	t		1001

<210> 363

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-640-413 : polymorphic base C or G

<220>

<221> misc_binding

<222> 479..498

<223> 12-640-413.mis1, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-640-413.mis2, potential complement

<220>

<221> primer_bind

<222> 885..905

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 412..432

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-640-413 potential probe

313

<220>
<221> misc_feature
<222> 94,112..113,116..120,122..124,128..138,141..144,146,148..153,155
157..160,163..166,318
<223> n=a, g, c or t

<400> 363
ttttacccca atgattaaat ctgaaaatat ttaaatttaa atattggtat acattgggga 60
actcaagtca gaataattct caatcaattg cagncaagca catcttcacc annagnnnnn 120
tnnngtgnnn nnnnnnnnct nnnnanannn nnnanannnn ccnnnngaag aaaggcctgg 180
tggcctcttc tattctggtg ccagtgtctg ctctgagaca caacaaagtg atgatgagag 240
ttcctcacat gcagttagaa atagcacatc aatttaacag tgtgatttca gggcaatagg 300
tgttccacct aaacaatnaa cctgaaaggt acaattattc aacaactaac tataaactct 360
acaattccat gtgataaatg agactcccaa gactgattca taaaaattcc aaatcacaaat 420
actagactca ggaatgtcag tgattcttaa ccaccagctt ttattttcat tttttgaaaa 480
actactggaa aactctgasa aactttaagt gaagcataaa gcattgtaga ggaacataaa 540
tgtagatata aaattatccc aactgtgaat agcttttcct cagtgtctcat atttagggaa 600
gtagaccact aatggcttca aactaaaaga attctacaga aaacctgcct gaaataaaca 660
caagtgtatt agtagaaca aaatatagga ttaaagccta gtgggtgccac ttttccaaga 720
acttatatta gtaattatag tattataagt gaagagtctg ggtatatttt ttcacattat 780
ctccctgact acaatgtaat agctccattt cttttctcca ttacacacat gcagacacat 840
acatacatat acacacatat ttacacaaaat atccttaaca gaggccaact atctcaaata 900
tcttcttgca aagaaactga gtgattgagt cagttaaaaa atattattta ctccaataat 960
tcctcaaaat acttgatttt ctctctttaa tatttggtac c 1001

<210> 364
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-641-120 : polymorphic base G or A

<220>
<221> misc_binding
<222> 479..498
<223> 12-641-120.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-641-120.mis2, potential complement

<220>
<221> primer_bind
<222> 600..618
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 127..147
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-641-120 potential probe

<220>
<221> misc_feature
<222> 5,519,564,828,846..847,850..854,856..858,862..872,875..878,880

314

882..887,889,891..894,897..900

<223> n=a, g, c or t

<400> 364

tgganaatat	tcacaaaatt	aacattagaa	gtaatccaac	atctttatac	gaaagaatga	60
ttaaaaactta	tgtgcatata	gtagcattaa	aataatttta	tcaatgaaat	gttcagttac	120
actttcagcc	ataatacaaa	caaagtgaat	tagaaaaatga	taaatatagc	aagatggcaa	180
gtttttgcag	gaggaaatgt	atatacaata	agattaaaaat	tttctaaata	agtgtcacat	240
gtatacattg	acctatataa	at ttgacaaa	atccataata	aaaaatacat	at ttttctaaa	300
aattatacct	ctagatagaa	at ttttagaaa	aattatcttt	taaaaagggt	ttcatacttt	360
tataaaat	cttacattaa	ttttgtatta	tttttataat	attatcacia	aaggagaaac	420
aagcagtc	tatcagtgat	gaatctctaa	acagagggtta	gattccttca	acacctggta	480
gaaaaacaag	gctctggtrt	caagccagtg	agatgaaanc	actgaaaacg	agttacatta	540
aatgtggcta	caggtaactg	caantcacat	acaacaccta	gaagccccag	gtattacgtg	600
gaatagtagt	acaaggactc	tcacgttaac	gtaagattaa	aaatcatatt	ttaagaaaac	660
actctgccat	atgtgatgca	ctgtttacat	ttagactttt	ttttctttgt	tttggtaaaa	720
accatttgga	aaagttttac	cccaatgatt	aaatctgaaa	atattttaa	ttaaatattg	780
gtatacattg	gggaactcaa	gtcagaataa	ttctcaatca	attgcagnca	agcacatctt	840
caccannagn	nnnnnnnnngt	gnnnnnnnnn	nnctnnnnan	annnnnnana	nnnnccnnnn	900
gaagaaaggc	ctggtggcct	cttctattct	ggtgccagtg	ctgcctctga	gacacaacaa	960
agtgatgatg	agagttcctc	acatgcagtt	agaaatagca	c		1001

<210> 365

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-641-122 : polymorphic base T or G

<220>

<221> misc_binding

<222> 479..498

<223> 12-641-122.mis1, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-641-122.mis2, potential complement

<220>

<221> primer_bind

<222> 602..620

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 129..149

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-641-122 potential probe

<220>

<221> misc_feature

<222> 7,521,566,830,848..849,852..856,858..860,864..874,877..880,882
884..889,891,893..896,899..902

<223> n=a, g, c or t

315

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<400> 365
tatgganaat attcacaaaa ttaacattag aagtaatcca acatctttat acgaaagaat    60
gattaaaaact tatgtgcata tagtagcatt aaaataatTTt tatcaatgaa atgttcagtt    120
acacttttcag ccataataca aacaaagtga attagaaaat gataaatata gcaagatggc    180
aagtTTTTtgc aggaggaaat gtatatataa taagattaaa attttctaaa taagtgtcac    240
atgtatacat tgacctatat aaatttgaca aaatccataa taaaaaatac atatttttcta    300
aaaattatac ctctagatag aaattttaga aaaattatct tttaaaaagg ttttcatact    360
tttataaaaat ttcttacatt aattttgtat tattttttata atattatcac aaaaggagaa    420
acaagcagtc catatcagtg atgaatctct aaacagaggt tagattcctt caacacctgg    480
tagaaaaaca aggctctgkt gtcaagccag tgagatgaaa nactgaaaa cgagttacat    540
taaagtgtggc tacaggtaac tgcaantcac atacaacacc tagaagcccc aggtattacg    600
tggaatagta gtacaaggac tctcacgtta acgtaagatt aaaaatcata ttttaagaaa    660
acactctgcc atatgtgatg cactgtttac atttagactt ttttttcttt gttttgttaa    720
aaaccatttg gaaaagtttt accccaatga ttaaattctga aaatatTTta atttaaatat    780
tgggtatacat tgggggaactc aagtcagaat aattctcaat caattgcagn caagcacatc    840
ttcaccanna gnnnnntnnn gtgnnnnnnn nnnnctnnnn anannnnna nannnnccnn    900
nngaagaaag gcctggtggc ctcttctatt ctggtgccag tgctgcctct gagacacaac    960
aaagtgatga tgagagttcc tcacatgcag ttagaaatag c                                1001

<210> 366
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 432
<223> 12-641-223 : polymorphic base G or A

<220>
<221> misc_binding
<222> 412..431
<223> 12-641-223.mis1, potential

<220>
<221> misc_binding
<222> 433..452
<223> 12-641-223.mis2, potential complement

<220>
<221> primer_bind
<222> 636..654
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 163..183
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 420..444
<223> 12-641-223 potential probe

<220>
<221> misc_feature
<222> 24,41,555,600,864,882..883,886..890,892..894,898..908,911..914
916,918..923,925,927..930,933..936
<223> n=a, g, c or t

<400> 366
atcataaaaa aatcaagggtg tatntattaa accttatgga naatattcac aaaattaaca    60
ttagaagtaa tccaacatct ttatacgaaa gaatgattaa aacttatgtg catatagtag    120

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316

cattaaaata	at tt t t a t c a a	t g a a a t g t t c	a g t t a c a c t t	t c a g c c a t a a	t a c a a a c a a a	180
g t g a a t t a g a	a a a t g a t a a a	t a t a g c a a g a	t g g c a a g t t t	t t g c a g g a g g	a a a t g t a t a t	240
a c a a t a a g a t	t a a a a t t t t c	t a a a t a a g t g	t c a c a t g t a t	a c a t t g a c c t	a t a t a a a t t t	300
g a c a a a a t c c	a t a a t a a a a a	a t a c a t a t t t	t c t a a a a a t t	a t a c c t c t a g	a t a g a a a t t t	360
t a g a a a a a t t	a t c t t t t t a a a	a a g g t t t t c a	t a c t t t t t a t a	a a a t t t c t t a	c a t t a a t t t t	420
g t a t t a t t t t	t r t a a t a t t a	t c a c a a a a g g	a g a a a c a a g c	a g t c c a t a t c	a g t g a t g a a t	480
c t c t a a a c a g	a g g t t a g a t t	c c t t c a a c a c	c t g g t a g a a a	a a c a a g g c t c	t g g t g t c a a g	540
c c a g t g a g a t	g a a a n c a c t g	a a a a c g a g t t	a c a t t a a a t g	t g g c t a c a g g	t a a c t g c a a n	600
t c a c a t a c a a	c a c c t a g a a g	c c c c a g g t a t	t a c g t g g a a t	a g t a g t a c a a	g g a c t c t c a c	660
g t t a a c g t a a	g a t t a a a a a t	c a t a t t t t t a a	g a a a a c a c t c	t g c c a t a t g t	g a t g c a c t g t	720
t t a c a t t t a g	a c t t t t t t t t	c t t t g t t t t g	t t a a a a a c c a	t t t g g a a a a g	t t t t a c c c c a	780
a t g a t t a a a t	c t g a a a a t a t	t t a a a t t t a a	a t a t t g g t a t	a c a t t g g g g a	a c t c a a g t c a	840
g a a t a a t t c t	c a a t c a a t t g	c a g n c a a g c a	c a t c t t c a c c	a n n a g n n n n n	t n n n g t g n n n	900
n n n n n n n n c t	n n n n a n a n n n	n n n a n a n n n n	c c n n n n g a a g	a a a g g c c t g g	t g g c c t c t t c	960
t a t t c t g t g t g	c c a g t g c t g c	c t c t g a g a c a	c a a c a a a g t g	a		1001

<210> 367

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 388

<223> 12-641-267 : polymorphic base T or C

<220>

<221> misc_binding

<222> 368..387

<223> 12-641-267.mis1, potential

<220>

<221> misc_binding

<222> 389..408

<223> 12-641-267.mis2, potential complement

<220>

<221> primer_bind

<222> 636..654

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 163..183

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 376..400

<223> 12-641-267 potential probe

<220>

<221> misc_feature

<222> 24,41,555,600,864,882..883,886..890,892..894,898..908,911..914
916,918..923,925,927..930,933..936

<223> n=a, g, c or t

<400> 367

a t c a t a a a a a	a a t c a a g g t g	t a t n t a t t a a	a c c t t a t g g a	n a a t a t t c a c	a a a a t t a a c a	60
t t a g a a g t a a	t c c a a c a t c t	t t a t a c g a a a	g a a t g a t t a a	a a c t t a t g t g	c a t a t a g t a g	120
c a t t a a a a t a	a t t t t a t c a a	t g a a a t g t t c	a g t t a c a c t t	t c a g c c a t a a	t a c a a a c a a a	180
g t g a a t t a g a	a a a t g a t a a a	t a t a g c a a g a	t g g c a a g t t t	t t g c a g g a g g	a a a t g t a t a t	240
a c a a t a a g a t	t a a a a t t t t c	t a a a t a a g t g	t c a c a t g t a t	a c a t t g a c c t	a t a t a a a t t t	300

317

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gacaaaaatcc ataataaaaa atacatatatt tctaaaaaatt atacctctag atagaaattt 360
tagaaaaaatt atctttttaa aagggtttyca tactttttata aaattttcta cattaatttt 420
gtattattttt tataaatatta tcacaaaagg agaaacaagc agtccatata agtgatgaat 480
ctctaaacag aggttagatt ccttcaacac ctggtagaaa aacaaggctc tgggtgtcaag 540
ccagtggatg gaaanactg aaaacgagtt acattaaatg tggctacagg taactgcaan 600
tcacatacaa cacctagaag ccccggtat tacgtggaat agtagtacia ggactctcac 660
gttaacgtaa gattaaaaat catattttta gaaaacactc tgccatatgt gatgcactgt 720
ttacatttag actttttttt ctttgttttt ttaaaaacca tttggaaaag ttttacccca 780
atgattaaat ctgaaaatat ttaaatttaa atattggtat acattgggga actcaagtca 840
gaataattct caatcaattg cagncaagca catcttcacc annagnnnnn tnnngtgnnn 900
nnnnnnnnct nnnnanannn nnnanannnn ccnnnngaag aaaggcctgg tggcctcttc 960
tattctggtg ccagtgtgc ctctgagaca caacaaagtg a 1001

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<210> 368

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 12-642-387 : polymorphic base A or G

<220>

<221> misc_binding

<222> 483..502

<223> 12-642-387.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 12-642-387.mis2, potential complement

<220>

<221> primer_bind

<222> 117..135

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 592..612

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 12-642-387 potential probe

<220>

<221> misc_feature

<222> 537,804,808,881,899,903,920,936,958,962..963,967,985,995

<223> n=a, g, c or t

<400> 368

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ttttattcgaa ttttttactc tcattaaaca ttaagtaata tataattata attttagaaa 60
acctaaaata actcaatatt aatgcttatt tatgtatatt tctaaactga aaaaaaacg 120
agattcactg aaaactcagg ctgtttattt gagaagggtca gaaatagtgt gtttctactg 180
tgcattttta gaaaaccctt ttttattttt attttatttt ttattttcaa catttattgt 240
aaatttcagag gtacatgtgc aagaggataa ggtttgttac ataggtaaaa aaacactctt 300
gtataaacia atacaatgat atggactata tgtgtccctg tcaagaaaaa cagagcaaaa 360
cccttcttaa aaatggcaag acacatttta ttctgactgg tgaattaggg gatagagact 420
acagtataaa ttgagctcaa ctctaattaa gacaaaggta actggggctt ttaaagagaa 480
aaccgatatg actaaaaatg acraaaacat aaaggagcta ggagggtata tgaaaantgg 540

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318

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aatattacat aaaaattcag tgtgaaataa ttgaaaatta ttaggtaagg tgggttaggc 600
agtgtatatt ttgcagtttg gcaggatcat attcctttga gccaaagacct accatggaag 660
ctagggtggc ctttaaagac aaattcatga cctagtgtccc atataagcta agctaaactt 720
ggcccagtcct cttaacatgg tgtttatgca agtcttttgt gttacgtggg agtgtaaaat 780
tcaagtcctt catgaaatac aaanatantt tcttaatggg aatattctgt gtttcaaaat 840
tattaacggg cgtaactgac ttcctatcca aaactgtgca ncctggtaaa aatccttgnt 900
tanaaagaca aaagatgtn tccacatgag gcctgnaata tgcttgagtt actatttnca 960
cnntagnaac aaccctttgt aatgngataa taatncacag a 1001

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<210> 369

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 12-642-417 : polymorphic base A or G

<220>

<221> misc_binding

<222> 484..502

<223> 12-642-417.mis1

<220>

<221> misc_binding

<222> 504..523

<223> 12-642-417.mis2, potential complement

<220>

<221> primer_bind

<222> 87..105

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 562..582

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 12-642-417 potential probe

<220>

<221> misc_feature

<222> 507,774,778,851,869,873,890,906,928,932..933,937,955,965,976,981
983,988..989,998,1001

<223> n=a, g, c or t

<400> 369

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ttaaagtaata tataattata attttagaaa acctaaaata actcaatatt aatgcttatt 60
tatgtatatt tctaaactga aaaaaaacg agattcactg aaaactcagg ctgtttattt 120
gagaagggtca gaaatagtgt gtttctactg tgcattttta gaaaaccctt ttttattttt 180
attttatttt ttattttcaa cattttattgt aaattcagag gtacatgtgc aagagggtata 240
ggtttggttac ataggtaaaa aaacactcct gtataaacia atacaatgat atggactata 300
tgtgtccctg tcaagaaaaa cagagcaaaa cccttcttaa aaatggcaag acacatttta 360
ttctgactgg tgaattaggg gatagagact acagtataaa ttgagctcaa ctctaattaa 420
gacaaaaggta actggggcctt ttaaagagaa aaccgatatg actaaaaatg acgaaaacat 480
aaaggagcta ggagggttata tgraantgg aatattacat aaaaattcag tgtgaaataa 540
ttgaaaatta ttaggtaagg tgggttaggc agtgtatatt ttgcagtttg gcaggatcat 600
attcctttga gccaaagacct accatggaag ctagggtggc ctttaaagac aaattcatga 660
cctagtgtccc atataagcta agctaaactt ggcccagtcct cttaacatgg tgtttatgca 720

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319

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agtcttttgt gttacgtggg agtgtaaaat tcaagtcctt catgaaatac aaanatantt 780
tcttaatggg aatattctgt gtttcaaaat tattaacggg cgtaactgac ttcctatcca 840
aaactgtgca ncctggtaaa aatccttgnt tanaaagaca aaagatgttn tccacatgag 900
gcctgnaata tgcttgagtt actatttnca cnntagnaac aaccctttgt aatgngataa 960
taatncacag aataanagaa nangatannt ccctttantt n 1001

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<210> 370

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 434

<223> 12-646-429 : polymorphic base C or T

<220>

<221> misc_binding

<222> 414..433

<223> 12-646-429.mis1, potential

<220>

<221> misc_binding

<222> 435..454

<223> 12-646-429.mis2, potential complement

<220>

<221> primer_bind

<222> 6..26

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 474..494

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 422..446

<223> 12-646-429 potential probe

<220>

<221> misc_feature

<222> 31..32,35,59,514

<223> n=a, g, c or t

<400> 370

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ctacacttgg aaaatatctg taccocaaat nnganagtca atataacctg gtgggttaana 60
gctggcactc tggatccaga tggccttgat tcaagtctta gaaaccactg tataatgatg 120
tgggactgga caagttactt gaacttcatt tgactcagct tcctcaccaa tgaaatggca 180
atagttgtca tcacattatc aatatcatgg gttgctgaaa gaacgaattc attaatattg 240
caaagcacta acaattgtgt gtacagcaaa ataaaattgt actattatca ttaaacaagt 300
caaaaaattt ccacaataat aatttttagtg ttcatataat tgcataatat attatagttt 360
caaaacatgc tatgttttcta atgcaaatga taaaaatgac agtatttact atttcaagca 420
tgtgggaatt aaayttggag cataaaccaa gggctgacaa actatggcct cttggctggg 480
caaattcttg cagctacttg ttttttaaaa aaantaattg gtataataat ttcacaccac 540
aaaattatac actttaagca tttaatcttt atgattcatt ggcatttaac acatttgaaa 600
tgttctgcca ctaccaccac tatctagatc caaattatct ttttcaactc aaaagggaagc 660
tttacacca ttagagagtc atctcgcatc ctccattat ccgtgccttg caacctggca 720
ttatgtgttg gcatcattgt atagcttatt gggatatataa cttcaacaaa gtgttttatt 780
ttttcttact cttaacatgt cctatttggt tctaaacagc aattttatga tgcataaaat 840
taaacttcta tgttctgatt tctctgttat taaatatatt cagaggtggt ctgatttaca 900
ttgttgtagg ttctctccaa ttttatattg aagtattttc ttgagaatgg ccataaacca 960

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320

agatcctgga aagctctgaa taaggtgggg aagtgagttt c

1001

<210> 371

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 438

<223> 12-646-433 : polymorphic base G or T

<220>

<221> misc_binding

<222> 418..437

<223> 12-646-433.mis1, potential

<220>

<221> misc_binding

<222> 439..458

<223> 12-646-433.mis2, potential complement

<220>

<221> primer_bind

<222> 6..26

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 474..494

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 426..450

<223> 12-646-433 potential probe

<220>

<221> misc_feature

<222> 31..32,35,59,514

<223> n=a, g, c or t

<400> 371

ctacacttg	aaaatatctg	taccccaa	at	nnganagtca	atataacctg	gtgggtaana	60
gctggcactc	tggatccaga	tggccttgat	tcaagtctta	gaaaccactg	tataatgatg		120
tgggactgga	caagttactt	gaacttcatt	tgactcagct	tcctcaccaa	tgaaatggca		180
atagttgtca	tcacattatc	aatatcatgg	gttgctgaaa	gaacgaattc	attaatatg		240
caaagcacta	acaattgtgt	gtacagcaaa	ataaaattgt	actattatca	ttaaacaagt		300
caaaaaat	ccacaataat	aatttttagt	ttcatataat	tgcataatat	attatagttt		360
caaaacatgc	tatgtttcta	atgcaaatga	taaaaatgac	agtatttact	atttcaagca		420
tgtgggaatt	aaacttgkag	cataaaccaa	gggctgacaa	actatggcct	cttggctggg		480
caaatcttgt	cagctacttg	ttttttaaaa	aaantaattg	gtataataat	ttcacaccac		540
aaaattat	actttaagca	tttaatcttt	atgattcatt	ggcatttaac	acatttgaaa		600
tgttctgcca	taccaccac	tatctagatc	caaattat	ttttcacttc	aaaagggaagc		660
tttacacca	ttagagagtc	atctcgcatt	ctcccattat	ccgtgccttg	caacctggca		720
ttatgtgttg	gcattcattg	atagcttatt	gggtatataa	cttcaacaaa	gtgttttatt		780
ttttcttact	tctaacatgt	cctatattgt	tctaaacagc	aattttatga	tgcatataaat		840
taaacttcta	tgttctgatt	tctctgttat	taaatatatt	cagagggtgt	ctgattttaca		900
ttgttgtgag	ttctctccaa	ttttatattg	aagtattttc	ttgagaatgg	ccataaacca		960
agatcctgga	aagctctgaa	taaggtgggg	aagtgagttt	c			1001

<210> 372

<211> 1001

321

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 12-647-145 : polymorphic base A or G

<220>

<221> misc_binding

<222> 483..502

<223> 12-647-145.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 12-647-145.mis2, potential complement

<220>

<221> primer_bind

<222> 359..378

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 788..808

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 12-647-145 potential probe

<220>

<221> misc_feature

<222> 351,951

<223> n=a, g, c or t

<400> 372

gcatcattgt	atagcttatt	gggtatataa	cttcaacaaa	gtgttttatt	ttttcttact	60
tctaacatgt	cctatttggt	tctaaacagc	aattttatga	tgcataaaat	taaacttcta	120
tggtctgatt	tctctgttat	taaatatatt	cagaggtggt	ctgatttaca	ttgttgtag	180
ttctctccaa	ttttatattg	aagtattttc	tgagaatgg	ccataaacca	agatcctgga	240
aagctctgaa	taaggtgggg	aagtgagttt	cagatatatg	agtccggtaa	aatataacga	300
aatgagaaaag	aaagaacaaa	atgcaaaggt	agaagaaatt	tattactcac	nagttcctaa	360
gtgatgttag	ggatgatgat	aggaaactga	cagaaagtcc	agaggtggta	gagagctcaa	420
ccagctgcct	agaagtgcga	gggggaaccc	ttgtaggaag	gcttttatta	aggaccttag	480
gtattatttc	ctaggcttct	ccrcaggagt	tgaggaatgg	ctagcttaag	ggaacacaca	540
tgaaggggaa	aattatcata	tgactctggt	attgatcatt	aggttatatc	atggtcatca	600
cctctgtgat	gtgttgcggt	tctgggtcat	taggatgaga	aacatgtaga	ctctatctca	660
aagaaggggaa	gttttaacaa	aggcaatagt	gacaacctat	gactaggtct	taagcaactc	720
atgttaagcc	taaaaatcaa	tgctgaggca	aaacaaactt	acgacgagaa	ggtagacaga	780
cattttagaa	gaaatgtgac	ctagctgctt	ctggattggg	agtataaaaa	gtaccatgaa	840
tcagcttcta	aatgtaacaa	gaataaatag	tgaaaattgt	tttttagagac	aactatgcaa	900
acatattagg	agaagttgac	tgcaaggcca	tgacacctata	gttccagcta	nctcaggagg	960
ctgaggaagg	tggattactt	gagcccagga	gttcaaggcc	a		1001

<210> 373

<211> 751

<212> DNA

<213> Homo Sapiens

<220>

322

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<221> allele
<222> 251
<223> 12-648-123 : polymorphic base A or G

<220>
<221> misc_binding
<222> 231..250
<223> 12-648-123.mis1, potential

<220>
<221> misc_binding
<222> 252..271
<223> 12-648-123.mis2, potential complement

<220>
<221> primer_bind
<222> 129..147
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 607..627
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 239..263
<223> 12-648-123 potential probe

<220>
<221> misc_feature
<222> 14,23,28,31..32,35,44,49,67,106,113,124
<223> n=a, g, c or t

<400> 373
atttcttttt tggnggggaaa gtncatchnag nnaentggga attnctcgnt ttacagaaaag      60
aaattgnatt ttaaaacctc gtaagtagaa gggatcacaa gtaagnataa ttntcaaaca      120
aatncaggaa aacaagtctt tagcaggagt tttctgaagc gtgaagtgag ctgctcaaga      180
gagtgaccgg atcttttctg gagaaaagcc tgggtggacct ctccactga agtgtgcatg      240
tgcactcctc rcataggaca tgggtgaggtg atgatgagag tccctcgaag ccagttgtac      300
ataacacatt ccatgagggt gccaatTTTA cagtaagata tcagagtaac aggtgtcacc      360
cataaaca aaa cccagaaata tgtaactata catgtttact tatggattat cagtaggatt      420
ttgaggacga gttcacagaa attcaaaacc atacaccagt caaaaccatg caccaggctt      480
cgggatgtca gcaattctta ccttatgtga tgaaggagtg atttagaagc aaggtttggg      540
aaattctgac aaattttaag ataggttaga aataattata cagttgagag aaatatataa      600
tatcttccca atcataagtg acttttcctt agtagcataa tcaaggaaat gaaattataa      660
tgactacatt aaagtaatga tttagaaaac ctccctgaaa taaaaacaag ttacttagga      720
gaacaataac aatataaaat taaagagaag t                                     751

<210> 374
<211> 928
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 428
<223> 12-648-300 : polymorphic base C or T

<220>
<221> misc_binding
<222> 408..427
<223> 12-648-300.mis1, potential

```

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<220>
<221> misc_binding
<222> 429..447
<223> 12-648-300.mis2, complement

<220>
<221> primer_bind
<222> 129..147
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 607..627
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 416..440
<223> 12-648-300 potential probe

<220>
<221> misc_feature
<222> 14,23,28,31..32,35,44,49,67,106,113,124
<223> n=a, g, c or t

<400> 374
atttcttttt tggngggaaa gtncatcnag nnacntggga attnctcgnt ttacagaaaag      60
aaattgnatt ttaaaacctc gtaagtagaa gggatcacaa gtaagnataa ttntcaaaca      120
aatncaggaa aacaagtctt tagcaggagt tttctgaagc gtgaagtgag ctgctcaaga      180
gagtgaccgg atcttttctg gagaaaagcc tgggtggacct ctccactga agtgtgcatg      240
tgcactctcc gcataggaca tgggtgagggt atgatgagag tccctcgaag ccagttgtac      300
ataacacatt ccatgagggt gccaatttta cagtaagata tcagagtaac aggtgtcacc      360
cataaacaata cccagaaata tgtaactata catgtttact tatggattat cagtaggatt      420
ttgaggayga gttcacagaa attcaaaacc atacaccagt caaaaccatg caccaggctt      480
cgggatgtca gcaattctta ccttatgtga tgaaggagtg atttagaagc aagggttggg      540
aaattctgac aaattttaag atagggttaga aataattata cagttgagag aaatatataa      600
tatcttccca atcataagtg acttttcctt agtagcataa tcaaggaaat gaaattataa      660
tgactacatt aaagtaatga tttagaaaac ctccctgaaa taaaaacaag ttacttagga      720
gaacaataac aatataaaat taaagagaag taaacagtgg tagtcttcct aagaatctat      780
attagtgatt acaagagctt ggttcccata tttttaactg tatctttccc tcactactgt      840
gtaaagatac taatttattt cttactttac atacttaatc aaatacatat acacacacac      900
gcacatgcac acacttacat aactacag                                     928

<210> 375
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-648-402 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-648-402.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-648-402.mis2, potential complement

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<220>
 <221> primer_bind
 <222> 100..118
 <223> upstream amplification primer

 <220>
 <221> primer_bind
 <222> 578..598
 <223> downstream amplification primer, complement

 <220>
 <221> misc_binding
 <222> 489..513
 <223> 12-648-402 potential probe

 <220>
 <221> misc_feature
 <222> 2..3,6,15,20,38,77,84,95,910..911,996..997
 <223> n=a, g, c or t

<400> 375
 gnnacntggg aattnctcgn ttacagaaa gaaattgnat tttaaaacct cgtaagtaga 60
 agggatcaca agtaagnata attntcaaac aaatncagga aaacaagtct ttagcaggag 120
 ttttctgaag cgtgaagtga gctgctcaag agagtgaacc gatcttttct ggagaaaagc 180
 ctggtggacc tctccactg aagtgtgcat gtgcatcctc cgcataggac atgggtgaggt 240
 gatgatgaga gtccctcgaa gccagtgtga cataacacat tccatgaggg tgccaatttt 300
 acagtaagat atcagagtaa caggtgtcac ccataaaca acccagaaat atgtaactat 360
 acatgtttac ttatggatta tcagtaggat tttgaggacg agttcacaga aattcaaaac 420
 catacaccag tcaaaacat gcaccaggct tcgggatgtc agcaattctt accttatgtg 480
 atgaaggagt gatttagaag saaggtttgg gaaattctga caaattttta gataggttag 540
 aaataattat acagttgaga gaaatatata atatcttccc aatcataagt gacttttcct 600
 tagtagcata atcaaggaaa tgaaattata atgactacat taaagtaatg atttagaaaa 660
 cctccctgaa ataaaaaca gttacttagg agaacaataa caatataaaa ttaaagagaa 720
 gtaaacagtg gtagtcttcc taagaatcta tattagtgat tacaagagct tggttcccat 780
 atttttaact gtatcttccc ctactactg tgtaaagata ctaatttatt tcttacttta 840
 cataactaat caaatacata cacacacaca cgcacatgca cacacttaca taactacaga 900
 ttaataatan ngagaaaatt gatgttgtat aacataagtc tttccaaaagg aactgagcga 960
 tgctgtattt aaaaaactgg cactactaga agtcanngtat t 1001

<210> 376
 <211> 798
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 298
 <223> 12-652-115 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 278..297
 <223> 12-652-115.mis1, potential

<220>
 <221> misc_binding
 <222> 299..318
 <223> 12-652-115.mis2, potential complement

<220>
 <221> primer_bind
 <222> 184..203

325

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 615..635

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 286..310

<223> 12-652-115 potential probe

<220>

<221> misc_feature

<222> 43..44,341

<223> n=a, g, c or t

<400> 376

aaataattgg	ttaaaaattt	ttatgccaca	aaattaaaca	ctnnaaccat	ttaatgtgta	60
caattcattg	gcgtttaata	tatttgcaat	attttgccac	taccaccact	ctctagatcc	120
aaagtatttt	gtcacttcaa	aaggaagctt	tatacccat	agacagtcac	ctcgcatctt	180
cccatcctcc	atctcctgca	acctggcatt	atctgttggc	atcattctat	agcctagtag	240
ataatgtttt	tttaaaggca	aatagggtaca	taacttcaac	aaagtgtttt	atttttcytt	300
atttttacat	ctcctatttg	ttcctaaatg	aaaattctgt	ngatgtataa	gaattagtta	360
ttatttctta	gttgctctgt	tattaaatat	attcagcagt	gttggtgattt	atattgttac	420
agtttctgtc	caattttgta	ttgaagtctg	tccctttaga	attgcaataa	accaagctct	480
gatggagggtg	aggaagtga	attcagatgt	gtgtgtcagg	taaaatacaa	tgaaatgtaa	540
aataaaaacca	aatgcatga	aatagaagaa	atgtattaca	gttcctagag	atattaagga	600
taatgacata	aaacggacag	aaaattcaga	agtggcagag	agctcaacca	gctgcctgga	660
agtgatagag	agaatccctg	tgtggggggc	tgtgggggtg	cttttcttaa	ggtctatgag	720
cattatttcc	tagtcttgtc	tgccggagtt	gtggagtggc	tatcttaaga	aaacacacat	780
gaagagggaa	aattatta					798

<210> 377

<211> 886

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 386

<223> 12-652-203 : polymorphic base A or C

<220>

<221> misc_binding

<222> 367..385

<223> 12-652-203.mis1

<220>

<221> misc_binding

<222> 387..406

<223> 12-652-203.mis2, potential complement

<220>

<221> primer_bind

<222> 184..203

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 615..635

<223> downstream amplification primer, complement

326

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<220>
<221> misc_binding
<222> 374..398
<223> 12-652-203 potential probe

<220>
<221> misc_feature
<222> 43..44,341
<223> n=a, g, c or t

<400> 377
aaataattgg ttaaaaattt ttatgccaca aaattaaaca cttnnaaccat ttaatgtgta      60
caattcattg gcgtttaata tatttgcaat attttgccac taccaccact ctctagatcc      120
aaagtatttt gtcacttcaa aaggaagctt tatacccatt agacagtcac ctgcgattct      180
cccatcctcc atctcctgca acctggcatt atctgttggc atcattctat agcctagtag      240
ataatgtttt tttaaaggca aataggtaca taacttcaac aaagtgtttt atttttcttt      300
atttttacat ctctatttg ttctaaatg aaaattctgt ngatgtataa gaattagtta      360
ttatttccta gttgctctgt tattamatat attcagcagt gttgtgattt atattgttac      420
agtttctgtc caattttgta ttgaagtctg tccctttaga attgcaataa accaagctct      480
gatggagggtg aggaagtga aatcagatgt gtgtgtcagg taaaatacaa tgaaatgtaa      540
aataaaacca aaatgcatga aatagaagaa atgtattaca gttcctagag atattaagga      600
taatgacata aaacggacag aaaattcaga agtggcagag agctcaacca gctgcctgga      660
agtgatagag agaatccctg tgtggggggc tgtgggggtg cttttcttaa ggtctatgag      720
cattatttcc tagtcttgtc tgccggagtt gtggagtggc tatcttaaga aaacacacat      780
gaagaggggaa aattattatt tgattctggt gttgaccatt aggttatctc atggtaatca      840
gctctgtggt atgttgcat tctgggtcag tgggatgaga aacaag                        886

<210> 378
<211> 957
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 457
<223> 12-652-274 : polymorphic base G or T

<220>
<221> misc_binding
<222> 437..456
<223> 12-652-274.mis1, potential

<220>
<221> misc_binding
<222> 458..477
<223> 12-652-274.mis2, potential complement

<220>
<221> primer_bind
<222> 184..203
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 615..635
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 445..469
<223> 12-652-274 potential probe

<220>

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327

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<221> misc_feature
<222> 43..44,341
<223> n=a, g, c or t

<400> 378
aaataattgg ttaaaaaattt ttatgccaca aaattaaaca cttnnaaccat ttaatgtgta      60
caattcattg gcgtttaata tatttgcaat attttgccac taccaccact ctctagatcc      120
aaagtatttt gtcacttcaa aaggaagctt tataccatt agacagtcac ctgcattct      180
cccatectcc atctectgca acctggcatt atctgttggc atcattctat agcctagtag      240
ataatgtttt tttaaaggca aataggtaca taacttcaac aaagtgtttt atttttcttt      300
atttttacat ctctatttg ttctaaatg aaaattctgt ngatgtataa gaattagtta      360
ttatttccta gttgctctgt tattaaatat attcagcagt gttgtgattt atattgttac      420
agtttctgtc caattttgta ttgaagtctg tcccttkaga attgcaataa accaagctct      480
gatggagggtg aggaagtga attcagatgt gtgtgtcagg taaaatacaa tgaaatgtaa      540
aataaaacca aaatgcatga aatagaagaa atgtattaca gttcctagag atattaagga      600
taatgacata aaacggacag aaaattcaga agtggcagag agctcaacca gctgcctgga      660
agtgatagag agaatccctg tgtggggggc tgtgggggtg cttttcttaa ggtctatgag      720
cattatttcc tagtcttgc tgccggagtt gtggagtggc tatcttaaga aaacacacat      780
gaagagggaa aattattatt tgattctggt gttgaccatt aggttatctc atggtaatca      840
gctctgtggt atgttgcat tctgggtcag tgggatgaga aacaagtgtg ctctgtaaca      900
aacaactaca caaggaaggg aagtttcaca aagccaaaag tgacaggcta tgacttg      957

<210> 379
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-652-371 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-652-371.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-652-371.mis2, potential complement

<220>
<221> primer_bind
<222> 131..150
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 562..582
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-652-371 potential probe

<220>
<221> misc_feature
<222> 288
<223> n=a, g, c or t

<400> 379

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328

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atgtgtacaa ttcattggcg ttaatatat ttgcaatatt ttgccactac caccactctc      60
tagatccaaa gtattttgtc acttcaaaaag gaagctttat acccattaga cagtcattctc    120
gcattctccc atcctccatc tcttgcaacc tggcattatc tgttggcatc attctatagc     180
ctagtagata atgttttttt aaaggcaaat aggtacataa cttcaacaaa gtgtttttatt    240
tttcttttatt ttacatctc ctatttggtc ctaaataaaa attctgtnga tgtataagaa     300
ttagttatta tttcctagtt gctctgttat taaatatatt cagcagtgtt gtgatttata    360
ttgttacagt ttctgtccaa ttttgatttg aagtcctgtcc ctttagaatt gcaataaacc     420
aagctctgat ggaggtgagg aagtgaattt cagatgtgtg tgtcaggtaa aatacaatga     480
aatgtaaaat aaaacaaaaa ygcataaaat agaagaaatg tattacagtt cctagagata     540
ttaaggataa tgacataaaa cggacagaaa attcagaagt ggcagagagc tcaaccagct     600
gcctggaagt gatagagaga atccctgtgt ggggggctgt ggggggtgctt ttcttaaggt    660
ctatgagcat tatttcctag tcttgtctgc cggagttgtg gagtggctat ctttaagaaa     720
cacacatgaa gagggaaaat tattatttga ttctggtgtt gaccattagg ttatctcatg     780
gtaatcagct ctgtggtatg ttgcatttct gggtcagtgg gatgagaaac aagtgtactc     840
tgtaacaaac aactacacaa ggaagggaag ttccacaaag ccaaaagtga caggctatga     900
cttgctctta aacaactcaa gttaagtcta aaaatggatg tggaatcaat aactatattc     960
aacaatgta  tgacaagaag gtagaaaagg gatgggtcca g                                1001

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<210> 380

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-653-423 : polymorphic base T or A

<220>

<221> misc_binding

<222> 479..498

<223> 12-653-423.mis1, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-653-423.mis2, potential complement

<220>

<221> primer_bind

<222> 903..921

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 390..410

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-653-423 potential probe

<400> 380

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aaaaactgtg taaaaactgt tatctccaga gaaaaaccaa tgctaaggaa gcatccagtg      60
tagataatag agagtatcct ggagtcactg atattaataa tttagatgag agctgaacta    120
tatgcaggaa taggtaaaag aatgaagaag agaaaaaac acaaaaagaa aagcaggtaa     180
agtgttcagg acagttctca agactcaaaag ttaggtttgc aagggaagata ctgagtaaga    240
atcagatgat gctgataggc aagataagag ccagatactc ctcaggagtt gaaatattta     300
ttaagcacat ttagggacta ctaaaaagag ttaagaaaag aaaaatgagg ataagattat     360
acttttttaa aaaagattcc aagatgttcg atggattaaa ttgtggaagg gccaaaactag     420
aaagagctga ccattgagga aattttgtat gaattcaggt agcagatgat ggaaaaatgg     480
actagaaagt ggatagaawt acctatgcct actttttacg taatatgact aacttcatat     540

```

329

```

tgtgttgtgt ggaaaaaagt taatacaaat aaaccactta aaatgtctct ggcataatagt 600
tagtgattca gaaatattat ttgcaatta tggttatttt tgttattact aatactatga 660
attacttaac atgtgtaagt cacttgagat attatcctc atttaataga aactaattat 720
tcagcatttc aagattatat tctctaacaa agtcctatgg tcttctatat gacagatacc 780
ctgtagactt gtttaaaata agacatatca gttttgacag taagatgagc aaaatgaaat 840
tgtaaaattc taccacaagt gacaaggatc ttcattcagta ttctaactta taagaaaata 900
atcccttacc gatataaatg tgtgattcta ttagtatttg cagccagacc cagtgttcac 960
ttgattttac taaagcattt aaatcattct gcgttgagat c 1001

```

<210> 381

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-654-115 : polymorphic base T or C

<220>

<221> misc_binding

<222> 479..498

<223> 12-654-115.mis1, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-654-115.mis2, potential complement

<220>

<221> primer_bind

<222> 595..613

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 76..96

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-654-115 potential probe

<400> 381

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ccatcaggaa gacccactac gttatctgag acaatggcaa aagctgacat atggcttatt 60
cgaaactact gggattttca atttcctcac ccactcttac caaatgttga gttcgttgga 120
ggactccact gcaaacctgc caaaccccta ccgaaggtaa actattactg tttgttttgt 180
ctgctttgaa gtttcagtac gaatggttct atattcattc aaagtgtttg acttacactg 240
gaagaaaggt ggaagtggga agagtaaagc agataccaat tagaaactga cgtacatggt 300
gatactatca caagtttatg aatttcatca ttattaccaa taaagaggga tactaaagag 360
actttgaaaa tagggtttgt aaattaaagc tttgattatg caacatgtaa gaaggtagtg 420
gccattcatt caaagaatat ttataaagag attagcacac accacaggta cgtgtatggg 480
acacagtttc tatcccaaya caccttacat tctattttga aagatagaat atatgcaagt 540
aataaaaact gtgtaaaaac tggtatctcc agagaaaaac caatgctaag gaagcatcca 600
gtgtagataa tagagagtat cctggagtca ctgatattaa taatttagat gagagctgaa 660
ctatatgcag gaataggtaa aagaatgaag aagagaaaaa aacacaaaaa gaaaagcagg 720
taaagtgttc aggacagttc tcaagactca aagtttagtt tgcaagggaag atactgagta 780
agaatcagat gatgctgata ggcaagataa gagccagata ctctcagga gttgaaatat 840
ttattaagca catttaggga ctactaaaaa gagttaagaa aagaaaatat gggataagat 900
tatacttttt aaaaaaagat tccaagatgt tcgatggatt aaattgtgga agggccaaac 960
tagaaagagc tgaccattga ggaaattttg tatgaattca g 1001

```

330

<210> 382
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 499
 <223> 12-654-207 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 479..498
 <223> 12-654-207.mis1, potential

<220>
 <221> misc_binding
 <222> 500..519
 <223> 12-654-207.mis2, potential complement

<220>
 <221> primer_bind
 <222> 687..705
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 168..188
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 487..511
 <223> 12-654-207 potential probe

```

<400> 382
tgcctacatt tttgcccaca ttattctaac ttctttcaga aaattaccta gtttaattat      60
cttgtgtcat ctatcttttc tttttttttc ccccatcagg aagaccact acgttatctg      120
agacaatggc aaaagctgac atatggctta ttcgaaacta ctgggatttt caatttcctc      180
accactctt accaaatggt gagttcgttg gaggactcca ctgcaaacct gccaaacccc      240
taccgaaggt aaactattac tgtttgttt gtctgctttg aagtttcagt acgaatgggt      300
ctatattcat tcaaagtgtt tgacttacac tggaagaaag gtggaagtgg gaagagtaaa      360
gcagatacca attagaaact gacgtacatg ttgatactat cacaagttta tgaatttcac      420
cattattacc aataaagagg gatactaaag agactttgaa aatagggttg gtaaattaaa      480
gctttgatta tgcaacatrt aagaaggtac tggccattca ttcaaagaat atttataaag      540
agattagcac acaccacagg tacgtgtatg ggacacagtt tctatcccaa tacaccttac      600
attctatttt gaaagataga atatatgcaa gtaataaaaa ctgtgtaaaa actggttatct      660
ccagagaaaa accaatgcta aggaagcatc cagtgtagat aatagagagt atcctggagt      720
cactgatatt aataatttag atgagagctg aactatatgc aggaataggt aaaagaatga      780
agaagagaaa aaaacacaaa aagaaaagca ggtaaagtgt tcaggacagt tctcaagact      840
caaagttagt tttgcaagga agatactgag taagaatcag atgatgctga taggcaagat      900
aagagccaga tactcctcag gagttgaaat atttattaag cacatttagg gactactaaa      960
aagagttaag aaaagaaaat atgggataag attatacttt t                                1001

```

<210> 383
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 12-657-396 : polymorphic base A or G

```

<220>
<221> misc_binding
<222> 483..502
<223> 12-657-396.misl, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-657-396.mis2, potential complement

<220>
<221> primer_bind
<222> 108..128
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 566..586
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-657-396 potential probe

<220>
<221> misc_feature
<222> 74,84,232,860,993
<223> n=a, g, c or t

<400> 383
ctgtataatt atcggttgt gtgctgcttc tagtaaataa ttattatata ctgaagctat      60
atgtttctaa cacnaaactt tatnaatttc tgttctaaca tgcattctcag aatatagggga    120
caatatagct atatgtatga caacttcaaa attttatttt aaaagtatac ataaactata      180
ttattttatg tggatttgca tctttataat gaagacaatt ttttctctgg angaaaatgg      240
aagaatttgc ccagagctct gatgaagacg gtggttggtt ttctctggag tcagctgtgc      300
aaaaccttac agaagaaaaa gctgatctta tcacttcggc cctggctcag attccacaaa      360
aagtcagtac aacctccaat ccttataaga aactattcac acaatggaga aagtatggct      420
ttccacctgg aacttgaatc tcatttttca atttgcataa caggcactag atttatgtaa      480
caatttggaa agtattatgg tartttatgt gagcacaact gattatttgt ctagtgatct      540
ttgctattac tttagtaaca catctcttgg ttgtcgtttg ttaataataa agtaaaaata      600
aagcattaag tccctatttc acgttgcagg atttgaaatc ttaagaccta ttctgatgac      660
tccaaaggaa acttcttaag tatactagct caaaggaacc taaacttttg gggatgatat      720
aagaaagata gagaagaatc atgctcaata ttatcttcaa catattttat tgtataggag      780
ctctattcag tgtgtttgaa cataaaaagta gaagcttaga tttatgtagt ctttctaata      840
aactggagtt ttctatagtn tacaaggcaa ttatgatttt aatattacag tctaacaacc      900
tgcattgtaat actttatgat attcaattaa ttttattact gtaattctag ttttcctctc      960
tttagttagt gctatttata cactagcctc aanggggttac t                          1001

<210> 384
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-658-120 : polymorphic base A or T

<220>
<221> misc_binding
<222> 483..502

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332

<223> 12-658-120.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 12-658-120.mis2, potential complement

<220>

<221> primer_bind

<222> 384..404

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 863..883

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 12-658-120 potential probe

<220>

<221> misc_feature

<222> 418,551

<223> n=a, g, c or t

<400> 384

atTTTTcaat	ttgcataaca	ggcactagat	ttatgtaaca	atttggaaag	tattatggta	60
gtttatgtga	gcacaactga	ttatttgtct	agtgatcttt	gctattactt	tagtaacaca	120
tctcttggtt	gtcgtttggt	aataataaag	taaaaataaa	gcattaagtc	cctatttcac	180
gttgcaggat	ttgaaatctt	aagacctatt	ctgatgactc	caaaggaaac	ttcttaagta	240
tactagctca	aaggaacctt	aactttgggg	gatgatataa	gaaagataga	gaagaatcat	300
gctcaatatt	atcttcaaca	tattttattg	tataggagct	ctattcagtg	tgtttgaaca	360
taaaagtaga	agcttagatt	tatgtagtct	ttctaataaa	ctggagtttt	ctatagtnta	420
caaggcaatt	atgattttta	tattacagtc	taacaacctg	catgtaatac	tttatgatat	480
tcaattaatt	ttattactgt	aawtctagtt	ttcctctctt	tagttagtgc	tatttatata	540
ctagcctcaa	ngggttactt	tttaaaattt	tatgttttaa	tttcaaaaaca	ctcaataaaa	600
gccagtatgc	taattaggaa	tgtgaaatta	gttttgatta	tgagattctc	tttttgggag	660
ttcagaatat	ctatgtaatc	ctttgttttc	aagtgttaaga	ttttcatata	ggtttccaga	720
aagaaaaaag	tatggaatta	aggtacaaat	acaaacaaaa	ttcagccttg	aacaatgaag	780
tataggtaac	ttctgtctct	ttcttttttg	attaaaaata	aatgaaataa	aggagagaat	840
gaagcataaa	gagaaaagac	aaccaactat	ccaaaaccag	acaaaagcca	aagcaatgtt	900
tgtctctggg	aaactgtaaa	tttgataata	gagctagaat	ggccaagtga	tttacattta	960
cacagcagtt	gtgtgtccac	aaggatattt	aacttccata	t		1001

<210> 385

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-659-382 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-659-382.mis1, potential

<220>

<221> misc_binding

333

<222> 502..521
 <223> 12-659-382.mis2, potential complement

<220>
 <221> primer_bind
 <222> 120..139
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 552..572
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-659-382 potential probe

<220>
 <221> misc_feature
 <222> 21,546
 <223> n=a, g, c or t

<400> 385
 atattgagat aataaatgaa ncattcaaat atttaagtaa tcattaggca gacataattc 60
 cagtgtaaag atgagtaaaa aattactaat ggtccccacc ctttttatta atgtatttac 120
 tacattccact ttcaacttcc aaataatggt aagcttttca tttctaaagc aatgaaaagg 180
 gagtgagttt acttatattc acttgtttca taagttatat tcccatatct gatgatttac 240
 aaagaaagca aatctatcaa tcatctatgt ctgagaaata cattaatctg cttaaaaggc 300
 acatataatt tgtttccgat taaaaattat taagcacttt ttccaagaaa aaaattcaag 360
 tgactttttt tcccatatgt gcagaataat atcgcattgt ctacaattgg aaattattta 420
 aagggtgaaa agactgattg gcagttcttt aataataggt ctgtttaaaa tatcccaaat 480
 ttgtgggtgat gctaaatttc rttctgctgg ctcttaactc ttcagtggca caatccaaag 540
 cgttgncagc agtggtttat atgggtctgct atagctaagc catgtagtac atgcctagta 600
 ccaacatgtg gtactgattt tggaattacc aagcaatctt cataaactag tgtataatct 660
 acaagttttt aacgtgtact tgctatctga gttttaaaag taactacaca tttgcatcaa 720
 aaaattagta taggtgatta caagaatggt atacaggata taaaactaaa aactgcttta 780
 taaatattca aatatcaaag ttgctgcac agctcagaga cgctgaagct gtgctggagg 840
 cagcagagtt aatggcggca agtccctgtg gagggacctt cactaacccta cattcctcct 900
 tcctgccctc catccttccc gatctccgc tcctcttggg gtcatttctt actgcaatag 960
 agttttgcgt ccacatacct acctagggct attattaaca a 1001

<210> 386
 <211> 983
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 306
 <223> 12-660-134 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 286..305
 <223> 12-660-134.mis1, potential

<220>
 <221> misc_binding
 <222> 307..326
 <223> 12-660-134.mis2, potential complement

<220>

334

<221> primer_bind
 <222> 173..193
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 692..712
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 294..318
 <223> 12-660-134 potential probe

<220>
 <221> misc_feature
 <222> 880..881,889,925..926,930
 <223> n=a, g, c or t

<400> 386
 agtgtagtta catctcacia ataatttttt caatcatttt ctgggttggtc tgtctactaa 60
 ttcaaagtgt acacctacct ttttctccta atagctagat attccaaatg taactgaaat 120
 ataacagccc ttcttttatt accagtgcac gcacttttta tgggaataaa tccccagtct 180
 ttattatgaa gtggtaacac attttgtcat ggagtgtggc ctgtccttct actactggag 240
 catcaccacc accccactcc ctgctgccgt ggacaccatg ccctatcaca ctcaagtgc 300
 tcactrtttc tctaagagaa tatgttctag catgcacccg gctttttggg ggctagagtg 360
 ggggatatgc agtttttttt gtctgcagtg tgctctttct atttgtccac ttgacaatct 420
 tgtattcatt cttcaagtct caagtcacat accacttctt caatatgtag ccatcactta 480
 tcgccccaga ggacttggtg cttctttctc tgagatctga aagtaatttt aatgcagttt 540
 tactgttaca gtaatttggt acctagagaa ccattgcccatt ttcattgcct catattgagc 600
 attgctcatt ttaagactca ccacgaataa ttattcaaaa atttatctaa tcctaggtca 660
 tctaacaacc aaagctttta tacctcatgg tggaggcaat gacatctatg agaggatcta 720
 ccatgggac cctatgggtg gccttccttt gttttagat caaccgata agttggttca 780
 catgaaggct aagggggaag ctgttacagt agactcaaaa acgatgtcat ctacaaattt 840
 gctcaatgca taaaaagcag tcattaatga ctcttcacgn ntgtaattnt tttaactacg 900
 tagcatgtat ttgctgacta cattnntttt tggtaatgct taaaggcaat cgtcaattaa 960
 ccactatgag tatcacgacg tgt 983

<210> 387
 <211> 1000
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 497
 <223> 12-662-80 : polymorphic base G or C

<220>
 <221> misc_binding
 <222> 477..496
 <223> 12-662-80.misl, potential

<220>
 <221> misc_binding
 <222> 498..517
 <223> 12-662-80.mis2, potential complement

<220>
 <221> primer_bind
 <222> 418..435
 <223> upstream amplification primer

335

<220>
 <221> primer_bind
 <222> 979..1000
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 485..509
 <223> 12-662-80 potential probe

<220>
 <221> misc_feature
 <222> 24,726,739
 <223> n=a, g, c or t

<400> 387
 atatatgctag tgactcagaa atgnttatta attttgcaat tatgggttatt ttattactaa 60
 tactactaac tacttaacat gtgcatgtca cttgagatat cattcctcat ttaagagAAC 120
 cagattattc agcacatcaa gggttatattg tcttggaag tcatagatga cagataccct 180
 tggacttgat taaaagtaga catatcagtt gtgacagcaa gataagctag ttgaaatttt 240
 aaaattcttc cataagtaat aaggatcttc accagtattc cagcttaaaa cacttcctca 300
 acaatataaa tgtgtgcctc aaatatgtgc agacaaacac aggggttcaca tgattttaat 360
 aaagcattta aatcattctg cattgagatc ccagaatttt acattttaga gcataaacat 420
 atcctattag agcagatgat ttctgcctta tgacaggcca ctcaataaag cttcctgggg 480
 gaactcgtct tgacatsata ggtgtctgac agagaagcac agagataatg aacaatgcat 540
 gtataataaa gaccaaataa ttcttgccac ttgtttctga atagtgccct tagtttcaat 600
 acgaaaaaaa attccgtcag catataagat tatattcttt tcgaaggaat acaagaactt 660
 catatatattt aattaacatc acattttaag gcatatgtaa aaagtaaggc ttcttcaatg 720
 gattanttat gcaatctcnt taaaagatca tttttgcttg cataaaactg agaatttggt 780
 ccattgttaa aactcagtat ctatgtttta tgcaagttgt ataggcttta tagagtcagt 840
 ttcttaagag acaaaagtgt aggttaagact aatgaaaaat atataccact ctaccctact 900
 cttgaaagat ttccccactc acactaaggg aaactgacag tgccagtaga aggaggaaga 960
 gagtaagaca atgtagaagg acaagaaaaa aaggttgact 1000

<210> 388
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-906-149 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-906-149.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-906-149.mis2, potential complement

<220>
 <221> primer_bind
 <222> 353..372
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 809..829
 <223> downstream amplification primer, complement

```

<220>
<221> misc_binding
<222> 489..513
<223> 12-906-149 potential probe

<220>
<221> misc_feature
<222> 750,853..854,860,942,945
<223> n=a, g, c or t

<400> 388
taattttata actgattgcc aggttggttaa gcctggcaag acattcagag ctaggtcaac      60
aaatatttca tttttttctg tttttatcctg tggcatatgg accacctcaa atttcagtgc      120
agaaggcttc ctgtagtcaa ttaacaaaga ctttgagtga gtcaatactg ttacctcatg      180
gccctcact atgatctcct ctagaatgac cttgacatta agccaatggc tcatgtcaca      240
gggccacacc aggaccttct cacagaattc acaactagca cagaagagtt gcaggagccg      300
aaataccaaa gctgacttct cgggcctcat gatgacattt ccctcacaca ctgatctgca      360
ctagctttgt agttactaag catgaaattg aaatgacaat ataagcacag aagttaaaaa      420
ttaatathtt aagtgtaaat aaagttcatt gggtgggtgc cagcttcaca tttattgaag      480
atatcaaaaa gaaatgcaat rttgcaatgt atcagggaaa atttgttcca accttctaga      540
gcttagaaat aaaacacata aagatacttt tattatctgg attgatgata aagaaatttt      600
ttaaaattct ttagatttaa taattcatgt gcagaaacat atgcacacaa ccacatttac      660
attcattcca cactaaatcc aaggtgtcag atggtttaga agaactcatg tttcacatcc      720
tttgctcaca aggacaatac aaagaattan ctgggaatac acttggagac tttgggtaac      780
tattttcatt aattctatat actaagtgc aagtgttcag tatttcagag gagaaaaatg      840
cacaattgct tttnaatatn ctgataatta ataaaagctt tagtaagaca tttgacttag      900
gaggtgagat gaaagcttca ttaggattta ttgttgccaa anggnaagca tttcacaaac      960
aatacaagca tgacgaaagt ataggatatt taaaagtcac t                        1001

<210> 389
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-906-154 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-906-154.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-906-154.mis2, potential complement

<220>
<221> primer_bind
<222> 348..367
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 804..824
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513

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337

<223> 12-906-154 potential probe

<220>

<221> misc_feature

<222> 745,848...849,855,937,940

<223> n=a, g, c or t

<400> 389

ttataactga	ttgccagggt	gttaagcctg	gcaagacatt	cagagctagg	tcaacaaata	60
tttcattttt	ttctgtttta	tcctgtggca	tatggaccac	ctcaaatttc	agtgcagaag	120
gcttcctgta	gtcaattaac	aaagactttg	agtgagtcaa	tactgttacc	tcattggcccc	180
tcactatgat	ctcctctaga	atgaccttga	cattaagcca	atggctcatg	tcacagggcc	240
acaccaggac	cttctcacag	aattcacaca	tagcacagaa	gagttgcagg	agccgaaata	300
ccaaagctga	cttctcgggc	ctcatgatga	catttccctc	acacactgat	ctgcactagc	360
tttgtagtta	ctaagcatga	aattgaaatg	acaatataag	cacagaagtt	aaaaattaat	420
attttaagt	ttaaataaagt	tcattgggtg	gttgccagct	tcacatttat	tgaagatatt	480
aaaaagaaat	gcaatgttgc	matgtatcag	ggaaaatttg	ttccaacctt	ctagagctta	540
gaaataaaaac	acataaagat	acttttatta	tctggattga	tgataaagaa	attttttaaa	600
attcttttaga	tttaataaatt	catgtgcaga	aacatatgca	cacaaccaca	tttacattca	660
ttccacacta	aatccaaggt	gtcagatggt	ttagaagaac	tcattgtttca	catcctttgc	720
tcacaaggac	aatacaaaaga	attanctggg	aatacacttg	gagactttgg	gtaactattt	780
tcattaattc	tatatactaa	gtgcaaaagt	ttcagtattt	cagaggagaa	aaatgcacaa	840
ttgcttttna	atatnctgat	aattaataaa	agcttttagta	agacatttga	cttaggaggt	900
gagatgaaag	cttcattagg	atttattgtt	gccaaaangn	aagcattttca	caatcaatac	960
aagcatgacg	aaagtatagg	atatttaaaa	gtcattccag	t		1001

<210> 390

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-906-251 : polymorphic base A or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-906-251.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-906-251.mis2, potential complement

<220>

<221> primer_bind

<222> 251..270

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 707..727

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-906-251 potential probe

<220>

<221> misc_feature

338

<222> 648,751..752,758,840,843

<223> n=a, g, c or t

<400> 390

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cacctcaaat ttcagtgcag aaggcttccct gtagtcaatt aacaaagact ttgagtgagt      60
caatactggt acctcatggc ccctcactat gatctcctct agaatgacct tgacattaag      120
ccaatggctc atgtcacagg gccacaccag gaccttctca cagaattcac aactagcaca      180
gaagagttgc aggagccgaa ataccaaagc tgacttctcg ggcctcatga tgacatttcc      240
ctcacacact gatctgcact agctttgtag ttactaagca tgaaattgaa atgacaatat      300
aagcacagaa gttaaaaatt aatattttta gtgtaaataa agttcattgg ttggttgcca      360
gcttcacatt tattgaagat atcaaaaaga aatgcaatgt tgcaatgtat caggggaaat      420
ttgttccaac cttctagagc ttagaaataa aacacataaa gatactttta ttatctggat      480
tgatgataaa gaaatttttt waaattcttt agatttaata attcatgtgc agaaacatat      540
gcacacaacc acatttacat tcattccaca ctaaatccaa ggtgtcagat gggttagaag      600
aactcatggt tcacatcctt tgctcacaag gacaatacaa agaattanct gggaatacac      660
ttggagactt tgggtaacta ttttcattaa ttctatatac taagtgcaaa gtgttcagta      720
tttcagagga gaaaaatgca caattgcttt nnaatatnct gataattaat aaaagcttta      780
gtaagacatt tgacttagga ggtgagatga aagcttcatt aggatttatt gttgccaaan      840
ggnaagcatt tcacaatcaa tacaagcatg acgaaagtat aggatattta aaagtcattc      900
cagtgagtag tgatcacaga gaaagttcag ggcaggacgt tacagaacaa agttagtttg      960
aaataggaga aattagtttt aaataaacia ttattagtct g                               1001

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<210> 391

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-906-451 : polymorphic base A or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-906-451.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-906-451.mis2, potential complement

<220>

<221> primer_bind

<222> 52..71

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 508..528

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-906-451 potential probe

<220>

<221> misc_feature

<222> 449,552..553,559,641,644

<223> n=a, g, c or t

<400> 391

339

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aataccaaaag ctgacttctc gggcctcatg atgacatttc cctcacacac tgatctgcac      60
tagcttttgta gttactaagc atgaaattga aatgacaata taagcacaga agttaaaaaat    120
taatatttta agtgtaaata aagttcattg gttgggtgcc agcttcacat ttattgaaga      180
tatcaaaaag aaatgcaatg ttgcaatgta tcagggaaaaa tttgttccaa ccttctagag      240
cttagaaaata aaacacataa agatactttt attatctgga ttgatgataa agaaattttt      300
taaaattctt tagatttaat aattcatgtg cagaaacata tgcacacaac cacatttaca      360
ttcattccac actaaatcca aggtgtcaga tgggttagaa gaactcatgt ttcacatcct      420
ttgctcaca ggacaataca aagaattanc tgggaataca cttggagact ttgggtaact      480
attttcatta attctatata mtaagtgcaa agtggtcagt atttcagagg agaaaaatgc      540
acaattgctt tnnaatatnc tgataattaa taaaagcttt agtaagacat ttgacttagg      600
aggtgagatg aaagcttcat taggatttat tgttgccaaa nggnaagcat ttcacaatca      660
atacaagcat gacgaaagta taggatattt aaaagtcatt ccagtgaagta gtgatcacag      720
agaaagtcca gggcaggacg ttacagaaca aagttagttt gaaataggag aaattagttt      780
taaataaaca attattagtc tgaatgataa tttataggta aataattact tactcaagtt      840
ttaaaggaca gtcacaagat cgagcttttc cttagcaaga aattcttgca tctcaacata      900
gagtgatatg taaagataag agtttagaaa cagggaaaat gataaaaatt gtatattagt      960
tactgagaca tgtcaacctt atggaataaa acataaattg t                                1001

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<210> 392

<211> 744

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 244

<223> 12-907-199 : polymorphic base G or T

<220>

<221> misc_binding

<222> 224..243

<223> 12-907-199.mis1, potential

<220>

<221> misc_binding

<222> 245..263

<223> 12-907-199.mis2, complement

<220>

<221> primer_bind

<222> 46..65

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 533..553

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 232..256

<223> 12-907-199 potential probe

<400> 392

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tgacttttagg aacatttaga aagtttaaag taaacaatgc tcaatgtaat tgagcatgag      60
gagtgggttga attatgatatt aaaaccagcc ttgtcttttt ttatagtgac ttgaagaggt    120
ttagtaattc cttcatgttt tggaccgaga ccgattccag gaacaaacgt catgtttttcc      180
attatatata gactgggaac actataagag ctatgtggaa tattaattgc agccccccat      240
tgtkccagct aatctctgcc tcaaagatta atggggattg gtgtgatata aggctgaatt      300
gtaccttttc accatcaggg ccagtgcaag gcaagataaa tgtgctctgg tgaacttcat      360
cagcttttcc aaccctact tatcccatgt tagtgggatg tttaagccag aaggaaggcc      420
atacattaga ggaaataata gaaacatcag cccagcatc cactatgccc tcaaaccttt      480
ttccttgaat gtgtatggtg caggtggggcc attgtttaga aattacttta atccaataag      540

```

340

cggtcttttc	actgttgag	cctatcccag	agccccctgt	cttatctcct	ttgtttaaaa	600
caatattagg	taataaaagt	aattgagcaa	ttgactcacc	aactggaatg	gaaacaggaa	660
ccttggcaga	caccataagt	ttaatctcat	cagaggaatc	agaattaatg	agaccagtag	720
gaactatgat	accttttagca	gagg				744

<210> 393

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-907-482 : polymorphic base A or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-907-482.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-907-482.mis2, potential complement

<220>

<221> primer_bind

<222> 20..39

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 507..527

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-907-482 potential probe

<400> 393

aaagtaaaca	atgctcaatg	taattgagca	tgaggagtgg	ttgaattatg	atttaaaacc	60
agccttgtct	ttttttatag	tgacttgaag	agggttagta	attccttcac	gttttgacc	120
gagaccgatt	ccaggaacaa	acgtcatggt	ttccattata	tatagactgg	gaacactata	180
agagctatgt	ggaatattaa	ttgcagcccc	ccattgttcc	agctaattct	tgccctcaaag	240
attaatgggg	attggtgtga	tataaggctg	aattgtacct	tttgaccatc	agggccagtg	300
caaggcaaga	taaatgtgct	ctggtgaact	tcattcagctt	ttccaacccc	tacttatccc	360
atgttagtgg	gatgtttaag	ccagaaggaa	ggccatacat	tagaggaaat	aatagaaaca	420
tcagccccag	catccactat	gccctcaaac	ctttttcctt	gaatgtgtat	ggtgcagggtg	480
ggccattggt	tagaaattac	wttaatccaa	taagcggctt	tttcactgtt	ggagcctatc	540
ccagagcccc	ctgtcttata	tcctttgttt	aaaacaatat	taggtaataa	aagtaattga	600
gcaattgact	caccaactgg	aatggaaaca	ggaaccttgg	cagacaccat	aagtttaatc	660
tcattcagagg	aatcagaatt	aatgagacca	gtaggaaacta	tgataccttt	agcagagggtg	720
gatgtcctac	ctaacaccag	gcccatggaa	ccttgaggta	aagggccagt	gacccctgtg	780
gggacaatta	aaagacaaga	attaggtagt	aaatttagag	gaatgggtact	atggagatca	840
accaccctgc	cccctactgt	ggaggtagac	aagcagtgtg	ctgtgacaga	agaagaggct	900
gggacccatc	tgggtttgct	gtaggtaaat	ttgtttgtac	tgggggctgc	gttaggaccg	960
cttcaattgg	aaatgcaaca	ttggtctgag	tctgagggtgt	g		1001

<210> 394

<211> 1001

<212> DNA

<213> Homo Sapiens

341

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<220>
<221> allele
<222> 53
<223> 12-909-36 : polymorphic base A or G

<220>
<221> misc_binding
<222> 33..52
<223> 12-909-36.mis1, potential

<220>
<221> misc_binding
<222> 54..73
<223> 12-909-36.mis2, potential complement

<220>
<221> primer_bind
<222> 18..38
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 505..525
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 41..65
<223> 12-909-36 potential probe

<220>
<221> misc_feature
<222> 480,526,538..539,545,554..556,573
<223> n=a, g, c or t

<400> 394
taacttgtgt tttgactcca ggaaaagtaa aatgttagtt tgagctcgag aargaatctg      60
gatactggta actttaccca gaccttgga atcttcccc tcagtacatt taattaatga      120
agtgttacia tgaattctca aaagatctaa gagatttgtt ttcacttcat tcgctgtgat      180
catgggccta atcagagtca ctgcactggc aaccactgct ggagtggcat tataccaatc      240
tattcaaaca gctcatTTTg tcaatgatta gcaagtcaat tccacccaaa tgtggaattc      300
tcaacaagac attgatcaaa aattagctaa tcaaattaat gatttaagac agtctgttat      360
ttggcttgga aatcagctga tgagtctcga acatcacatg caaatgcagt gtgatttgaa      420
tacttctgat ttctgtatca caccatattc ctacaatgag actgatcatt catggaaaan      480
tgggtcaaagg acaccttctg ggtagggaag ataatttatt cttggnacat aactaaannt      540
taaangaaac aaannntttc tgaagcctct cangctcatt taccatttgt gtctggagct      600
gaggcgtag atcagggtggc agaaagtatt tctggactaa accccacgac ttggattaag      660
tctactgggg gctccatggt agtaaatttt ggaataatat ttctctgttt aatcgacttg      720
tttttagtgt gctggaccag tcaaagattc ccgtgtcaaa acctagagaa caaacaagac      780
tttgcaccat ggcacattta tataaaaaga aagggaggga tgttgtggga agtcaggggac      840
cctgaatgga gggactggct ggagctgtgg cagaggaaca taaattgtga agatttcatt      900
ttaatatgga cctttgtcag ttcccaaata atacttttct aatttcttat gcctgtctta      960
ctttaatctc ttaatcctgt tatcttcata acctgaggat g                                1001

<210> 395
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 193

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342

<223> 12-909-176 : polymorphic base C or T

<220>

<221> misc_binding

<222> 173..192

<223> 12-909-176.mis1, potential

<220>

<221> misc_binding

<222> 194..213

<223> 12-909-176.mis2, potential complement

<220>

<221> primer_bind

<222> 18..38

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 505..525

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 181..205

<223> 12-909-176 potential probe

<220>

<221> misc_feature

<222> 480,526,538..539,545,554..556,573

<223> n=a, g, c or t

<400> 395

taacttgtgt	tttgactcca	ggaaaagtaa	aatgttagtt	tgagctcgag	aaggaatctg	60
gatactggta	actttaccga	gaccttgga	atcttcccc	tcagtacatt	taattaatga	120
agtgttacaa	tgaattctca	aaagatctaa	gagatttgtt	ttcacttcat	tcgctgtgat	180
catgggccta	atyagagtca	ctgcactggc	aaccactgct	ggagtggcat	tataccaatc	240
tattcaaaca	gctcattttg	tcaatgatta	gcaagtcaat	tccacccaaa	tgtggaattc	300
tcaacaagac	attgatcaaa	aattagctaa	tcaaattaat	gatttaagac	agtctgttat	360
ttggcttga	aatcagctga	tgagtctcga	acatcacatg	caaatgcagt	gtgatttgaa	420
tacttctgat	ttctgtatca	caccatattc	ctacaatgag	actgatcatt	catggaaaan	480
tggtcaaagg	acaccttctg	ggtagggaag	ataatttatt	cttggnacat	aactaaannt	540
taaaangaaac	aaannntttc	tgaagcctct	cangctcatt	taccatttgt	gtctggagct	600
gaggcgtag	atcaggtggc	agaaaagtatt	tctggactaa	acccacacgac	ttggattaag	660
tctactgggg	gctccatggg	agtaaatttt	ggaataatat	ttctctgttt	aatcgacttg	720
tttttagtgt	gctggaccag	tcaaagattc	ccgtgtcaaa	acctagagaa	caaacaagac	780
tttgcaccat	ggcacattta	tataaaaaga	aaggaggagg	tggtgtggga	agtcagggac	840
cctgaatgga	gggactggct	ggagctgtgg	cagaggaaca	taaattgtga	agatttcatt	900
ttaatatgga	cctttgtcag	ttcccaaata	atacttttct	aatttcttat	gcctgtctta	960
ctttaatctc	ttaatcctgt	tatcttcata	acctgaggat	g		1001

<210> 396

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-909-484 : polymorphic base G or T

<220>

<221> misc_binding

343

<222> 481..500

<223> 12-909-484.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-909-484.mis2, potential complement

<220>

<221> primer_bind

<222> 18..38

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 505..525

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-909-484 potential probe

<220>

<221> misc_feature

<222> 480,526,538..539,545,554..556,573

<223> n=a, g, c or t

<400> 396

taacttggtgt	tttgactcca	ggaaaagtaa	aatgttagtt	tgagctcgag	aaggaatctg	60
gatactggta	actttaccca	gaccttggga	atcttccccc	tcagtacatt	taattaatga	120
agtggttacia	tgaattctca	aaagatctaa	gagatttggt	ttcacttcat	tcgctgtgat	180
catgggccta	atcagagtca	ctgcactggc	aacctctgct	ggagtggcat	tataccaatc	240
tattcaaaca	gctcattttg	tcaatgatta	gcaagtcaat	cccacccaaa	tgtggaattc	300
tcaacaagac	attgatcaaa	aattagctaa	tcaaattaat	gatttaagac	agtctgttat	360
ttggcttgga	aatcagctga	tgagtctcga	acatcacatg	caaatgcagt	gtgatttgaa	420
tactttctgat	ttctgtatca	caccatattc	ctacaatgag	actgatcatt	catggaaaaa	480
tggtcaaaag	acaccttctg	kgtaggggaag	ataatttatt	cttggnacat	aactaaannt	540
taaangaaac	aaannnttct	tgaagcctct	cangctcatt	taccttattg	gtctggagct	600
gaggcgtag	atcaggtggc	agaaagtatt	tctggactaa	acccacagac	ttggattaag	660
tctactgggg	gctccatggt	agtaaatttt	ggaataatat	ttctctgttt	aatcgacttg	720
tttttagtgt	gctggaccag	tcaaagattc	ccgtgtcaaa	acctagagaa	caaacaagac	780
tttgcacat	ggcacattta	tataaaaaga	aaggaggagg	tggtgtggga	agtcaggggac	840
cctgaatgga	gggactggct	ggagctgtgg	cagagggaaca	taaattgtga	agatttcatt	900
ttaatatgga	cctttgtcag	ttcccaaata	atacttttct	aatttcttat	gcctgtctta	960
ctttaatctc	ttaatcctgt	tatcttcata	acctgaggat	g		1001

<210> 397

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 347

<223> 12-910-76 : polymorphic base A or G

<220>

<221> misc_binding

<222> 327..346

<223> 12-910-76.mis1, potential

<220>

344

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<221> misc_binding
<222> 348..366
<223> 12-910-76.mis2, complement

<220>
<221> primer_bind
<222> 272..292
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 704..724
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 335..359
<223> 12-910-76 potential probe

<220>
<221> misc_feature
<222> 17,38,54,57,59,62,69,76,87,95,106,109,115,118,122,128,857,876,888
<223> n=a, g, c or t

<400> 397
aataattata cagaacnttt aagtgagaaa tgtccagntt gtttaatat tggagnent 60
cnaattctna aaacanaatg gtttgcnac tcatnaaact atttcnacna tatcnagngt 120
cnatttgntg acattttgtg atgtcaacaa aatgataaaa ttttagaaac ccaacatcaa 180
ttccctcaca aaagtacaac cagtagctat ccaaatacaa aaatgccact ctgaattcac 240
cagatctcaa ggcagaagga gaaaacccga agactcacag acatgagaaa acttatgatt 300
ggtaagatga ttaatttttt tggactgtac cccccgctt ccacaarcca aaatgacacc 360
actgtgaggg aacttccttt cacctgcagt tattgaaatg ggaggaggga atttcaagtg 420
gacattttaat ttcttcattg atctgtaaat ttgaggggaa agcccacatt tgtcccaccc 480
cacagacggt attaagagt ttcagagggc tgaaccacct ggggtaaatt ggggacagga 540
gatggagtag taatcacagt gatcaccaca cagatcttgg catctgcttt gtgttcctag 600
atacggggat gccacacaga ggagtctcac cagaaccata gcaactgcagg gggcaaaatc 660
ttaaggaagg cctgaatctt tgacaaaatt ttacaattcc caggtagtca tgtggagatt 720
ttccatgact gggaaacaag tataagactt gaaattaagt tccaaggctt gtttaaagt 780
ctcccagatc tagaaatcac tgcaagtctg ggtttaagta ccagtgcagc atttaagttc 840
agatgctcac aataagntct cccaagactg gaaaanaca attaaagnaa atactgagtt 900
ttggtgcagt attaaattct ggtggcaaat attcagtcct tgcctaaaca aaaagcaact 960
ggtggcaagg aattagattc caatattaag tagtaaaggt t 1001

<210> 398
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-910-295 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 12-910-295.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-910-295.mis2, potential complement

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345

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<220>
<221> primer_bind
<222> 209..229
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 641..661
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-910-295 potential probe

<220>
<221> misc_feature
<222> 6,13,24,32,43,46,52,55,59,65,794,813,825
<223> n=a, g, c or t

<400> 398
attctnaaaaa canaatgggtt tgcnaactca tnaaactatt tcnacnatat cnagngtcna      60
tttgntgaca ttttgtgatg tcaacaaaat gataaaatth tagaaaccca acatcaattc      120
cctcacaaaa gtacaaccag tagctatcca aatacaaaaa tgccactctg aattcaccag      180
atctcaaggc agaaggagaa aaccggaaga ctcacagaca tgagaaaact tatgattggt      240
aagatgatta attttttttg actgtaccac cccgcttcca caagccaaaa tgacaccact      300
gtgaggggaa ttccctttcac ctgcagttat tgaaatggga ggaggggaatt tcaagtggac      360
atttaatttc ttcattggatc tgtaaatttg aggggaaagc ccacatttgt cccacccac      420
agacggtatt aagagtgttc agagggtga accacctggg gttaaattggg gacaggagat      480
ggagtagtaa tcacagtgat caycacacag atcttggcat ctgctttgtg ttcctagata      540
cggggatgcc acacagagga gtctcaccag aaccatagca ctgcaggggg caaaatctta      600
aggaaggcct gaatctttga caaaatttta caattcccag gtagtcatgt ggagattttc      660
catgactggg aaacaagtat aagacttgaa attaagttcc aaggcttggt taaatgtctc      720
ccagatctag aaatcactgc aagtctgggt ttaagtacca gtgcagcatt taagttcaga      780
tgctcacaat aagntctccc aagactggaa aancaacatt aaagnaaata ctgagttttg      840
gtgcagtatt aaattctggt ggcaaatatt cagtccttgc ctaaacaaaa agcaactggt      900
ggcaaggaaat tagattccaa tattaagtag taaaggttga acaacacaag aatacaccta      960
taaaagttag aacatgtgga tatctcttta agtatggaaa c                                1001

<210> 399
<211> 740
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 240
<223> 12-911-22 : polymorphic base G or C

<220>
<221> misc_binding
<222> 221..239
<223> 12-911-22.mis1

<220>
<221> misc_binding
<222> 241..260
<223> 12-911-22.mis2, potential complement

<220>
<221> primer_bind
<222> 219..237
<223> upstream amplification primer

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<220>
<221> primer_bind
<222> 653..673
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 228..252
<223> 12-911-22 potential probe

<220>
<221> misc_feature
<222> 354,703,732,739
<223> n=a, g, c or t

<400> 399
atattttcca ctgtaatatt ttatcttagc tatatagcct aaaattttaa caattaatct      60
cggggggggag tgtcgcattc ttttgttgta ttttcctagg cgatttgatc cttttctaata      120
acattgctga cacaagatca ctaacaattc taaaatgtcc tattcatgat atcactatctt      180
ttatgatgtc acatttttta aaccttagtt gatatgttta ttcacaatat gctgggccts      240
tgtagtgcat aaatatgaac tgacatcaat agatgtaaaag aagtcaaaag cataaaaattc      300
acaggaggca atagactata caagtcattg aagtggttcta tgatattagt ttgntattaa      360
aaacataaca atgttcacct tttgataaaa ataagccatt ttacatagcc aacagtactg      420
ggcttagacc atgaattggt aatgataata atgatagtgc attactctgg aaaagggttta      480
gtatatttct ctagaactca tctagatatt atggcctaca tttctgcctt tagtccaata      540
ttttttgtgt cctcaatgag aaagagatag ttatcatcaa tgtgttcaaa caaaagggtta      600
agtgatcctt tcttagggag agaatatgtc aacaagggtga tcaagttgaa cagattattt      660
taggagaggt aacgacagga aacattttat taaaaatact aantttttaa aaactttgat      720
cgtttacttg ancaaagant                                     740

<210> 400
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-912-65 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-912-65.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-912-65.mis2, potential complement

<220>
<221> primer_bind
<222> 437..457
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 908..928
<223> downstream amplification primer, complement

<220>
<221> misc_binding

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347

<222> 489..513
 <223> 12-912-65 potential probe

<220>
 <221> misc_feature
 <222> 24,47,131,137,440
 <223> n=a, g, c or t

<400> 400
 acaacaggaa gctgcaccct tctnctgcat tcagacagaa gtgaganctg ctgggccgga 60
 agctctagca aggatgatag caatacaagt tgattccttaa ttaattaaag cacattgaga 120
 agctgatcca naaaagncaa acactattaa atctctcaga ctttaaaaat acagtcatat 180
 tccaggagtt aaggggtcca gtcaccaac atggcacatg tatacatacg taacaaacct 240
 gtacgttggtg cacatgtacc ctagaactta aagtataata aaaaatatat atatacatag 300
 tcatattcat ttttcacaac atagcatatt gtgacaggtc tttcttgatt tactaagttt 360
 acttattatc ctgtgaagta tattttcata cctgaatttt acctagcttc agccttccat 420
 taacgttgca ttcattcttn aacatttgta aaccaccata ttttctagaa attggtgact 480
 atattctaaa atcattgtag ycacgaaatc atatgaatac ctgcttgcc tctccggata 540
 ggggtcaagtt tctcacataa gcaaaattta cttatttggc atatacaatg tgaacataat 600
 cttaaaacct gactttggct tttggtgta ttaataaggt tcttaatcca atttttgttt 660
 tttttttaca gaagtgtac agctatactg taatcctagc attcctgagt tttgtatata 720
 gcttggaat aatattttatt gtcaaattt tttaaatct tcaacttctt ctaatatatt 780
 tattaacctt agcatctttt tttgcatttt ttccctgtga agtgtcattc actctatcaa 840
 ttactatcag aaaaatctgt tatcatcttg cctatttatg caaagcaaat gattctccaa 900
 ctgttgactc taatccttcc tctcaaatag gttctgctaa ataaatgacc ctgagtctct 960
 gagacatttg ttgtatcaaa gcacaacaac attaacagta a 1001

<210> 401
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 384
 <223> 12-914-106 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 365..383
 <223> 12-914-106.mis1

<220>
 <221> misc_binding
 <222> 385..404
 <223> 12-914-106.mis2, potential complement

<220>
 <221> primer_bind
 <222> 279..298
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 773..793
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 372..396
 <223> 12-914-106 potential probe

<220>

348

<221> misc_feature
 <222> 536,990
 <223> n=a, g, c or t

<400> 401
 aactcctatt atattggaggt agttttctta ataatgtttg atactttcca tatgcctact 60
 tcactaatTT taattatttc tctttttttg ctcttctgat tgggtaatta catatgtttt 120
 atcttttagga ttgctgattc cttactctgt ttgaccaagt ctgctgttga agttttctac 180
 tgagtttttc aattcacttc acataattttt tattaattgg atttcttttt atttttaaaa 240
 cattttccact tctttgcaaa atttatcatc attttcctgg attattctct aaagtgtggt 300
 ttttttcaac tctctattca tatgtgctgt gattttctgaa ctttttaaaat aggtgtgcac 360
 tgaatttctt gtcaaaaatt ttayggagca tctgaacctt aattctgcac tgtaacttaa 420
 aactagactt gcagtgattt ctaggctctgt gagatactta agcaataact ggagcttaat 480
 ctcaaagtgt atacttggtt gcaggtcata gaaaagctcc gtatgagtaa ctgggnatta 540
 taaaaatacc tgccaaagat tcaggccttc ctttggattt tggccctgc agtggtatgg 600
 aactggtcag actcctcagc gtggcattcc tgctaatagg aacaccaagc agttgctgag 660
 atgtgtgtgc ctgtcactgt gatttagtact tccactcttg tttccaattc accccaggtc 720
 attcaactct atagccactc ctaatgcctc tcctgaggta ggacaaaagt gggcttccca 780
 aacaaaaaag attcacagat ccatgaagaa actgaacatt cacttcaaat ttcctcctct 840
 gatcttgcca actgcaggta aaataaaagt ctgtcacagt ggtgtcttct tgggtgtgtg 900
 aaggggtgcc ataatccaaa aaattattca ttttacagat catgagtttt cccatgtcta 960
 tgagtcttgg gattttcttc ttctcttttn agctctggtg a 1001

<210> 402
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 12-914-252 : polymorphic base A or T

<220>
 <221> misc_binding
 <222> 483..502
 <223> 12-914-252.mis1, potential

<220>
 <221> misc_binding
 <222> 504..523
 <223> 12-914-252.mis2, potential complement

<220>
 <221> primer_bind
 <222> 252..271
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 746..766
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 491..515
 <223> 12-914-252 potential probe

<220>
 <221> misc_feature
 <222> 509,963
 <223> n=a, g, c or t

349

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<400> 402
ttaataatgt ttgatacttt ccatatgcct acttcactaa ttttaattat ttctcttttt 60
ttgctcttct gattgggtaa ttacatatgt tttatcttta ggattgctga ttccttactc 120
tgtttgacca agtctgctgt tgaagttttc tactgagttt ttcaattcac ttcacatatt 180
ttttattaat tggatttctt tttattttta aaacatttcc acttctttgc aaaatttatc 240
atcattttcc tggattatc tctaaagtgt gtttttttcc aactctctat tcatatgtgc 300
tgtgatttct gaacttttaa aataggtgtg cactgaattt cttgtcaaaa attttatgga 360
gcactctgaac cttaattctg cactgtaact taaaactaga cttgcagtga tttctaggtc 420
tgtgagatac ttaagcaata actggagctt aatctcaaat gttatacttg tttgcaggtc 480
atagaaaagc tccgtatgag tawctgggna ttataaaaat acctgccaaa gattcaggcc 540
ttccttttga ttttggtccc tgcagtgtta tggaactggt cagactcctc agcgtggcat 600
tcttgcta at aggaacacca agcagtgtgt gagatgtgtg tgcctgtcac tgtgattagt 660
acttccactc ttgtttccaa ttcaccccag gtcattcaac tctatagcca ctcctaatagc 720
ctctcctgag gtaggacaaa agtgggcttc ccaaaccaaa aagattcaca gatccatgaa 780
gaaactgaac attcacttca aatttcctcc tctgatcttg gcaactgcag gtaaaaataaa 840
gttctgtcac agtgggtgtc tcttggtgtg tggaaggggt gccataatcc aaaaaattat 900
tcattttaca gatcatgagt tttcccatgt ctatgagtct tgggattttc ttcttctctt 960
ttnagctctg gtgaattcag tgtggctttt tgtatttaca t 1001

<210> 403
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-448-266 : polymorphic base A or C

<220>
<221> misc_binding
<222> 483..502
<223> 10-448-266.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-448-266.mis2, potential complement

<220>
<221> primer_bind
<222> 238..257
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 660..679
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-448-266 potential probe

<220>
<221> misc_feature
<222> 772,907,915
<223> n=a, g, c or t

<400> 403
gaattatcac attgcacaag gatggctctg aaatggacta cagttctgct gatacaactc 60
agtttttact ttagctctgg gagttgtgga aagggtgctgg tatgggccgc agaatacagc 120
ctttggatga atatgaagac aatcctgaaa gaacttggtc agagagggtca tgagggtgact 180

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350

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gtactggcat cttcagcttc cattcttttt gatcccaacg actcatccac tcttaaactt 240
gaagtttatc ctacatcttt aactaaaact gaatttgaga atatcatcat gcaattgggt 300
aagagattgt cagaaattca aaaagataca ttttggttac ctttttcaca agaacaagaa 360
atcctgtggg caattaatga cataattaga aacttctgta aagatgtagt ttcaaataag 420
aaacttatga aaaaactaca agagtcaaga ttgacatcg tttttgcaga tgcttattta 480
ccctgtgggt agctgctggc tgmgtatatt aacataccct ttgtgtacag tcacagcttc 540
agtcttggt actcatttga aaggcacagt ggaggattta tttccctcc ttcctacgta 600
cctgttggt tgtcaaaatt aagtgatcaa atgactttca tggagagggg aaaaaatatg 660
ctctatgtgc tttattttga cttttggttc caaatattta atatgaagaa gtgggatcag 720
ttttacagtg aagttttagg taagattttt ttcagttagt aacatgaagc tnctaactta 780
tttgtgtctt tgaagcacia cttgcataaa gccataaagt cagggagtg gagtttttga 840
taaataaatt tatgaaatga aaatacaaga tgatctacca atctcaciaa tattatagaa 900
aagcttnaaa ttatnggggt cagtgaatac gctgtgacca tcaactcaca agaacacccc 960
aggaaatcat aaacctatat attagtagac ctaagacttt a 1001

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<210> 404

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-453-330 : polymorphic base C or T

<220>

<221> misc_binding

<222> 483..502

<223> 10-453-330.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 10-453-330.mis2, potential complement

<220>

<221> primer_bind

<222> 172..189

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 578..597

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 10-453-330 potential probe

<220>

<221> misc_feature

<222> 19,31,101,212,337,520,661

<223> n=a, g, c or t

<400> 404

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cattagtcca actggaaant cttgtattaa ngttttgcag tctgaagtca caccaccata 60
tagccttcag ttacatctcc aacacaagta cctgtttttt ncctctgaaa tctgaaaagt 120
aatagcaaat tagttcagtg tgttatctag aaaacactgt cactttcaga gcctttcatt 180
gtgcattctca ttttattcct atgaataatt tntgctaaaa ttcattccaat cctaggteat 240
ccaaaaacca gagctttttat aactcatggt ggagccaatg gcatctatga ggcaatctac 300
catgggatcc ctatgggtggg cattccattg ttttttngat caacctgata atattgctca 360
catgaaggcc aaggagagcag ctggttagagt ggacttcaac acaatgtcga gtacagacct 420

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351

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gctgaatgca ctgaagacag taattaatga tccttcgtga gtagaacaat atttttcact 480
agatgggtatt aatagatagc ttytcttgtc agtagtgagn catgagtttc atccttttta 540
taagagagtg attttgaaag aatttaaagtg atttaaccaa tccgaaatct gcttttactt 600
tttatctggt atttaaaaaat tgtatttgaa ccccatatct ctaatgagta accagttagt 660
ngaaacagtt ttctaaataa aaataatttt aaaatgatat agataatata aaaaaatata 720
tttcttaaaa atttgacata atgaatccat agtagaaagg aagaataatc ttgaaataat 780
ataataaaat gttttaatta aatatctaaa atgtctcaga atataactat tttcttgcag 840
aaaaattaat ttttattatt atctttattg taacagactt gaaaatgaga ttttaattttg 900
atagcataaa acccacctat ttatggcaaa aattccaaat atttttacta tgtttacaga 960
gtcatgaagt catcaccagt gtataagttt ggaacatttt t 1001

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<210> 405

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-455-367 : polymorphic base C or T

<220>

<221> misc_binding

<222> 483..502

<223> 10-455-367.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 10-455-367.mis2, potential complement

<220>

<221> primer_bind

<222> 135..152

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 545..564

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 10-455-367 potential probe

<220>

<221> misc_feature

<222> 161,248

<223> n=a, g, c or t

<400> 405

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tttaaaagcc aaactttgta tgatgactca aattaaaata cataaattct atatcaattc 60
tttgacattt actttgaatt atttgacact tttaaagcct ttcatagact tgatatctac 120
aggcaaatta acttactttc agtggtcgga tctttatttt ntatccttca gatataaaga 180
gaatattatg aaattatcaa gaattcaaca tgatcaacca gtgaagcccc tggatcgagc 240
agtcttctntg gattgaattt gtcatgcgcc acaaaggagc caaacatctt cgagttgcag 300
cccacaacct cacctgggtc cagtaccact ctttggatgt gattgggttc ctgctggctt 360
gtgtggcaac cgtgctatth atcatcacia agtggtgtct gttttgtttc tggaaagttt 420
ctagaaaagg aaagaaggga aaaagggatt agttatatct gagatttgaa gctggaaaac 480
ctgatagata ggaatacttc agytgattcc agcaataaat attgtgatgc aagatttctt 540
tcttcctgtg acaaaaaaaa atccttttca agtctacctt gtcaagtaaa aatttgtttt 600
tcagagattt accacccagt taatgggttag aaatattctg tggcaatgaa gaaaacacta 660

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352

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ggggaaataa aaaataatat aaagccatat gagcttgtat tgaaatttgt tgcacttata 720
ttgaaatgtg atcatggctc acttcagcct caacttacta agctcaagag gttctctcac 780
ctcagccccc caagtagctg ggaccatagg tgcattgtcac catgtccaac taatttttta 840
ttttttgtag tgatgagatc tcatttgtgt ctccatgctg atttcaaact cctgggctca 900
aacaatcctc ccatttttag atcccaaagg gatgagatta caggtatgta ccaccataac 960
tttacaaaat gagattttta tataagaatg attcaaattg t 1001

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<210> 406

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 12-5-158 : polymorphic base C or T

<220>

<221> misc_binding

<222> 484..502

<223> 12-5-158.mis1

<220>

<221> misc_binding

<222> 504..523

<223> 12-5-158.mis2, potential complement

<220>

<221> primer_bind

<222> 346..366

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 801..821

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 12-5-158 potential probe

<220>

<221> misc_feature

<222> 314,336,793

<223> n=a, g, c or t

<400> 406

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caaaggatga aggtcctctg gaccagaagc acccaaccag attattcagc aacaggactg 60
aggggtgcctg gggcaagtgc cagctcatgc catcacctc acagagcccc gggtaagttt 120
aaccattgag ggccaggaag tggacttcc cctgggcact ggcgcgccct tctcaatttt 180
aatccctga cccagatgac tgttctcaaa gtccgttact atctgaggaa tcttaggaca 240
gctgttaacc aggtatttct ctgcctcct cagctgcaat tgagagactt tgctctttca 300
catgcctttt ctgnntatgt ctgaaagtcc cacacnctt attagggaga gacatatttg 360
ccaaagctgg ggccattatc tacatgaata tggggaacaa gtgaccatt tgttgtcccc 420
tacttgaaga agaaatcaac tttgagctct gggccttaga aggacaattt ggaagggcaa 480
agaatatcca tccagtccac atyaagctaa aagacaccac cacttttct tatcaaagga 540
aatatcactt aaggcctgaa gttctcaaag gattacagga tattgttaga aattttaaag 600
ctcaaggttt agtaaaaaaa tgtagcagtc tttgaaacac cccaatccta ggaatacaaa 660
aaccaaatag tggagactag ggcaagacct caggtttcac ctatctacct tcaggaaatt 720
tttttcatct gtgataacac agcctatcga tgccaaaaatg gactccaaa agaactatgc 780
tatgtctcat ttntagcac ctcccatgtc catatatact gaacaagagt tacaagtct 840
ccttataccc caatctcgcc acaccgcagc ccttattgtc ccttttacag taggagcagg 900

```

353

aatactaggc aggcttggga ctggaattgg aggcataacc tcctccaccc aattctatta 960
 taaattatca tgagaattaa atgatgacat ggaatgagtt g 1001

<210> 407

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-9-367 : polymorphic base G or A

<220>

<221> misc_binding

<222> 500..518

<223> 12-9-367.mis1, complement

<220>

<221> misc_binding

<222> 479..498

<223> 12-9-367.mis2, potential

<220>

<221> primer_bind

<222> 847..865

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 386..406

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-9-367 potential probe

<220>

<221> misc_feature

<222> 231,891

<223> n=a, g, c or t

<400> 407

gggagcaaca agcagctagg ggaacccac cctcccaggg aagcattgag taattgtgca 60
 accacaggaa accatacttc tcccaagaat ctttgcaacc ctcaagtcaa gaagtctacc 120
 tgtgaactca catcaacagg gccttcattc tgacagccag aaaaagggtg agtctcagca 180
 gagcatctac tcaggcatgc gaggtgacct tggaacctta gctatgtggg nctttctggc 240
 aaaagtaact gcagctttgg caaattagga gattagaacc acatacatat ccctaggaaa 300
 aaggctgaat ccaagggact gagaagatac agcctgcagg cccactttc acagcacctc 360
 acaggtgagc acccactggc ttaaaattcc agcaagccac caatagcggc attgcacctc 420
 cataagaagg agctctcagt gggagtggca ggctgccacc tttgctggcc tttattctta 480
 gtttttctct cccatcacrg aaattccatc ctatgagtgg actggggcaa tggctatttg 540
 gtactcagta ttctttgtgc cgttcttgag ttgaatctct gagttatgac tgtggctgaa 600
 tgaaagatgt gagacccttc ttagccacac ttgcctagaa ttaagcttct ggagcatatg 660
 cctgagtcata tatatataaa aaaatcagag agacaccttt tctcaactgc ataccctgac 720
 actcaactgg gagctttgaa gagtgagagc cctgtggtag catcagcacc tccctggaag 780
 agagggagtt tctgtcactg aactaggagg gggggcaaat gagcatgttg tggcttaaat 840
 gccaaagaca cttgtgtgtt tcaactacaa ttactggatt ttcttcagt naatgttact 900
 ttatttatatg cctttaggat tattgccagg gacaccaaatt gggtgtttta aaaaacaatt 960
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<210> 408

354

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<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-10-303 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-10-303.mis1, potential complement

<220>
<221> misc_binding
<222> 482..500
<223> 12-10-303.mis2

<220>
<221> primer_bind
<222> 787..807
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 335..355
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-10-303 potential probe

<220>
<221> misc_feature
<222> 67,85,89,608,657,722..723,752,854,885
<223> n=a, g, c or t

<400> 408
agttgcccca ccttttcaga ccaaaccat gtatcattta catgtattga ttgatgtgga      60
acatctnctc taaattgtat aaanccang gttgtagcct gaggacattg ggcacatggt      120
ctaaacagct gaaggctgtg ttatgggcca ttagtcactc atatttggtc cagaataaat      180
ctctttgaat attttacaga gtttgactca ttccctcaca ataatttgac acttgaacat      240
gtgggaactc ccagaaaacc caggaccccc aaaatgtttc ctgaacttga aactaaagta      300
ccagaagggg ccatttgaag gcctttcaaa ctttaagctc ctctgatgga actggtcagt      360
cctcttgagc cctggatctc cctttgggtg acagacatca atttttcctg aacttatttt      420
tttcctagga agttgttgtt taggattcta attctagttc tgggggtgcat tctgaagagt      480
cttctccatt gccttttata yaaaagataa actcaattgg cttgtctgca catttgcattg      540
aagatagaac tgtcatttta tagataaatg agggactgag ctccctcagc ttgaagagaa      600
agaacatntt tgctcctccc agaaaatgag ccctggatga ccagaggcta agtgggnaac      660
atctagatgt ttgactccca ttcccgttat gtgcagtgcc cctacagaag atgccccaac      720
anntaattag ttcttctgtg gtttaaatgt tntttaactg ctgagatatt taaaagcttg      780
tagaatcaat ctctaagaag cagacacatc atattattgc aatttttgta gttcaattta      840
ctatggaatt ttnatgact ctccatcaag tataccttca tgttncatat attttcctaa      900
gtatatatgt acatatcact ttatgtagaa agtcttcctc aaattaaact agtgaaaata      960
ttacttggtc actcatggat agacatagat ttatgtatct g                                1001

<210> 409
<211> 1001
<212> DNA
<213> Homo Sapiens

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355

<220>
 <221> allele
 <222> 501
 <223> 12-14-264 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 482..500
 <223> 12-14-264.mis1

<220>
 <221> misc_binding
 <222> 502..521
 <223> 12-14-264.mis2, potential complement

<220>
 <221> primer_bind
 <222> 237..257
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 680..700
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-14-264 potential probe

<220>
 <221> misc_feature
 <222> 307,577,897
 <223> n=a, g, c or t

<400> 409
 tgaaatgtta acttcataca atataagtaaa tgggtcacata tcaactgttcc tgttatcttt 60
 actgggggct ggaaaaaatg ggaagaactg ggccctccaga cttttcttgg atgcctcatt 120
 gtcaaagtgt aataaagagc acagtgggac tttgtgtttt ctatttttga tgggtgccc aa 180
 atggtctgtta ctttcagatg tattgcacat ttacattctc aataaagtat attaatgata 240
 aaagacttgt aacatggaga ataactcaag gagaaagtct tttattagtt ttctgttgct 300
 gcattancaa actacctcat ttcttaatat cttaaaaaaa aaactgttta actcatgggt 360
 tcatggttct tctcacaatt ttgatctagg ctagtatagc tgatctcagc aggtcctgcc 420
 cactttcagg tgcataatgaa actataggaa cctggctgat cctaaaagcc gttagtgtgca 480
 tgctttgcat ttgcctgagc ygtgtctttg taggtatatg tcatgtgggt gtctctcatc 540
 atcacaatgt gtaactgtag tacaagtgtc aataggnaaa gtctcataca cttaaagtaaa 600
 caacattaag catactatat ttatgtaata aatgtatgat tgtgcaccat atgtcctact 660
 ggaaacaatt tttaaaattc tcaaaactact gcctttcaat ttaagactct actggggtac 720
 ataattttaa gaaattttaga aattttctctc atgaaaaaat atacatttcg tgaaaaatat 780
 ccatacacgt taaataaata tgaagagtgt tttaataggc cccagatttt taggacagtc 840
 cagattacac cttttctgct tgagtcactt taatgatgcc tcaaaaattg gataatnttt 900
 aacattccac atgaaacttt gtaataaatt atatatatcg cacatatattt acatacatat 960
 aactttatat aaaaacttta aaaatagtaa atatacagat a 1001

<210> 410
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 499
 <223> 12-17-86 : polymorphic base T or A

<220>
 <221> misc_binding
 <222> 500..518
 <223> 12-17-86.mis1, complement

<220>
 <221> misc_binding
 <222> 479..498
 <223> 12-17-86.mis2, potential

<220>
 <221> primer_bind
 <222> 565..584
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 121..140
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 487..511
 <223> 12-17-86 potential probe

<220>
 <221> misc_feature
 <222> 44,197,388..389,398,407,627,852,856,941
 <223> n=a, g, c or t

<400> 410
 gaagttgagg tgtacaggtg aggcaacttg ccaaacccca catnaattct ctagagggtt 60
 tgcagggact tgaatccagg ctaactggat ccagagtgcg ggagctctta accaccatgc 120
 tacgctgact cccctttctg agttagtatt tttcaaaatg tcacatttgt agtttccatt 180
 ttcttgtctc tatattnaag tgtatattat tatgaatgta taattaaatt tttagaaata 240
 tccttgtagc tatttatcac ttcctaaca actaccctca atcatgggga ctttgaaaaa 300
 caattagcat tttattacaa tttccatagc atgagtgttg ggtagggttca gcaagatggt 360
 tcatacacag tattttctcag gtcattannc tttaatangg gtggctnggg gatgtaatca 420
 tctgaaggtc attcattcac gtacttgggt atggatgtca aaagactcaa attcctgtgg 480
 gactgaataa tcatgactwc ttagtctctt ctttgcata ttccccgagt tgtcatttat 540
 catcaggact ttgggtgtaa cactgggctc caaagtatat agaggggagaa aaagggaag 600
 agggaggaga gagagagaga gagaaangag gtataagtaa aagacataga cagacagaca 660
 aacggagaca gactgccttt tctaacacag tcttcaaac tatgctgtca cttccagtat 720
 actttctttg ctgagaaagc cagcagtcct gccaaaattc aaggggaggg accacggttt 780
 gataagaatg tcaaagtgtt tgcagtgatg tctcaaaatt ccacaaatat aacctattga 840
 gttagtcaac angaangcct ctaagcaact atgaaattca ttacatatgg acattaaaaa 900
 cacaataaaa tcctaaaaag tgtgaattta tattttttac naactactga aacattaagc 960
 attttaaaat atttactcat agatttttat atatgaaata g 1001

<210> 411
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-19-163 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 481..500

357

<223> 12-19-163.misl, potential

<220>

<221> misc_binding

<222> 502..520

<223> 12-19-163.mis2, complement

<220>

<221> primer_bind

<222> 339..357

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 781..801

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-19-163 potential probe

<220>

<221> misc_feature

<222> 612,814,950

<223> n=a, g, c or t

<400> 411

accttgaaaa	gaggttagat	gaatttctaa	ctagaataac	cagtgtttga	cttcttcctg	60
gtttaagctt	gggaaagtgt	acgtgtccag	gaatttatca	atttgttcta	aattttctag	120
tttatttgcg	tacaggtggt	tatagtattc	tctgatggca	gtttgtattt	ctgtgggatc	180
agtggtgata	tcccccatat	cattttttat	tgcgtctatt	tgattctgcc	aattcatagc	240
acatacagca	ttctggagaa	ctttggccca	gccatgaaaa	gtactgttac	ctagctgaca	300
ctgtaactat	aacttctaata	ggccatttca	ctatagtaca	aaggcagttg	cttcaggaga	360
atgaggaaca	tggtaaaacc	agtaaatttc	atgagcatga	gctcattggt	gcacttcttt	420
gtcagtaaag	ccagttcctt	agtcagaaac	aatactgtgt	ggaagaccat	gatagagaat	480
taggcatacca	gtaaatttat	rgatggtagt	tttgacagat	gtatatgttc	agagaagata	540
aatccatatt	caaaataagt	atgtattcca	gtaagaaaaa	aatgcagctc	cttctatgat	600
ggaggtgggc	tnaaggtaat	caatctgcca	ctgggaagct	ggttgattat	cttggagaat	660
gatgccatat	caggggctta	gcatggctct	ctgttcctgc	atattgggca	cacagtgggtg	720
gcttttagcca	ggttgaactt	agtgaagtga	agattatggt	gcttaaccca	tgcataaactt	780
ccatcaatgc	catcatagcc	actttgctca	tgangcccat	tgggtgataa	caggggtagc	840
tgaggaaaga	gtctgacccc	agatctacag	gaggggtcat	cccatccact	ttattattaa	900
aattttcttc	tagtgatgtc	attctttgaa	gaacattcac	atgactcacn	aaatgtcttc	960
atatattttg	ccccctcaaa	gaggtttatc	cagatagttt	t		1001

<210> 412

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-457-284 : polymorphic base G or T

<220>

<221> misc_binding

<222> 483..502

<223> 10-457-284.misl, potential

<220>

<221> misc_binding

358

<222> 504..523
 <223> 10-457-284.mis2, potential complement

<220>
 <221> primer_bind
 <222> 220..238
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 621..639
 <223> downstream amplification primer, complement

<220>
 <221> misc_binding
 <222> 491..515
 <223> 10-457-284 potential probe

<220>
 <221> misc_feature
 <222> 715
 <223> n=a, g, c or t

<400> 412
 gggtcataaaa attattgctt gactagagta attgtaaaca taaaagaaca ccaaacacac 60
 taaaataaat atgagggtcat caatcttttg ttggctctcct tggcatgcac ctattcagac 120
 tgttagtatt atgtatttac ttcaaatttt agcagttata ttttaacttg attgattttt 180
 cctcagatat aagtatgaga aatgacagaa agaaaacaaca actggaaaag aagcattgca 240
 taagaccagg atgtctctga aatggacgct agtctttctg ctgatacagc tcagttgtta 300
 ctttagctct ggaagctgtg gaaaggtgct agtgtggccc acagaatata gccattggat 360
 aaatatgaag acaatcctgg aagagcttgt tcagaggggt catgagggtga ctgtgttgac 420
 atcttcggct tctactcttg tcaatgccag taaatcatct gctattaaat tagaagttaa 480
 tcctacatct ttaactaaaa atkatttgga agattctctt ctgaaaattc tcgatagatg 540
 gatatatggt gtttcaaaaa atacattttg gtcataattt tcacaattac aagaattgtg 600
 ttgggaatat tatgactaca gtaacaagct ctgtaaagat gcagttttga ataagaaact 660
 tatgatgaaa ctacaagagt caaagtttga tgcattctg gcagatgccc ttaantccct 720
 gtggtgagct actggctgaa ctatttaaca taccctttct gtacagtctt cgattctctg 780
 ttggctacac atttgagaag aatgggtggag gatttctgtt ccctccttcc tatgtacctg 840
 ttgttatgtc agaattaagt gatcaaatga ttttcatgga gaggataaaa aatatgatac 900
 atatgcttta ttttgacttt tggtttcaaa tttatgatct gaagaagtgg gaccagtttt 960
 atagtgaagt tctaggtaag tcatgtgtct aactggtgct t 1001

<210> 413
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 10-460-221 : polymorphic base C or T

<220>
 <221> misc_binding
 <222> 483..502
 <223> 10-460-221.mis1, potential

<220>
 <221> misc_binding
 <222> 504..523
 <223> 10-460-221.mis2, potential complement

<220>

359

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<221> primer_bind
<222> 283..301
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 686..704
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-460-221 potential probe

<220>
<221> misc_feature
<222> 128,707,966
<223> n=a, g, c or t

<400> 413
atggggatta taattcaaga tgagaggaga tttgggtggg gacagtcaaa ccatattagt    60
gacttatttt aataattatt tatgattgtg aatatactga tgttacatta aagatgtgat    120
ttcttctnac agatctctga atacatttgc cttccttata tatacatatg agcaacatat    180
gcaataaaata aaatctaaat tatgactata tataaatgta tttatatata ttttatcaat    240
gcacagacat tttatatatg tttgggtatg ttattccaag tcctttcagg aaaataacctg    300
catattcaaa taacaattct cgtgttagct accttttgtt ttgttttgtt tttttccatc    360
aggaagaccc actacattat ttgagacaat ggggaaagct gaaatgtggc tcattcgaac    420
ctattgggat tttgaatttc ctgcccatt cttaccaaat gttgattttg ttggaggact    480
tcactgtaaa ccagccaaac ccytgccata ggtaaatgta ttcttgtttc atttgttgc    540
ttgacatttt cagaaggaat ggctggatat gtttctttca gagtgtttaa ctcagagtga    600
ggggaatatg ggaggtcaaa aacaaggact tgccattaga aaatcatata tttctgtagt    660
atcacaagta tgtgaatgtt attatcatta aagaccaaag aggtttnact agggagattt    720
tgaaaaacagg gttggttaaa gtaaggcctt cattgtgcca cccaaaagat agtatgattc    780
atttcttcaa aaaatatattg tagagtgatt aatacaaaacc acaggtaagt gctggatttt    840
cagagaataa aggtagcaca gtttctgctc cctcatgcct tacattgtac tttgaaagat    900
agaataaaaa caagtgaaaa agaaaagtct aaaaagtgtt ataaggaaag accacaatga    960
taaagnaaat atgcagaaga gatcccaaac tcattgacaa t                                1001

<210> 414
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-232 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-232.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-232.mis2, potential complement

<220>
<221> primer_bind
<222> 272..290
<223> upstream amplification primer

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360

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<220>
<221> primer_bind
<222> 675..693
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-460-232 potential probe

<220>
<221> misc_feature
<222> 117,696,955,992
<223> n=a, g, c or t

<400> 414
aattcaagat gagaggagat ttgggtgggg acagtcaaac catattagtg acttattttta      60
ataattatatt atgattgtga atatactgat gttacattaa agatgtgatt tcttctnaca      120
gatctcttgaa tacatttgcc ttccttatat atacatatga gcaacatatg caataaataa      180
aatctaaaatt atgacctatat ataaatgtat ttatatatat tttatcaatg cacagacatt      240
ttatatatgt ttgggtatgt tattccaagt cctttcagga aaatacctgc atattcaaat      300
aacaattctc gtgttagcta ccttttgttt tgttttgttt ttttccatca ggaagaccca      360
ctacattatt tgagacaatg gggaaagctg aaatgtggct cattcgaacc tattgggatt      420
ttgaatttcc tcgcccatte ttaccaaagtg ttgattttgt tggaggactt cactgtaaac      480
cagccaaacc cctgcctaag gtraatgtat tcttgtttca tttgtttgct tgacattttc      540
agaaggaaatg gctggatatg tttctttcag agtgtttaac tcagagttag gggaaatatgg      600
gagggtcaaaa acaaggactt gccattagaa aatcatatat ttctgtagta tcacaagtat      660
gtgaatgtta ttatcattaa agaccaaaga ggtttnacta gggagatttt gaaaacaggg      720
ttggttaaag taaggccttc attgtgccac caaaagata gtatgattca tttcttcaaa      780
aaatattttgt agagtgatta atacaacca caggtaagtg ctggattttc agagaataaa      840
ggtagcacag tttctgctcc ctcatgcctt acattgtact ttgaaagata gaataaaaac      900
aagtgaaaaa gaaaagtcta aaaagtgtta taaggaaaga ccacaatgat aaagnaaata      960
tgcagaagag atcccaaact cattgacaat tnaaagttag t                                1001

<210> 415
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-235 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-235.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-235.mis2, potential complement

<220>
<221> primer_bind
<222> 269..287
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 672..690
<223> downstream amplification primer, complement

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<220>
<221> misc_binding
<222> 491..515
<223> 10-460-235 potential probe

<220>
<221> misc_feature
<222> 114,693,952,989
<223> n=a, g, c or t

<400> 415
tcaagatgag aggagatttg ggtggggaca gtcaaaccat attagtgact tattttaata      60
attatttatg attgtgaata tactgatgtt acattaaaga tgtgatttct tctnacagat      120
ctctgaatac atttgccttc cttatatata catatgagca acatatgcaa taaataaaat      180
ctaaattatg actatatata aatgtattta tatatatatt atcaatgcac agacatttta      240
tatatgtttg ggtatgttat tccaagtcct ttcaggaaaa tacctgcata ttcaaataac      300
aattctcgtg ttagctacct tttgttttgt tttgtttttt tccatcagga agaccacta      360
cattatttga gacaatgggg aaagctgaaa tgtggctcat tcgaacctat tgggattttg      420
aatttcctcg cccattctta ccaaagtgtg attttggttg aggacttcac tgtaaaccag      480
ccaaacccct gcctaaggta aaygtattct tgtttcattt gtttgcttga cattttcaga      540
aggaatggct ggatatgttt ctttcagagt gtttaactca gagtgagggg aatatgggag      600
gtcaaaaaca aggacttgcc attagaaaat catatatatt tgtagtatca caagtatgtg      660
aatgttatta tcattaaaga ccaaagaggt ttnactaggg agattttgaa aacagggttg      720
gttaaagtaa ggccttcatt gtgccacca aaagatagta tgattcattt cttcaaaaaa      780
tatttgtaga gtgattaata caaaccacag gtaagtgtcg gattttcaga gaataaagg      840
agcacagttt ctgctccctc atgccttaca ttgtactttg aaagatagaa taaaaacaag      900
tgaaaaagaa aagtctaaaa agtggtataa ggaaagacca caatgataaa gnaaatatgc      960
agaagagatc ccaaactcat tgacaattna aagtgagtac t                          1001

<210> 416
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-236 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-236.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-236.mis2, potential complement

<220>
<221> primer_bind
<222> 268..286
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 671..689
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515

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<223> 10-460-236 potential probe

<220>

<221> misc_feature

<222> 113,692,951,988

<223> n=a, g, c or t

<400> 416

caagatgaga	ggagatttgg	gtggggacag	tcaaaccata	ttagtgactt	attttaataa	60
ttattttatga	ttgtgaatat	actgatgtta	cattaaagat	gtgatttctt	ctnacagatc	120
tctgaatata	tttgccctcc	ttatatatac	atatgagcaa	catatgcaat	aaataaaaatc	180
taaattatga	ctatatataa	atgtatttat	atatatttta	tcaatgcaca	gacattttat	240
atatgtttgg	gtatgttatt	ccaagtcctt	tcaggaaaat	acctgcatat	tcaaataaca	300
attctcgtgt	tagctacctt	ttgttttggt	ttgttttttt	ccatcaggaa	gacccactac	360
attatttgag	acaatgggga	aagctgaaat	gtggctcatt	cgaacctatt	gggattttga	420
atttcctcgc	ccattcttac	caaagtgtga	ttttgttgga	ggacttcact	gtaaaccagc	480
caaaccctcg	cctaaggtaa	atrattctt	gtttcatttg	tttgcttgac	attttcagaa	540
ggaatggctg	gatatgtttc	tttcagagt	tttaactcag	agtgagggga	atatgggagg	600
tcaaaaacaa	ggacttgcca	ttagaaaatc	atatatttct	gtagtatcac	aagtatgtga	660
atgttattat	cattaaagac	caaagagggt	tnactaggga	gattttgaaa	acagggttgg	720
ttaaagtaag	gccttcattg	tgccacccaa	aagatagtat	gattcatttc	ttcaaaaaat	780
attttagag	tgattaatac	aaaccacagg	taagtgtctg	attttcagag	aataaaggta	840
gcacagtttc	tgctccctca	tgctttacat	tgtactttga	aagatagaat	aaaaacaagt	900
gaaaaagaaa	agtctaaaaa	gtgttataag	gaaagaccac	aatgataaag	naaatatgca	960
gaagagatcc	caaactcatt	gacaattnaa	agtgagtact	c		1001

<210> 417

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 503

<223> 10-460-285 : polymorphic base A or T

<220>

<221> misc_binding

<222> 483..502

<223> 10-460-285.mis1, potential

<220>

<221> misc_binding

<222> 504..523

<223> 10-460-285.mis2, potential complement

<220>

<221> primer_bind

<222> 219..237

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 622..640

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 10-460-285 potential probe

<220>

<221> misc_feature

363

<222> 64,643,902,939

<223> n=a, g, c or t

<400> 417

tattttaata	attatattatg	attgtgaata	tactgatgtt	acattaaaga	tgtgatttct	60
tctnacagat	ctctgaatac	atttgccttc	cttatatata	catatgagca	acatatgcaa	120
taaaataaaat	ctaaattatg	actatatata	aatgtattta	tatatatttt	atcaatgcac	180
agacatttta	tatatgtttg	ggtatgttat	tccaagtcct	ttcaggaaaa	tacctgcata	240
ttcaaataac	aattctcgtg	ttagctacct	tttgttttgt	tttgtttttt	tccatcagga	300
agacccacta	cattatattga	gacaatgggg	aaagctgaaa	tgtggctcat	tcgaacctat	360
tgggattttg	aatttcctcg	cccattctta	ccaaatgttg	attttgttgg	aggacttcac	420
tgtaaaccag	ccaaaccctt	gcctaaggta	aatgtattct	tgtttcattt	gtttgcttga	480
cattttcaga	aggaatggct	ggwtatgttt	ctttcagagt	gtttaactca	gagtgaaggg	540
aatatgggag	gtcaaaaaca	aggacttgcc	attagaaaat	catatatattc	tgtagtatca	600
caagtatgtg	aatgttatta	tcattaaaga	ccaaagaggt	tnactaggg	agattttgaa	660
aacagggttg	gttaaagtaa	ggccttcatt	gtgccacca	aaagatagta	tgattcattt	720
cttcaaaaaa	tatttgtaga	gtgattaata	caaaccacag	gtaagtgtctg	gattttcaga	780
gaataaaggt	agcacagttt	ctgctccctc	atgccttaca	ttgtactttg	aaagatagaa	840
taaaaaacaag	tgaaaaagaa	aagtctaaaa	agtgttataa	ggaaagacca	caatgataaa	900
gnaaatatgc	agaagagatc	ccaaactcat	tgacaattna	aagtgaagtac	tcaataatgt	960
gcagagatag	gtgaaacgat	gaggggttga	taaacacca	a		1001

<210> 418

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-605-58 : polymorphic base G or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-605-58.mis1, potential

<220>

<221> misc_binding

<222> 502..520

<223> 12-605-58.mis2, complement

<220>

<221> primer_bind

<222> 444..464

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 901..921

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-605-58 potential probe

<400> 418

gttcagcaga	acagcagaca	aattactttt	atttttaatt	tcaatactct	ttgcttttaga	60
aacaattttg	ctgtggcact	tcctagtctg	tgactctgtc	ttgaaaaggg	ctggaactca	120
ggctgcgtag	acatacatat	ttcattttatc	tggtcttcaa	cttaaacatt	cacctcttta	180
taaaaacttc	tctgtaattc	tgaaggtaat	tccccttttt	ttgatggagt	tcaaaaattg	240
ctgacttgca	ctgttgggaa	atcatcactg	actgtgattt	cattttccat	actttcatat	300

364

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ttacatccac ctgctttttc tgttcagtg gagacaagca gttggagcca accttctgag 360
cttcttcaaa aaggctatca acaaaatatt cacaatttgt tgattatcac tgagagattg 420
attgtcagat actgtttcac aaacccatct tcttttatac tttcgagatt atctacctct 480
ttcattctct tttgtcttat kctgggcagg gtctcctggc ctcagcctca ctcagctcag 540
aggccacgag cacccttttg ccccgggctc cgtctggagc ccgctgctcc agacctcctt 600
aggttcgccc gcggcacagc taggatcctg acggactctc taggtctctg ccaggcacca 660
gacaccaaaa gcatgctgat gtagtctcaa ttgatttgtt tttaaattgg taattaaacc 720
tccaccttta ttgaaagatc atttggaaga ttttgttctc atactcggtc agttaataaa 780
catatgattt gtcaaaagat agattttaga aacattttat gaattcaaaa aatttgaggg 840
aaatatttgg gttgttttag aagctctgtc aagatgtagt tttaatcaag aaacttatgt 900
caaaagttta agaatcaagc cttaatatta ttcttgacga tgtccttggt aaaatctgct 960
ggtggggata attaaaatac acattgtata tactttgtat t 1001

```

<210> 419

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-607-207 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-607-207.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-607-207.mis2, potential complement

<220>

<221> primer_bind

<222> 689..707

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 179..199

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-607-207 potential probe

<220>

<221> misc_feature

<222> 531,558

<223> n=a, g, c or t

<400> 419

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atgtacatgt atatatgtgt tcactttctc caaaacaagg cacagaatta ttgagctgcc 60
ttacagatgt ttgtgaaact gaatgtgttt gtagaagaca gttaaaaatg ataattattc 120
tatataaccc tattttatat aaggatgtct catgtttctc tctttcctca gaagcctgta 180
actctattca tcccataaca ctaatatgaa aacataagtc atttagcatg accaaaaata 240
ggataatgat tttttaaaat gtaagcatat tgcaactaat cataatcagt aacaattaaa 300
agaccacaaa aattaccaaa aattggcaaa taataaaatc tcaggaattc tcaaggccct 360
cttaaaagct acacatcaag gaaacacttt atgatcaaa tagtatgggt taacacaaac 420
ctatgtgtct ttattggtaa gaagaccatc atccaagtct cacaataacc actctatgac 480
ctatggcatg aatgtattct raaaataaat taaaattttg atgctaaggg naattattgg 540

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365

aagagattgc agcaacantt tttataaaat gtatctagat aaatgaaaca tttttaagaa	600
aaattgaatg aatatagtgt catagtagat aatattgcta aatcatgcat acaaacctaa	660
agtaatttac atcaagctta tcctgcaaca catagataaa ggactggtat ctcttgata	720
gtgagagcta ttatatatca ccaacccaaa agacaaacag accaatatga aaatagatga	780
aggatatgaa ttgacaattc acagaagtaa aaatggccaa tcacatcaaa aagatggcta	840
cttgtagtag aaagttggac attataattt agtaagtcaa taaccttaag tcaatgaatt	900
tattttaact tttattttaa gctcaggggt acatgtgcaa gtttgttaca taggtaaata	960
tgtgtcaaca cccaggtatt aagcctagta cccactaatt a	1001

<210> 420

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-609-119 : polymorphic base T or G

<220>

<221> misc_binding

<222> 500..518

<223> 12-609-119.mis1, complement

<220>

<221> misc_binding

<222> 479..498

<223> 12-609-119.mis2, potential

<220>

<221> primer_bind

<222> 597..615

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 114..134

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-609-119 potential probe

<220>

<221> misc_feature

<222> 454

<223> n=a, g, c or t

<400> 420

ttttaaaaat acttaccaat atatggtctg aattgacata ttttagaatt tcttttttta	60
tttgtaaaca gttttataaa gaaatttccc ccaatgatta ggaccagaaa gtatatattgt	120
tatgacagaa ggggttggtc attattttac tgagaaaaag agaatttaga acaaaaggga	180
caacagcaac aaaaagatga gtatacaatt ttgatattgat atccaggaaa ctatgggtc	240
tacatttctt ttcctctttc tctctctctt tttttttttt ttggtgtgag aatacattga	300
gcgatgtggc attagagaat ggatttaagt ttaaaaaacag ggacacatca ggaaacacaa	360
gtcagaataa ttctcattca tttcaaagca aacacatatt caccaggagc ttcatatagt	420
gtgaggggagc tactctaggg ggtgagcaga tctnccactg gagaaagtcc tgggtgacctc	480
tcccactgtg gttcaagtkc cccctgtgag acacagcaaa gtgatgatga ggggtcccca	540
cattcagtta tacatagcac atcaaattca cagtgtgatt tcaggacaaa aggtgtcata	600
gtcatacctt agcaatgacc tgagaaataa gatcacttaa ttatgtaact atatagtata	660
taatactgta ttataaatgg aattctcaga actatttccc agaaattcca aaccacaata	720
ccagactgct gaatgtcagt gattcttata ctccagcttt taagggtgtt ttgggggggtg	780

366

ggggtgtcgg	gggcagtgag	gggtagtggg	gtaagactag	gaaaccctaa	ctttaagtga	840
aatataaagg	gttagagagc	tagaagctaa	ataaatgtag	atataatata	attccaattg	900
taactaactt	ttcctcaatg	ctcatagtca	tgtaatggct	ccaatgactc	ctaactaaaa	960
gaactgaaca	gaaaaaata	aaataaaata	aaactacccc	a		1001

<210> 421

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 499

<223> 12-609-180 : polymorphic base T or G

<220>

<221> misc_binding

<222> 479..498

<223> 12-609-180.mis1, potential

<220>

<221> misc_binding

<222> 500..519

<223> 12-609-180.mis2, potential complement

<220>

<221> primer_bind

<222> 658..676

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 175..195

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 487..511

<223> 12-609-180 potential probe

<220>

<221> misc_feature

<222> 34,53..54,515

<223> n=a, g, c or t

<400> 421

ggtgacagag	aaagactcca	tctggaaaaa	aaanaaaagat	gtcataaaagt	tannttatat	60
tttttaaaaa	tacttaccaa	tatatggtct	gaattgacat	attttagaat	ttcttttttt	120
atttgtaaac	agttttataa	agaaatttcc	cccaatgatt	aggaccagaa	agtatatattg	180
ttatgacaga	aggggttggt	cattatttta	ctgagaaaaa	gagaatttag	aacaaaagg	240
acaacagcaa	caaaaagatg	agtatacaat	tttgatatga	tatccaggaa	acttatgggt	300
ctacatttct	tttcctcttt	ctctctctct	tttttttttt	tttgggtgtga	gaatacattg	360
agcgatgtgg	cattagagaa	tggattttaag	tttaaaaaca	gggacacatc	aggaaacaca	420
agtcagaata	attctcattc	atttcaaagc	aaacacatat	tcaccaggag	cttcatatag	480
tgtaggggag	ctactctakg	gggtgagcag	atctnccact	ggagaaaagtc	ctgggtgacct	540
ctcccactgt	ggttcaagtg	ccccctgtga	gacacagcaa	agtgatgatg	aggggtcccc	600
acattcagtt	atacatagca	catcaaattc	acagtgtgat	ttcaggacaa	aaggtgtcat	660
agtcatacct	aagcaatgac	ctgagaaata	agatcactta	attatgtaac	tatatagtat	720
ataatactgt	attataaatg	gaattctcag	aactatttcc	cagaaattcc	aaaccacaat	780
accagactgc	tgaatgtcag	tgattcttat	acttcagctt	ttaagggtgtt	tttgggggggt	840
gggggtgtcg	ggggcagtg	gggtagtgg	ggtaagacta	ggaaacccta	actttaagtg	900
aaatataaag	ggtagagag	ctagaagcta	aataaatgta	gatataatat	cattccaatt	960
gtaactaact	tttcctcaat	gctcatagtc	atgtaatggc	t		1001

367

<210> 422
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 499
 <223> 12-609-233 : polymorphic base G or A

<220>
 <221> misc_binding
 <222> 479..498
 <223> 12-609-233.mis1, potential

<220>
 <221> misc_binding
 <222> 500..519
 <223> 12-609-233.mis2, potential complement

<220>
 <221> primer_bind
 <222> 711..729
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 228..248
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 487..511
 <223> 12-609-233 potential probe

<220>
 <221> misc_feature
 <222> 87,106..107,568
 <223> n=a, g, c or t

<400> 422
 ctgggaggca gaggttgcaa tgagccaaga ttgcatcatt gcactccagc ctgggtgaca 60
 gagaaagact ccatctggaa aaaaaanaaa gatgtcataa agttanntta ttttttttaa 120
 aaatacttac caatatatgg tctgaattga catatttttag aatttctttt tttatttgta 180
 aacagtttta taaagaaatt tcccccaatg attaggacca gaaagtatat ttgttatgac 240
 agaaggggtt ggtcattatt ttactgagaa aaagagaatt tagaacaaaa gggacaacag 300
 caacaaaaag atgagtatac aattttgata tgatatccag gaaacttatg ggtctacatt 360
 tcttttcttc tttctctctc tctttttttt ttttttggtg tgagaataca ttgagcgatg 420
 tggcattaga gaatggattt aagtttaaaa acagggacac atcaggaaac acaagtcaga 480
 ataattctca ttcatttcra agcaaacaca tattcaccag gagcttcata tagtgtgagg 540
 gagctactct aggggggtgag cagatctncc actggagaaa gtcctggtga cctctcccac 600
 tgtggttcaa gtgccccctg tgagacacag caaagtgatg atgaggggtcc cccacattca 660
 gttatataca gcacatcaaa ttcacagtgt gatttcagga caaaagggtg catagtcata 720
 cctaagcaat gcactgagaa ataagatcac ttaattatgt aactatatag tatataatac 780
 tgtattataa atggaattct cagaactatt tcccagaaat tccaaaccac aataccagac 840
 tgctgaatgt cagtgattct tatacttcag cttttaagggt gtttttgggg ggtgggggtg 900
 tcgggggtag tgaggggtag tggggtaaga ctaggaaacc ctaactttaa gtgaaatata 960
 aaggggttaga gagctagaag ctaataaat gtagatataa t 1001

<210> 423
 <211> 1001
 <212> DNA

368

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<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-611-294 : polymorphic base G or A

<220>
<221> misc_binding
<222> 502..520
<223> 12-611-294.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-611-294.mis2, potential

<220>
<221> primer_bind
<222> 776..795
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 251..271
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-611-294 potential probe

<220>
<221> misc_feature
<222> 406,571,773,943..944
<223> n=a, g, c or t

<400> 423
taaactgtgc acactggacc aaaacttgta agtaccaaat ttcaattaat cttttgagag      60
atgagacaat aaataattca ttcgaatggg ctagatatag ggaaagtaaa tcttgcagag      120
ccattcatct ctaatgtctt ttagcaacat gccgaagcac acaagtaaag ggccactaat      180
ccaaagacaa atgaggaatg tgaaagttaa aaatctcagg accatcaagc aaggtctctg      240
caaagaaaca gtaagtatag tcagcagtca gaaaattggc agacagcaga cagtctttag      300
tgaatgacag agagcacagg gagggctaag tgaaagggag tagtaattaa cattttgtag      360
cattgaaccc atttcttggt gtgaagggct tctaaccctt ttagcntttc ggaaaggcct      420
ctaaacctct tatctgtcag aagggcctct aactgtccta agttgggcct ctaaaccgat      480
tttgaacagt gtctctgttc ragtataaaa atatgttcca ccacttacct aaatcagcca      540
attggtgttg catagtctat ttcttttggg nttggaatct cacctcattt aggtcccgag      600
agagtcacca gagggaaaata ttactggaaa agtgggtcttg tcccagacgt taaggggtggg      660
tttgtggatc tcatgtggga aagaatgcaa ggtgagtcgc agagtacagt aaaattaaca      720
gtttgttaga gactactcta ttacagaata gggcatcctc agaaagcaag aangagaaat      780
acccctacct taaacttagt gcttgcttat atagggtgtt aagaatactg tactttatta      840
caaagggttg tgatcagctt gtgacaggct attaatattg ttattttcct atgtattatt      900
gatttcagca agattttaca agtgggctag ttttttaaag gannaaacta attcttaaat      960
taagaagttt ttgttttcaa actattggga cattttcata a                                1001

<210> 424
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

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369

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<222> 501
<223> 12-612-41 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-612-41.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-612-41.mis2, complement

<220>
<221> primer_bind
<222> 461..481
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 981..1001
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-612-41 potential probe

<220>
<221> misc_feature
<222> 383
<223> n=a, g, c or t

<400> 424
gtagaagctg agaaactagt taggagacat ttcaccagtt gtgacacaat tcttctttaa      60
atatgtcaaa atgggctggg cacagtgggt catgtctgta gggccaacac tttgggagac      120
agaggcagaa tgattagacc acaggagttc cagatgagta tgggcactac agcaagacct      180
catatctaaa aatgtaaaaa ataaaaaata tagccaggca tgggtggtgcg cagctgtagc      240
cccagcttct catgaggctg aggtggagga ttacctgaga ccgaaacgga aaggctgcac      300
tgagccatga tcatgtgact gcactcagcc tgtgtaatgg agcaaaagcc tgtctcaaaa      360
aaaaataaaa actaaaaata tcnaaaatga tcattcccag attctatttc cactatctta      420
cttatagcac ttagaatggc tcacaatatt ttctgtctta gaaaaacatt aactttccca      480
ccgaaaattc catttttcat ytttaaaggt atttgtcaat gataaaactc caatttataa      540
accaaacttt ctgtaatgac atacattaaa acattaatat tttatgtcaa ttcaatgaca      600
cttactttga atcacttggt tggcgctttt caaagaccat ccatagactt gatatgctta      660
agcaataaat ttacttttaa tggttgatatc tttatattta tccttcagct ataaagagaa      720
tatcatgaaa ttatcaagaa ttcacatcatga tcaaccggtg aagcccctgg atcgagcagt      780
cttctggatt gagtttgtca tgcgccataa aggagccaag caccttcggg tcgcagccca      840
caacctcacc tggatccagt accactcttt ggatgtgata gcattcctgc tggcctgcgt      900
ggcaactatg atatttatga tcacaaaatg ttgcctgttt tgtttccgaa agcttgccaa      960
aacaggaaaag aagaagaaaa gggattagtt atatcaaaag c                               1001

<210> 425
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-613-302 : polymorphic base C or G

<220>

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370

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<221> misc_binding
<222> 479..498
<223> 12-613-302.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-613-302.mis2, potential complement

<220>
<221> primer_bind
<222> 781..799
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 343..363
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-613-302 potential probe

<220>
<221> misc_feature
<222> 309
<223> n=a, g, c or t

<400> 425
agaaagtgat agtgccagta gcagggggaa gagagtagca gaataaggac aagggataaa      60
tgactagtag tacaatagtg attattactg atactagcat gatctcggct cactgaaacc      120
tccaccccc aggttcaagc gatctgattc tcctgcctca gcctcccag tagctgggat      180
tacaggcacc tgccaacaca tctgactaat ctttgtgttt ttagtagaga cagagtttca      240
ccatgttggc caggctgggc ttgaactcct gacctcaggt gatccacatg cctcagcctc      300
ccaaagtgnc tgggattaca agtgtgagcc tccgttgttg ttaacttgca gaaggtagac      360
ttgaatccaa gtaaataaatt gtgaaactga ttctctaatt cttttgtaca caaaataaatt      420
gttgcgacaa atttgcttgc ttttccatta tgtattagat tctcagataa tgtttgtata      480
tttcaaaaaga ataagactst tgccaaaaag tatcaagtgt ttgaaaaatg catataggca      540
ttgcctttat aatatactca catgaaactg tacagagaat aaatcatgat ggtaagattc      600
aatatcggtg gcaaatactc attaaaaaaa ctctggaaat aattcaaata tcttacatta      660
agaaatggtt aaaaacttac ataatgtgca taccaagcca ttacaatcct tttttcaaaa      720
caatgtttta ttacactgtc agccgtggta caggtatagt tggaaactaa ggaacaaaat      780
gatgagtaga acaagatcac agtttttttg tagaataaaa aggcataatac aatgagaata      840
aaattttcta aataaacatc acatatgtac attgagttat ataaatagaa ttaaaccat      900
aatgaaatgg cacacatttt aaattgagat agagatatgg gtaaattgatt ttctttttct      960
aaattttcat acttttataa aactacttac attgatcttc t                                1001

<210> 426
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-614-471 : polymorphic base T or A

<220>
<221> misc_binding
<222> 502..520
<223> 12-614-471.mis1, complement

```

371

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-614-471.mis2, potential

<220>
 <221> primer_bind
 <222> 952..971
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 424..442
 <223> downstream amplification primer

<220>
 <221> misc_binding
 <222> 489..513
 <223> 12-614-471 potential probe

<220>
 <221> misc_feature
 <222> 109,479
 <223> n=a, g, c or t

<400> 426
 gagctggatt ggtaaagtaa aatgaggaca tgcacgttgc aagagtcaag atagaatgaa 60
 accaaaattg agataaaatc aaaattgaga taaacacatg aaatatttnc acaaatactt 120
 cagtgaagaa tagcatgaat gattaagacc agtaaaacaa ttagaaataa gagagttttg 180
 ggaataaagc aggcaatcgg gagagcacta attcagcttt tttttctttt ttaacaaata 240
 acacttttat attttaatca ctttagtggc aattcctaga gtattagggtg attcctattg 300
 gggctctatg agtcaagatt cagggagaaa aatagaaaga ttcactagtt ctttctactg 360
 ctgttattgt ttgttctttt gttcattcat tcagttccat tttatttcat gttatcaatt 420
 acattttagt gtaaccagtg agtttatttc taatttctag aattgatgtg tttcttttnt 480
 atgtttatgg ttctcgatc wttccataca tatattatat gaactatttt tcatctctgg 540
 acatttgaac tatgtttatt ataaaacatc attttgattt attttctata tctataatcc 600
 tttggtgcaa atgttactat tatacatagt atatagttgt atactattgt aaactattgt 660
 atattgtata tagttgtata ctattgtata ttgtatatag ttggttattt cttcatttgg 720
 ttttcattag ttaatcttca acaggatttg atttctgcaa acattcttca tattctgcat 780
 tgtgagaaca tcagaataat ttattgattg cctctgctgt aacctaggca gatcactttc 840
 attacaattt ggcttttctt gtcatttttt ttacaattta ttgttacaat taatttttat 900
 agcagaaatt ccctgaactc tgtagataca tttttttcct agttttaagg tctttgtctc 960
 attttgattc cttccaaaac cacttctttt tatagtcct a 1001

<210> 427
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 12-620-192 : polymorphic base G or T

<220>
 <221> misc_binding
 <222> 483..502
 <223> 12-620-192.mis1, potential

<220>
 <221> misc_binding
 <222> 504..522
 <223> 12-620-192.mis2, complement

<220>
 <221> primer_bind
 <222> 309..326
 <223> upstream amplification primer

 <220>
 <221> primer_bind
 <222> 777..797
 <223> downstream amplification primer, complement

 <220>
 <221> misc_binding
 <222> 491..515
 <223> 12-620-192 potential probe

 <220>
 <221> misc_feature
 <222> 461..463
 <223> n=a, g, c or t

<400> 427
 tatgagaaaa ctacaagagt caaaatttga tgtccttctg gcagatgccg ttaatccctg 60
 tgggtgagctg ctggctgagc tacttaacat accctttctg tacagtctcc gcttctctgt 120
 tggctacaca gttgagaaga atgggtggagg atttctgttc cctccttcct atgtacctgt 180
 tgttatgtca gaattaagt atcaaatagat tttcatggag aggataaaaa atatgatata 240
 tatgctttat tttgactttt gggttcaagc atatgatctg aagaagtggg accagtttta 300
 tagtgaagtt ctaggtaagt cgtgtgtcca attgggtgtt attaagttct aattttcctg 360
 tgcctttgaa ggtgggctta tataaatata atgtcagaag atagtgtttt tatgggaaat 420
 tatgaattgc aaatgtaaga tgatctatga gtctcaaaaa nnntatagaa tgttgacctt 480
 atagaatcag ttagaacctt ggkgccatca ctgctacagg acaccaagag agtcataaac 540
 cttcaatgta aaacacttat gatttcttta agccatcaca tatcattttg ctatacattt 600
 tttcatcttt aaaaaagtca atagataact caagaaacat cttcatgaag gcagacatac 660
 aaattttata tttacacata tttctaaaaa tattatcaat gcaggattga ggaacttgta 720
 cctgagtacc tcagtttcct catttagaaa ttaaattttg tttttcatat aagaaggatt 780
 ccttcacagt tgagaaatat agtggctcta ctccagaaac agaagcctaa aacttgagat 840
 ttctaattgt tataattcc ttcaataaca acttcacaat tatttccttc aaaaactgaa 900
 atcttggtga aagtgaacat ctaagtttta atctatattt tattaactg catctctcca 960
 tcaaagaaaa taggggccaa aataaggaag agcacatatc t 1001

<210> 428
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 503
 <223> 12-621-49 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 483..502
 <223> 12-621-49.mis1, potential

<220>
 <221> misc_binding
 <222> 504..523
 <223> 12-621-49.mis2, potential complement

<220>
 <221> primer_bind
 <222> 455..473

373

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 907..927

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 491..515

<223> 12-621-49 potential probe

<220>

<221> misc_feature

<222> 634

<223> n=a, g, c or t

<400> 428

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aaaggacagc	ccaaagaata	aaaaaaaaac	aaggaaatca	tatatgtgat	aaggttctta		180
tatcagaaag	atattaaaaa	cacaagtcca	taagaagaca	aataattcaa	ccaaaattag		240
gcaaaacatg	ctcaacatga	tttcatatca	aagaaaggta	aagcataacc	agatatcact		300
tcattcacac	tggctataat	caaacgaaat	ataatcccaa	gtgttggcaa	ggttgggaag		360
aaattaaaa	tcttatacat	tgctgggtgag	aatggaaatt	gaagcatcca	ctgtgaaaaa		420
caatctggaa	attcctatgg	taatttagaa	atttatgggt	aacagacaat	tcctatggta		480
atttagaaat	tatatggtaa	ctrctacttt	gaattgtagc	agttatactt	tcacttgatt		540
gatttatctt	cagatataag	taggagaaaa	acagaaagaa	acagcgattt	gaaaagaagc		600
attgcattgc	accaggagaa	ctatgaaatc	gatngtcaaa	tattctcctg	atacaactca		660
gttgctcactt	tagttctggg	agttgtggaa	aggtgctagt	gtggcccaca	gaatacagcc		720
attggatgaa	tataaagaca	atcctggatg	aacttgtttg	gagaggccat	aagatgactg		780
tgctgtcatc	tttggcttcc	attattattc	accctagtaa	atcatctgct	attagatttg		840
aggtttatcc	aacatctcta	attaaaaata	attttgaggg	tcttgttgtg	aaactgatca		900
atagatggat	atacgatctt	cagaaagatg	cattttggtc	atatttctca	caagcacaag		960
aactcttttg	ggaatctaca	gactgtgtta	ataatctctg	t			1001

<210> 429

<211> 710

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 364

<223> 12-622-325 : polymorphic base C or T

<220>

<221> misc_binding

<222> 344..363

<223> 12-622-325.mis1, potential

<220>

<221> misc_binding

<222> 365..384

<223> 12-622-325.mis2, potential complement

<220>

<221> primer_bind

<222> 40..59

<223> upstream amplification primer

<220>

<221> primer_bind

374

<222> 551..569
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 352..376
<223> 12-622-325 potential probe

<220>
<221> misc_feature
<222> 333,685,688
<223> n=a, g, c or t

<400> 429
tattgttaga gttcatgttc ctttctcctt cactgatctc tcaaactaac aagactcagt 60
tcatttccag aagaccctac ctcttatatt agggagtttc agtaccttac ccagtcttat 120
gcactaacct ggtatgacct ctacttatcc tgtcttccac cctcaccttc tacttatcct 180
ctcttccacc ctcaccccag aagacaggga ccatatttgg accctgggtc aggagcatgc 240
taatacaatt catcatcaag ctcttgccca gcctactggc acggaggcag tccccaacca 300
ggagccccac caggattatc aagacagggc ctntctggaca ctgccatcaa gaccacatga 360
ttgygtatct ccttgcagga ctcaaaaagg gtgcccataa agtggttaaacc tataaaaacc 420
tttcagaaat cacccaaggt cctgacagaa acccagcctt ttttctctct tgtttaactg 480
aagccatgag aaaatatacc aacctagacc cagccaaccc agaaggaatc actattttaa 540
acctttggtt cctcatccaa tctaccctg atatttgggtg caagattcag aagcttgaca 600
atggccctga aacccacaa tgacaccttc ttaatttagt cttcaaagtc ttaaacagtt 660
ataacgagga aagtaaaaag aaaanaanaa aagacagagt ttcaaatgct 710

<210> 430
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-82 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-82.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-82.mis2, potential complement

<220>
<221> primer_bind
<222> 562..582
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 114..134
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-82 potential probe

<220>

375

<221> misc_feature
<222> 464..639
<223> n=a, g, c or t

<400> 430
tgtcttatgt caacatttta tgaattctac agtagtttag tgatttcttc taatttttaa 60
ggttatatatt gcagtaattt tgagatgtga ttacaaatgc attggcaatc ctctcatcaa 120
gtcatataacc cttcctgtga aatttagcaa attttgtggc tgtctcaaaa aagagaatat 180
agtgggaagtg aggagcttaa cttccaaagc tcaaaaaaat tgtaataca ttttctctgt 240
ctgtccttct gtccttttct ctgtgtttct gtcattcttt tttccttttt ctctgtctct 300
ccactcgctt tggagccctg tgctatatcc acagtcacca ggagaaatat accatttggg 360
gtagaaatac atatgtatgc ctaataagtc acaattggcc cagcactgca gtagcttgag 420
acttttaata ctaatcacca gatatgtgag tgattaacct tcangatgat tagccaagc 480
taccttagga cagtaacca ytgagaaatg ctgtgccata aacacctaatt tgagcctggc 540
caacaacctt gaattaaaac agatgatgat aaaatgttgc tgttctaagc accttcattt 600
cagagcagtt ggttaagcag tgatagacaa ccagaaaana tatttttaca tatttgagtt 660
atactcctgt aataatatta aaattaatat atacctacaa aaaaagtga tctatattac 720
atthttgtaac tacctgtaac ccagaaagag tagtcagcat aggatggtgg gtaagagctt 780
gcactctgaa tccagataac ctatatcatc ttgcaaaac cattacagaa tcatgtatag 840
ttaagcaaat tacttatcag gtctatgcct cacattctcc ttcagtgaat tgtagatgaa 900
gcaatgtcac tactactta atagcattgc tgagactaaa agagttgctg tatgtaattg 960
ctgtatatag caaaattcaa tttgctataa ctattattat t 1001

<210> 431
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-83 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-83.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-83.mis2, potential complement

<220>
<221> primer_bind
<222> 563..583
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 115..135
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-83 potential probe

<220>
<221> misc_feature
<222> 465..640
<223> n=a, g, c or t

376

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<400> 431
atgtcttatg tcaacatttt atgaattcta cagtagttta gtgatttctt ctaattttta 60
aggttatatt tgcagtaatt ttgagatgtg attacaaatg cattggcaat cctctcatca 120
agtcataata ccttcctgtg aaatttagca aattttgtgg ctgtctcaaa aaagagaata 180
tagtggaagt gaggagctta acttccaaag ctcaaaaaaa ttgttaatac attttctctg 240
tctgtccttc tgccttttcc tctgtgtttc tgtcattctt ttttcctttt tctctgtctc 300
tccactcgct ttggagccct gtgctatatc cacagtcccc aggagaaata taccatttgg 360
tgtagaaata cataatgtatg cctaataagt cacaattggc ccagcactgc agtagcttga 420
gacttttaat actaatcacc agatatgtga gtgattaacc ttcangatga ttagcccaag 480
ctaccttagg acagtaacca rctgagaaat gctgtgccat aaacacctaa ttgagcctgg 540
ccaacaacct agaattaaaa cagatgatga taaaatgttg ctgttctaag caccttcatt 600
tcagagcagt tgggttaagca gtgatagaca accagaaaan atatttttac atatttgagt 660
tatactcctg taataatatt aaaattaata tatacctaca aaaaaagtga atctatatta 720
cattttgtaa ctacctgtaa cccagaaaga gtagtcagca taggatgggt ggtaagagct 780
tgcactctga atccagataa cctatatcat ctttgcaaaa ccattacaga atcatgtata 840
gttaagcaaa ttacttatca ggtctatgcc tcacattctc cttcagtga atgtagatga 900
agcaatgtca ctacctactt aatagcattg ctgagactaa aagagttgct gtatgtaatt 960
gctgtatata gcaaaattca atttgctata actattatta t 1001

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<210> 432

<211> 989

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 489

<223> 12-624-107 : polymorphic base T or C

<220>

<221> misc_binding

<222> 469..488

<223> 12-624-107.mis1, potential

<220>

<221> misc_binding

<222> 490..509

<223> 12-624-107.mis2, potential complement

<220>

<221> primer_bind

<222> 575..595

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 127..147

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 477..501

<223> 12-624-107 potential probe

<220>

<221> misc_feature

<222> 477,652

<223> n=a, g, c or t

<400> 432

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tttaaaattt taatgtctta tgtcaacatt ttatgaattc tacagtagtt tagtgatttc 60
ttctaatttt taagggttata tttgcagtaa ttttgagatg tgattacaaa tgcattggca 120
atcctctcat caagtcatat acccttctctg tgaaatttag caaattttgt ggctgtctca 180

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377

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aaaaagagaa tatagtggaa gtgaggagct taacttccaa agctcaaaaa aattgttaat    240
acattttctc tgtctgtcct tctgtccttt tctctgtgtt tctgtcattc ttttttcctt    300
tttctctgtc tctccactcg ctttgagacc ctgtgtctata tccacagtcc ccaggagaaa    360
tataccattt ggtgtagaaa tacatatgta tgcctaataa gtcacaattg gcccagcact    420
gcagtagcct gagactttta atactaatca ccagatatgt gagtgattaa ccttcangat    480
gattagccya agctacctta ggacagtaac caactgagaa atgctgtgcc ataaacacct    540
aattgagcct ggccaacaac ctagaattaa aacagatgat gataaaatgt tgctgttcta    600
agcaccttca tttcagagca gttgggtaag cagtgataga caaccagaaa anatattttt    660
acatatattg gttatactcc tgtaataata ttaaaattaa tatataccta caaaaaaagt    720
gaatctatat tacattttgt aactacctgt aaccagaaa gagtagtcag cataggatgg    780
tggttaagag cttgcactct gaatccagat aacctatc atctttgcaa aaccattaca    840
gaatcatgta tagttaagca aattacttat caggtctatg cctcacattc tccttcagtg    900
aaatgtagat gaagcaatgt cactacctac ttaatagcat tgctgagact aaaagagttg    960
ctgtatgtaa ttgctgtata tagcaaaat    989

<210> 433
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-146 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-146.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-146.mis2, potential complement

<220>
<221> primer_bind
<222> 627..647
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 179..199
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-146 potential probe

<220>
<221> misc_feature
<222> 529,704
<223> n=a, g, c or t

<400> 433
tagaatgtta attaaaaatt ttaattatgg ctaaaatttt agtaaacaaa tttttaaaat    60
tttaagtgtc tatgtcaaca ttttatgaat tctacagtag tttagtgtatt tcttctaatt    120
tttaagggtt tatttgcagt aattttgaga tgtgattaca aatgcattgg caatcctctc    180
atcaagtcac atacccttcc tgtgaaattt agcaaatatt gtggctgtct caaaaaagag    240
aatatagtgg aagtgaggag cttaaccttc aaagctcaaa aaaattgtta atacattttc    300
tctgtctgtc cttctgtcct tttctctgtg tttctgtcat tcttttttcc tttttctctg    360
tctctccact cgctttggag ccctgtgcta tatccacagt cccaggaga aatataccat    420

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378

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ttggtgtaga aatacatatg tatgcctaata agtcacaaat tggcccagca ctgcagtagc 480
ttgagacttt taatactaata yaccagatat gtgagtgatt aaccttcang atgattagcc 540
caagctacct taggacagta accaactgag aaatgctgtg ccataaacac ctaattgagc 600
ctggccaaca acctagaatt aaaacagatg atgataaaat gttgctgttc taagcacctt 660
catttcagag cagttgggta agcagtgata gacaaccaga aaanatattt ttacatatatt 720
gagttatact cctgtaataa tattaaaatt aatatatacc tacaaaaaaa gtgaatctat 780
attacatttt gtaactacct gtaaccagaga aagagtagtc agcataggat ggtgggtaag 840
agcttgact ctgaatccag ataacctata tcctcttgc aaaaccatta cagaatcatg 900
tatagttaag caaattactt atcaggtcta tgccctcacat tctccttcag tgaaatgtag 960
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<210> 434

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-624-288 : polymorphic base T or G

<220>

<221> misc_binding

<222> 481..500

<223> 12-624-288.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-624-288.mis2, potential complement

<220>

<221> primer_bind

<222> 769..789

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 321..341

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-624-288 potential probe

<220>

<221> misc_feature

<222> 113,671,846

<223> n=a, g, c or t

<400> 434

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gttttaatat aatattatca atccattagt gccatttaga aaacttaaat tgaccagcaa 60
tccggtgctc tctatctgat aaatttacag cctgtttttg gacacctact tgnatatttt 120
aaatatttat taataaatat attagaatgt taattaaaaa ttttaattat ggctaaaaatt 180
ttagtaaaca aattttttaa attttaatgt cttatgtcaa cattttatga attctacagt 240
agttagtgga tttcttctaa tttttaaggt tatatttgca gtaattttga gatgtgatta 300
caaatgcatt ggcaatcctc tcatcaagtc atataccctt cctgtgaaat ttagcaaaatt 360
ttgtggctgt ctcaaaaaag agaatatagt ggaagtgagg agcttaactt ccaaagctca 420
aaaaaattgt taatacatatt tctctgtctg tccttctgtc cttttctctg tgtttctgtc 480
attctttttt cttttttctc kgtctctcca ctgcttttgg agccctgtgc tatatccaca 540
gtccccagga gaaatatatac atttggtgta gaaatacata tgtatgccta ataagtcaca 600
attggcccag cactgcagta gcttgagact ttttaacta atcaccagat atgtgagtga 660

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379

ttaaccttca	ngatgattag	cccaagctac	cttaggacag	taaccaactg	agaaatgctg	720
tgccataaac	acctaattga	gcctggccaa	caacctagaa	ttaaaacaga	tgatgataaa	780
atgttgctgt	tctaagcacc	ttcatttcag	agcagttggt	taagcagtga	tagacaacca	840
gaaaaatat	ttttacatat	ttgagttata	ctcctgtaat	aatattaaaa	ttaatata	900
cctacaaaaa	aagtgaatct	atattacatt	ttgtaactac	ctgtaaccca	gaaagagtag	960
tcagcatagg	atggtgggta	agagcttgca	ctctgaatcc	a		1001

<210> 435

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-624-293 : polymorphic base T or C

<220>

<221> misc_binding

<222> 481..500

<223> 12-624-293.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-624-293.mis2, potential complement

<220>

<221> primer_bind

<222> 774..794

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 326..346

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-624-293 potential probe

<220>

<221> misc_feature

<222> 118,676,851

<223> n=a, g, c or t

<400> 435

cttgggtttt	aatataatat	tatcaatcca	ttagtgccat	ttagaaaact	taaattgacc	60
agcaatccgg	tgctctctat	ctgataaatt	tacagcctgt	ttttggacac	ctacttgnat	120
attttaaata	tttattaata	aatatattag	aatgttaatt	aaaattttta	attatggcta	180
aaatttttagt	aaacaaattt	ttaaaatttt	aatgtcttat	gtcaacattt	tatgaattct	240
acagtagttt	agtgatttct	tctaattttt	aaggttatat	ttgcagtaat	tttgagatgt	300
gattacaaat	gcattggcaa	tcctctcatc	aagtcataata	cccttcctgt	gaaatttagc	360
aaatttttg	gctgtctcaa	aaaagagaat	atagtgggaag	tgaggagcct	aacttccaaa	420
gctcaaaaaa	attgttaata	cattttctct	gtctgtcctt	ctgtcctttt	ctctgtgttt	480
ctgtcattct	tttttccttt	ytctctgtct	ctccactcgc	tttggagccc	tgtgctatat	540
ccacagtcct	caggagaaat	ataccatttg	gtgtagaaaat	acatatgtat	gcctaataag	600
tcacaattgg	cccagcactg	cagtagcctg	agacttttaa	tactaatcac	cagatatgtg	660
agtgattaac	cttcangatg	attagcccaa	gctaccttag	gacagtaacc	aactgagaaa	720
tgctgtgcca	taaacaccta	attgagcctg	gccaacaacc	tagaattaaa	acagatgatg	780
ataaaatgtt	gctgttctaa	gcaccttcat	ttcagagcag	ttgggttaagc	agtgatagac	840
aaccagaaaa	natattttta	catatttgag	ttatactcct	gtaataatat	taaaattaat	900

380

atatacctac aaaaaaagtg aatctatatt acatttttgta actacctgta acccagaaag 960
 agtagtcagc ataggatggt gggtaagagc ttgcactctg a 1001

<210> 436
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-421-135 : insertion T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-421-135.mis1, potential

<220>
 <221> primer_bind
 <222> 367..385
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 797..817
 <223> downstream amplification primer, complement

<400> 436
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 gttctacttt ctcagataat tttaataagg ttggaagagt gtgttccttc aagggttggt 120
 agaacttgcc ttaaaataat ctgggcctaa tgtttttctg gtgggaaatt tttaaattat 180
 gggatttgca ttctttaatg attattggac taggcaggct ttttgttaca tcttgaatca 240
 attttggtag gccttggtcc ttgagatgat aacattggtc tcttgattat ccacttgctc 300
 caaggagggt ttacagact actccctagg cttgaaagcg tgggggtgaat accaccggga 360
 gtacacgaga taattgtaag aggtgtgtag acttggtttt aaataacatt gaactacatg 420
 atgagaagtc attctcattt caattatctt tgaatcctta tgggttaagtc aagtggaaaag 480
 tattggtttg gagccagcat gtccacaccc tcaaaattaa tgtttatattt tatcaaagta 540
 atttatgtac gtgatctgaa gataaagtgg gattacaggt tttatgacaa caaataactc 600
 ttcttctgct ctacctcccc tctccctcta tccctagaga taaccctttt tgattactac 660
 tttgggtatt tacttctgta tttctaaaca ttatactttc actgctattt attgattcac 720
 aaattttaga cattgtcagt tggcttcttt ttatggaaga aataatttca tgctccttta 780
 cttcttcttt tccttacctc atccttccag taacattata tcaactctgtt aggttaaactc 840
 aatagccaat gtttataatt attgtgatta agaaaataat gttgaaagca gggccttata 900
 gtatactgtg gttacatttc cttcttgtgc aatttttttt ccctaggggt aataattgct 960
 ctttatttct ttgtttgctt agtttcatgc ccaaactctt t 1001

<210> 437
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-442-133 : insertion C

<220>
 <221> misc_binding
 <222> 502..520
 <223> 12-442-133.mis1, complement

<220>

381

<221> primer_bind
 <222> 616..633
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 184..203
 <223> downstream amplification primer

<220>
 <221> misc_feature
 <222> 94,734
 <223> n=a, g, c or t

<400> 437
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 cccattcat ttaactatct gcacacagag acangaagcc agaaatctga ctgggaagaa 120
 attcctaccc ttttgccagc atgctaagct tctgggttct ctttccctga gtggccctag 180
 tgatctggct tgtggcacia ctgcctttgg gggccaagcc gcatcataaa ggaaaagtat 240
 ttctttttgt tctggccaaa gcaaaatacg cgtaataaaa catagatatt aaccaggctg 300
 cttagcatcc aatatcaaac tggcaaggct taaatttgcc ctgagggtgg ccctgtcatc 360
 tttaatctaa cctccgacta ggagtttcaa catgtgtgtc ctgggcaaga tggtcgccct 420
 gagtaataga aaagaaagag aaaggagaga gagaaaaaca ttgcctgtgg cagggcgggg 480
 aagggtgaaat gatcagggag gcagagaaag aaccacccat tgcagcgaca ctaaaaagtt 540
 caggtggctg ctgtcgggtg agcaaggatc ttttccagta atcctaccag ctctcaaatt 600
 tcccttggtt gggaggaaaa agctcccat gtcccaggat cctgtacatt cctaattctg 660
 tcaaccatag ccacagcaa agtacaaggg agattaatcc aaagagaata gcagttaaca 720
 tcccatagt ccgnaacctg ttcttagccg agagggactt taccgaagag gggcctctaa 780
 cccgctaaat cttagaaggg actctaactc tcctaagtcg ggctctaac cagaggtcag 840
 tcaagcatcc ttgcctttta ttaaggggga gcctttaacc acctctatct taggagagac 900
 tctaactcca ctaagctggg cctctaacc aatcccatc tttaccagg taccacacca 960
 cttacccaaa gtcttccaat cagtgtgca gtctatttcc t 1001

<210> 438
 <211> 756
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-449-63 : insertion AT

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-449-63.mis1, potential

<220>
 <221> primer_bind
 <222> 546..563
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 86..106
 <223> downstream amplification primer

<220>
 <221> misc_feature
 <222> 123,277
 <223> n=a, g, c or t

382

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<400> 438
ggggacggaa gaaaggaaaa gaaaaaatag tttatatgta tatacatttg tatcaaaata    60
agaaataaat atccataaatt attacaattt tcctctgaaa gtagtcacat gggtatacct    120
ggntatattt ttattttttt ttattattat tattatttga gacagggtct caccctgtca    180
cacaggctgg agtgcagtggt tgcaattatg gctcactgct acctctgcca cctgggctca    240
agccatcctc tcaccttagc cttctgaaca gctgggnata catgtgcact aatttttttt    300
tttttgaaac aaaaatattt gtgtagaagg cacaaaagct acaatcacag actccactgt    360
gcaaaggcgc aacctgcctc attgatctct agtgtacacc aaccagctt ccctttccat    420
tcagcctgtg aaaggagata gtgcttgggc catttggtta aagaagggga tgggagatga    480
tcaaaacccc aagtaagggt catccaatat ggtgtctaag cagcaaatga ctaattgctg    540
aagaaggaga ctagacagag gattagaggc agccatgggg ccagtgcagc tgtggagagc    600
tctgagcaaa gaaacaaggt tggcagggtga ggaggcctag gatagaggcc agaaggccaa    660
gcctggggct gcatgtgcac taatttttgt atttttttgc ttttttgata gagatgagat    720
ttcatcatgt tgcacagggt ggtcttgaag tcctgg                                756

<210> 439
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-454-242 : deletion AT

<220>
<221> misc_binding
<222> 481..500
<223> 12-454-242.mis1, potential

<220>
<221> primer_bind
<222> 260..279
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 755..773
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 795..800
<223> n=a, g, c or t

<400> 439
caaatggaaa aaatgaaaac tgtcacactt cttacataac ttcttttatt atctgtattg    60
taaatacaga gtctcaatta ttgactaatt tatactaata gtgggaagca gtgtctagat    120
aatcccagat gattactaat ttaaaactac tttacatttt atttagtaat gtgtttggaa    180
cagttacatt ttgtagctac ttacaatttt actttaactg aaataataag acaaggccat    240
aaatattggc ctccctggct ggggagttgt gtgggtttcc tttccaggca gttgaggttt    300
tccatggagc ctactctaca gtgtcagcag gagtataaca tagaaggctt ccaggtcagg    360
tggcccagag tcaaatcaaa gcccacatccc tttttagcaa attttcagc cttacttagc    420
tgtgccggcc tgccctcttc taaaatgagg aaaataataa taccacttc actggtttat    480
tgagaggatt aaatgaggac atgtgttatt tcacaccatt attgcttctg ttgttattat    540
tttaaaatct aggttggtga ttgcatcagt ttcttagggc tgctctaag aaagtaccac    600
aagctgagtg acttacatag cagaaaagtg ttttcttaca ggtaagagg ctggaagtct    660
gaaatcaagg tgtcagcagg gccatgctcc cactgaaacc catagcgggg aatcctttct    720
tgcttctaag ttctagtgt ttcttggct tgtagatgtg tcacttcagt cacacggcca    780
tctttctctt tcttnnnnnn cttcttcttc ttcttctctt tcttctctt cttcttcttc    840
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cttcttcttc ttcttctctt tcttctcttc cttcttcttc ttcttctctt tcttctcttc    960
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<210> 440
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-463-230 : deletion CAT

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-463-230.misl, potential

<220>
 <221> primer_bind
 <222> 255..272
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 773..790
 <223> downstream amplification primer, complement

<220>
 <221> misc_feature
 <222> 136,400,713,730
 <223> n=a, g, c or t

<400> 440
 aatcaatgca taaacaaaaa ggatgcccga gaaaacctgt gcttttcaga cacacacaca 60
 catacacaca cactcactca ctactcact ctgaattggg tcaagtataa aaaaattttt 120
 tttaaaggaa ggaatncttt agcccaactg ggatttcgac gaaattgtat atatcaaaag 180
 atagctacat ccaacctctc accagaatcc agaggcttct tcctgcaaag atactattga 240
 aagttttatt agtaagtttg agaaggcgaa agtatgtatc agagggtgaa gctaacatga 300
 caattgcttg gccaaagagc gcagcagttt tatgttattg agcagcacag gatgaatcga 360
 acaccacga tggctagaca gaggcgcctg gctgtgactn ccagagggtc aggcaagcca 420
 tctgacctct ctgagtcctc acccctgaa atgaaaacca tactcataag actccttgac 480
 aatggaaaatt ttggagggtga catagttaat gaagtgtcat agaaaggaaa tagctaagaa 540
 tactctaaaa cctccccatt cccagtatgg gcaatttggg aaaaatgagt aactaaaaat 600
 taggggttct caaagtgttg ttccaggatc aaatgcatta gtccccacct gggagcttgt 660
 tagaaatgca aattcccagg ctccccctga ggctcctga attagaactt ttnggggggtg 720
 tttaacaan gctctccagg tggttacgat gtcccataga gaatcattgg ggcaataaat 780
 cctgtgccct gattagattg caaagctgca ctttcaaaag caagtcaggg tgctgagttg 840
 cttagtttct attgcaaaat ttctgcttt ggaacaaaat tttcaaaatt tttagaggggt 900
 tgctcaggcc agtgatgttt gcaatgcaaa cccaagaatt ctgaaaggag cccatggctg 960
 aaaggagcca attcttccag gacggactac tccagttgca a 1001

<210> 441
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-462-199 : deletion ATGTCCCACAGCTG

<220>
 <221> misc_binding
 <222> 481..500

384

<223> 12-462-199.mis1, potential

<220>

<221> primer_bind

<222> 303..322

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 736..756

<223> downstream amplification primer, complement

<220>

<221> misc_feature

<222> 255

<223> n=a, g, c or t

<400> 441

caaaagcaag tcagggtgct gagttgctta gtttctattg caaaatttcc tgctttggaa	60
caaaattttc aaaattttca gaggggttgc caggccagtg atgtttgcaa tgcaaaccga	120
agaattctga aaggagccca tggctgaaag gagccaattc ttccaggacg gactactcca	180
gttgcaactg tgctgtggag gctgaggagc atccatgact gaggaagggc gagtccccta	240
taatgccctt gctangggga gcatcagaca tccctagact tacaagtccc tcgtgtaata	300
aggtgaacta tggaaagcta tgatttgagg aaagttccct ctgattgaaa gagttcttca	360
aatatgaaga atgtaacact tatggggcac ctactcattg caaaacactc tactaggggc	420
tttcacctgt atgtttaact cattttgttg atttttttt ttttaagccc aaatttctga	480
gaggttaagg aacttgtctg gtggtggcgt ctctgggatt ctgacttttc cactgaccat	540
aacatgcac tggtctaaat tgagcggacc acccaggagg acgttggaat aaaaagaaat	600
gggaaggggg tggggagagg aatgggcata gaataaaaag gtagaaaccc ttgggatcaa	660
aggatgcaac tgaaagagca ccaaaatatg catcattttt tttaatatgt tgtctggtac	720
ccaaaattgg gatgcctctg tggatatcaac tttgacattt aaagaaaggc cataagatta	780
gatcattcaa ccataagtgg aaggaagaaa caaaataaaa taaaacctta caattccctt	840
tgaagtgtgat caggtgtcaa ggcagtgatt tggttttctt ttacaaactt tctttttcca	900
gaaaaatttt tactgtgggt ttggagaggt gtttacaata aattcatagc agagctccaa	960
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<210> 442

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-430-287 : insertion T

<220>

<221> misc_binding

<222> 481..500

<223> 10-430-287.mis1, potential

<220>

<221> primer_bind

<222> 215..233

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 617..635

<223> downstream amplification primer, complement

<220>

<221> misc_feature

385

<222> 938,965,972
 <223> n=a, g, c or t

<400> 442

cgaacaatat	aattatttaa	attatatattt	gcatggccat	ttgttaatgc	tagttctcac	60
atgtctgtaa	aattaggatt	tttaatatca	attaaatgaa	ggactttgtt	ttgttcactg	120
ttacatctcc	attgcctaga	acattgacat	ataaatattt	gttaaacgaa	tgaatgaaat	180
aacattctga	caattgaaga	agagatttta	agaatagctg	taacacatca	tacataaaaa	240
tgtaagcat	aaatatttgt	aatatatgta	ccgaaattta	ttgacctca	catgtttggc	300
agattcttaa	ttttttctta	ctggctttac	ttagggacgt	gcttccttaa	cacaagagaa	360
agagaagttt	gcccatgaac	atgaagaaat	gaagaaccta	gaagccattg	ttcaagaaat	420
aaaaccaact	gccctcatag	gtaagcattt	tctcctctcc	cttctccccct	accctttatt	480
ttgacctgat	tgtttttttt	actaccaatt	tttgagggtat	aatttagcct	ttttgaattc	540
aaaaaactac	acgttcgctc	aagcgacagt	accctgtaga	gacctagatt	tttaacttta	600
gtcctgtcgt	ctttctctta	ctgatctgag	atgaagcgta	tggccccctc	ctctaactca	660
gcctgttaat	acctggcacg	ttcagcactt	ttctaggcct	gattactcca	gatagacagt	720
ggttctcaaa	taagagggat	ttttgccctg	caggaaacat	ttggcaatgt	ctggaagctt	780
tgagttgtct	taactagggt	agcgggggtg	gaagggagta	aagggagggg	ctactgacat	840
ctagcagata	gaggcagcgg	aatgattcta	ctaaatatcc	tgtagtgcac	tggacagccc	900
ctgcgacaag	gaattatcca	gcctaaaatg	tcaatagntg	ctgaggttga	gaaatactgc	960
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<210> 443
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-718-432 : deletion T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-718-432.mis1, potential

<220>
 <221> primer_bind
 <222> 913..932
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 479..499
 <223> downstream amplification primer

<220>
 <221> misc_feature
 <222> 346,853..854,883..884
 <223> n=a, g, c or t

<400> 443

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gtaaatgct	aatagtacct	tcagtagtac	cttcagacag	ttgttatgat	gattgagaga	120
aaacatataa	aacaaattac	ttttatcaag	tgctataaat	agtaactata	atTTTTattt	180
ttcaggaagg	attactagga	ccataattta	gttaaaagat	gtaggctggc	aaatttggtc	240
taatattaaa	tagagcattt	aatagttgga	attgtcccca	aagaaaataa	tgtatataaa	300
agtacttgca	cataaaaatt	actcagaggt	tgttattcct	tattgntttc	tgttgttaat	360
attattttgt	aactctccat	cactctgaga	acatggacag	atgtgcttaa	agatataaag	420
atttctactt	ttatgtgaga	tgatggatta	gaattaaatg	tttctaaagt	gttccaactt	480
taggattcta	tgaaagtggg	aaaaaaaaaa	tcgtattttg	tttcaacatt	caggactggg	540
tgtttcataa	aattcagtga	ttcagccatg	cttgtgatca	ttatgagtca	gttgaaattg	600

386

atcatcacaa	tatatttgac	ccagaggaat	aaacttctca	ttcaacattg	taaattat	660
tgttttgc	aacaaaacaa	ctttaataaa	cttcagtaag	cttttagctt	cccttgctac	720
ccaaagtta	tttcataaa	agctcaagag	acaattggca	agttaaataa	ttcaagagaa	780
aaaatgttc	caagaagttt	ttatttgctt	tgcattctat	tccttatgct	acatattaat	840
tgtacagtt	gcnncaaagt	aagttttgta	gtaaaaatta	ctnncaaat	aaaaaaggta	900
catagatac	agcaactagc	aaattaactt	cgcaaagaat	aagatgtggg	ttacataag	960
ccatttatgc	cagttaacta	gaccagtctc	caactctctc	t		1001

<210> 444

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-269-301 : deletion T

<220>

<221> misc_binding

<222> 482..500

<223> 12-269-301.mis1

<220>

<221> primer_bind

<222> 204..222

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 634..654

<223> downstream amplification primer, complement

<220>

<221> misc_feature

<222> 626

<223> n=a, g, c or t

<400> 444

acacagaggc	accatctgtg	tcaactctgtg	tgtgggtctgc	catgttggtg	gggtggcact	60
acagactcag	gcagctgggc	agacaatacc	ttagccttag	atgatgctga	tgagcccag	120
gagtcagaaa	ctgtagtgca	gacaatgccc	tccttagggc	aacacaatta	agtgcaatag	180
atgactggct	tttctgttag	cctcttcatt	ggaacaaaaa	gcagcattac	tctaccaaac	240
agagggggagc	tggaaagaaa	ctacacagtt	tgcccagcct	agcctctgcc	ttgacacgga	300
accatgtgag	tctagacatt	cacctagatc	attccttggg	gaccaatgct	gctgacacat	360
taactcaata	gtttgtcctg	gcctgagagg	tcatgtaact	tgtagaaagt	ttagaagcag	420
agattagtgt	cattttatttg	ccatggctgt	gacaacaaaag	gaagggaacag	gagtgggaaa	480
acccaaggcc	accctggttt	tggtagatgg	tgacacgct	tccactaact	gttctggggc	540
aaagatccaa	atgcactatt	gggcctggct	atgctgcttc	tgctgggtcc	cccaaacatg	600
agcctccacg	ccatttctca	gttgtnattt	taccacatat	tatcacagtc	accggatttg	660
tacagaatat	ttggaacct	tactgtctta	agggctaccc	tttaaagaag	agaaaacaag	720
gttttaattc	aactgtctgg	aacattttat	gtttacttat	gtggaatact	acatcttttg	780
ttataaacag	gagggaatgt	ggacattcga	aggccccctac	cttttagcta	aaagcccata	840
tgaagcatat	ggatccattt	atacacacca	tgcttttcag	ctacattttc	ctaatttgcc	900
tctctggggc	caaccttgtg	ggactagcag	attcatgggt	gagttgaagg	atggtgacct	960
cttccatcag	cttttcttct	tcctccagtc	ttccaaccct	c		1001

<210> 445

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

387

<221> allele
 <222> 501
 <223> 2-13-398 : insertion G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 2-13-398.misl, potential

<220>
 <221> primer_bind
 <222> 104..121
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 506..525
 <223> downstream amplification primer, complement

<400> 445
 tgagctccca tcccgcatcc tgtgtggcac tctgtccatc aagccagtg tgaaggagtt 60
 cacggaaacc tcagctgtgt ttgaggatgg gaccatgttt gaggtatcg actctgtcat 120
 ctttgcaaca ggctatgatt attcctaccc cttccttgat gagaccatca tgaaaagcag 180
 aaacaatgag gttaccttgt ttaaaggcat cttcccccca ctaatggaga agccaacctt 240
 ggctgtgatt ggcttggttc agtcccttgg agctgccatc cccacagcag acctgcaagc 300
 ctggtgggct gctaaagtat ttgcaagtag gtggggccatt ctgtctttca ttcattttat 360
 caatgaacat ttactgaaca cctgctatat gcaaagcact gtgctaggga tacaatgaga 420
 acaagacaaa catgttcctt gacctctcaa ggcttaaaat ggggtgtggg ggatgccata 480
 ataggggaaa tttggggggg ttctagttag gggagttgga ctgttgaca gagcaaacag 540
 tatacaggaa gtcataaagg tgagggaag catgaaatgt gtaaggaccc agaaacattt 600
 tgggtggaag gaataaaag cagaggcagg gagtggcaag aaatataggt ttataagcca 660
 cgtaaagag cttaaacttc tcatagggat taaggacttc gcaagatttt aagcaagaaa 720
 aaaatagcag aggataactg caatgtcagg ctacattata aagattggaa gggccctggt 780
 gaggttgga ggtgtgccag aaacctcact ggtgtcaact tctgtcagaa taacaaagtc 840
 aggccactct gattctcatg acaatcttct tcttctctcc ctctactcta gacctcatgg 900
 tctccagggg ctacaagtat gcttatgtga ggaaatcaag aatatgagga ttacatggag 960
 aaaggcaatg tctcaaatat attaatattac tccagtcata c 1001

<210> 446
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 2-28-132 : insertion T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 2-28-132.misl, potential

<220>
 <221> primer_bind
 <222> 370..387
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 769..793
 <223> downstream amplification primer, complement

388

<400> 446

tattcagggg	gttaaaggaa	gacaaagggt	tttaaattggg	gaaaaaatac	aattacataa	60
ttgttttgaa	ataattatat	aaagagcaat	aacaagggtg	atgccagtct	gagattggac	120
agttactgag	cagatgttct	tgtagaagtc	atTTTTgtgt	aagattatga	tggcttttgt	180
gtaagggtgt	ggTTTTgtta	gtTTTTgtta	tcaggcacac	atcatgagaa	cccgtctctt	240
ctggcctttc	ccaattctat	ttgtcgggtt	tcttaacatt	agtgactcca	tctagattct	300
gacagttttc	atgagaactt	gcttttcttt	tctctctcaa	gtccttattc	agtattcagc	360
acccttaaca	gattagtccc	actgctgagt	caggcctctt	gcatgaagca	gcaatgagaa	420
agacacactt	ggccaatgtt	atcctggagt	aattctcaat	gatgccttct	ctgtgtttct	480
tcaagacaac	tgtccttagt	gtgagaaaat	gtccagattt	ctcatcctct	ggccaatgga	540
aggttgtcac	tcagagcaac	ggcaaggagc	agagtgtgtg	ctttgacgca	gttatggttt	600
gcagtggcca	ccacattcta	cctcatatcc	cactgaagtc	atttccaggt	gagaccgct	660
gggattccca	gcttttttga	gtaggtttcc	aggtacttta	tatgtagtgt	ggattgacaa	720
gcaggattca	ttgtgcaac	tgggcagaac	ttggctcaat	aagattgaga	cagagctaga	780
aagatgaaag	acaccaaaaca	tcattctttgt	ttctattggc	ctctgagtct	tcattcacaca	840
tagatctcag	agccaacttc	cttgggaagtc	actaagtcct	tggcataatt	ttagagaatt	900
cacatcaaac	tgggtctctg	ttggagaggc	ccttttagcc	atgtgcctgc	gttggccttt	960
ttctaccctg	ccaaacaccg	agcctttttc	acagggccat	a		1001

<210> 447

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 2-39-27 : deletion ACAATGACAGCATCATCATCA

<220>

<221> misc_binding

<222> 481..500

<223> 2-39-27.mis1, potential

<220>

<221> primer_bind

<222> 475..495

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 870..892

<223> downstream amplification primer, complement

<400> 447

ccagggacaa	gttaagtccc	accattagtg	taccaaattcc	cagtacttac	atacttacct	60
tgatgtgtat	atgctgcaca	ccaaggtaaa	ttacaaatca	aacatattct	gatttttgaa	120
aacataacttg	aactaatagt	cattttaaag	gcttactctc	tgggtataat	taagcttgaa	180
atcatccaaa	tattattatt	ttcatagctg	cagcaaagca	gctgaatttc	acagagctaa	240
caatgctgtc	tctgtgctga	atacttaata	agccagaaat	gaggcaaaag	gtgagcccaa	300
tgagcaagca	gtatactcag	tgatacacag	gacctccagg	tcaaagggtt	ataccatgtt	360
gaaaatcaag	gaaaaagaca	tattcttttc	gaaatttctc	tctgcttcag	tccaccaacc	420
tctcatggaa	tttattctct	gtacctgtgg	gagtcatttc	agtgttatga	accagcaatc	480
aagacacctt	atctgggtcca	acaatgacag	catcatcatc	atcatcatta	tcatcattac	540
aatcatcac	agtatttact	atatatacac	aaatctcttg	acatagatta	tctcatctaa	600
tccccaccac	aactatctga	tgcagatgtt	attatgcctg	ttttatttat	tttttagaat	660
tttttatttt	atttatttca	atagcttttg	ggggagcagg	tgggtgtttg	ttacctggat	720
aagttcttta	atgggtgattt	gtgggttttg	gtgcacccat	catctgagca	gtgtacacta	780
tacccaatgt	gtagtctttt	atgcatcacc	ccccactcca	acacttaccc	ccaagtcccc	840
aaagtccatt	gtatctttt	tatgcctttg	tattctcata	gcctagctcc	aacttatgag	900
tgagaacata	gaatgttcag	ttttccactc	ccaagttact	tcacttagga	taatggctctg	960
caactccatc	caggttgctg	tgaatgccat	tatttcatcc	c		1001

389

<210> 448
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 2-45-155 : insertion GAC

<220>
 <221> misc_binding
 <222> 481..500
 <223> 2-45-155.misl, potential

<220>
 <221> primer_bind
 <222> 347..367
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 764..788
 <223> downstream amplification primer, complement

<400> 448
 ttatgttctc tgcccagtggt cccagggttt attgggtttc aaagaggtag tgggtatata 60
 cagcctcccc aaggggaatt taggaagtaa gctgggtgtc acaaagactg gcattaaata 120
 ggtagagacc taggatgcta atatcttgca atgtgccaaa ataattgtcc ctgtccccaa 180
 cctcaccatt gccaatatta cccctacccc tcacagttag cgtcacaggc aggcaacaaa 240
 ctggtgtcgt cacagaatga ttgatggaac acatagactg cattcattac ctaaaccattg 300
 tcgtcacact gcagcaacca aagacaatcg cattaccagc ggggttagatg taggaagagt 360
 aaaaaacaaa aaatttttga atgctgaatt atcactaatt attttatttg atccttcagg 420
 agaattgtgga agatggccga gcaagtatct atcaatctgt cgttaccaac accagcaaag 480
 aaatgtcctg tttcagtgc tttccaatgc ctgaagattt tccaaacttc ctgcataatt 540
 ctaaacttct ggaatatttc aggatttttg ctaaaaaatt tgatctgcta aaatatattc 600
 agttccaggt attgtatttt tggggaaatg ggtttctctg cattagtcca gctcatattt 660
 agatagaaaa gttactctga taatgaaagc aattatgaat gaagtatccc attctaagta 720
 tttgttgaaa tataacagcc tcatataaaa cccaaaaagt agtgtcatta cccttggtat 780
 tatagattat atacattaat tgaagaggaa aatcatctgt taaaattaaa ggtttgaata 840
 ataatatatt gatgtcaaaa cttttttttt tttttttctc cctgagacag agtctcactc 900
 tgttgctcag gctggagtgc agtggcatga tctcagctca ctgcaacctc tgccttccag 960
 gctcaagtga ttctcctgcc tcggcctcca gagtagctgg g 1001

<210> 449
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 2-4-391 : deletion G

<220>
 <221> misc_binding
 <222> 481..500
 <223> 2-4-391.misl, potential

<220>
 <221> primer_bind
 <222> 111..132
 <223> upstream amplification primer

390

<220>
 <221> primer_bind
 <222> 513..537
 <223> downstream amplification primer, complement

<400> 449
 ttatccctat atgttcattt gtgaatgaat atttattaca tcattataaa aaggattttt 60
 aaactatctg tatgtttaag agtatatgtt gctactatgt aagagtatat gctgttactg 120
 taaagacatt gcattactac tgttgacctc agagcacgcg cctcttgctt aattctagga 180
 ctccctaacta agtcttttga gtttcagctg gaagaatgct ggaggaatac ggaactcctc 240
 ccattttctca cagccacctc caactcttaa aaacgcttcc aactgcctcc cagcacacaa 300
 ccaagggaga aaactattct gtcaaagaga cgggtgccaaa aggcaaaaac aaaggtaagg 360
 atgatcgctg gggaaagaag ctgaaaagga aaagctcaga actctagctg gaaatttggc 420
 tcacatccct agtatgttac tgcatagtct ggctttgttc aatgggtcgc ttttaaata 480
 taaagctaga tgtaagcaag gtttgcaaca aagtccataa gaaactcagc ttttctcaa 540
 ggcaagaaga gagcaggatt tttgactggc tctttattca atagtgtctg ttattaaatt 600
 accactgcta caatgtttaa agccaattac ctgagcacat cataaggatt ctcttaccgg 660
 ttgtcccagt taagtaatgt tgattgatca actccttgac aggagctgat ggcaaagaag 720
 gtagctgtga ttggagctgg ggtcagtgcc ctaatttctc tgaagtgtctg tgtggatgag 780
 ggacttgagc ccacttgctt tgagagaact gaagatattg gaggagtgtg gaggttcaaa 840
 gtaagtgaga ttttcttggg tcttgaacag gttgtgttgt tatttcaggg tgaatcacag 900
 ttactgatgg gtcataattga gaaatttatt aaacaactct gatcagattt tatttctatt 960
 tattgatgtg gccataatgg aactgaagtc ataggctggc a 1001

<210> 450
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-345-410 : deletion TAA

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-345-410.misl, potential

<220>
 <221> primer_bind
 <222> 96..113
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 601..621
 <223> downstream amplification primer, complement

<400> 450
 actcctaagc tgctaggaat gctaaaatgc taggtctcct tctcagatcc caatgggcag 60
 ccctgccaaag ctagcttgac tagatgggtt gtctcataat cctgagacaa cgcagacgct 120
 ctgcatacct tatcaccacc tttcaacctc ctggggctct gtgattgatt tatttaacga 180
 cttcagagca ggggtgaaaca ctgctctgca tgtctcacta tatatctcac tatttctaga 240
 tcttccattt ttaaaaggaa ttgggattca ctcatctac aagtattgtt cagcatctac 300
 tctagagcag atacagtggg gagggaaaaa aagtctcagc ctccatggaa cctataaatc 360
 tagtgggaag aagagagact aaacaagtgc accaacaat aattacaata tgctacttgc 420
 tatgagggta catagagaac atgaaagacc aagttagaat acacagctga gacattaaaa 480
 atgaatataa atcctcttaa taaccactac tgcattgcaca aatgaggcct tatacagtat 540
 gtcgtattgg ggtaaaaaaa aaatcttcta aattaaaaaa acgcaaagt ggtaggagg 600
 cattcaccaa acattaactg aagtcattct tggcttttaa caccagagta aagtgcattc 660
 acttttttat tttaaattaa ataccgaagc tgggtgcggg ggctcatgcc tgtaatccca 720

391

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gcacttggga ggctgaggtg ggcagatcac ttgaggtcag gagttcgaga ccagcctggt 780
caacatggtg aaaccccatc tctactaaaa aaaaaaatac aaaaattagc cgggtatggt 840
ggtgggcgcc tgtaatccca gctacttgag aggggtgaggc aggaaaatca cttgagctca 900
ggagggcgag gttgcagtga gccaaagatca tgccactgca ctccagcctg ggcaacagag 960
cgagagactg tctcaaaaaa aaaaaaattg aatacctaaa a 1001

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<210> 451
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-358-353 : deletion AGCC

<220>
 <221> misc_binding
 <222> 481..500
 <223> 10-358-353.mis1, potential

<220>
 <221> primer_bind
 <222> 149..167
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 577..596
 <223> downstream amplification primer, complement

```

<400> 451
actggatgta tgtgttctca ttgcctgcct gcaacctaga attcctgccc aggaggagtt 60
cttcaaacgc tatgaaagat gttcccaccc cctgccatgc agctacacta aaaggacata 120
ttgatttctc tccagaattg tgtttatgct gaccactaaa tatcaactta ttaaaaaaaaa 180
aacttacgtg gttttaattt ttttttcgct cccccctcgc ccacaggaga actaatgaca 240
gttgccagat ggatgaggga gtttatcgca aaccatcctg actacaagca agacagtgtc 300
ataactgatg aaatgaatta tagccttatt ttgaagtgtg accaaattgc aaatgaatta 360
tgtgaatgcc cagagttact tggatcagca tttaggaag taaaatatag tggaagttaa 420
actgactcat ccaactagac attctacaga aagaaaaatg cattattgac gaactggcta 480
cagtaccatg cctctcagcc agcccggtgtg tataatatga agaccaaag atagaactgt 540
actgttttct gggccagtga gccagaaatt gattaaggct ttcttttggt ggtaaatcta 600
gagttttatac agtgtagatg tacatagtaa agtatttttg attaacaatg ttttttaata 660
acatatctaa agtcatcatg aactggcttg tacattttta aattccttact ctggagcaac 720
ctactgtcta agcagttttg taaatgtact ggtaattgta caatacttgc attccagagt 780
taaaatgttt actgtaaatt tttgttcttt taaagactac ctgggacctg atttattgaa 840
atttttctct ttaaaaacat tttctctcgt taattttcct ttgtcatttc cttgtgtgtc 900
tacattaaat cacttgaatc cattgaaagt gcttcaaggg taatcttggg tttctagcac 960
cttatctatg atgtttcttt tgcaattgga ataatacatt g 1001

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<210> 452
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 10-360-190 : insertion T

<220>
 <221> misc_binding
 <222> 481..500

392

<223> 10-360-190.misl, potential

<220>

<221> primer_bind

<222> 312..329

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 713..731

<223> downstream amplification primer, complement

<400> 452

gtataatatg aagaccaa	gatagaactg tactgttttc	tgggccagtg agccagaa	60
tgattaaggc tttctttggt	aggtaaatct agagtttata	cagtgtacat gtacatagta	120
aagtattttt gattaacaat	gtattttaat aacatatcta	aagtcacat gaactggctt	180
gtacattttt aaattcttac	tctggagcaa cctactgtct	aagcagtttt gtaaattgtac	240
tggtaatgtt acaatacttg	cattccagag ttaaaatgtt	tactgtaaat ttttgttctt	300
ttaaagacta cctgggacct	gatttattga aatttttctc	tttaaaaaa ttttctctcg	360
ttaattttcc tttgtcattt	cctttgttgt ctacattaaa	tcacttgaat ccattgaaag	420
tgcttcaagg gtaatccttg	gtttctagca ccttatctat	gatgtttctt ttgcaattgg	480
aataatcact tgggtcacctt	gccccaaagt ttcccctctg	aataaaatcc cattgaactc	540
tgatggctgt tatcaaagga	acttttcttt gtttaaattt	gctgatgcag gaattaagtt	600
taaacacaac tctatagaaa	gaaaggagat tattaccag	aattcacatg tagtgattat	660
taaggacaat tttttttttt	aactaaaaaa gttggcggca	ggggtggggg gtggcaatca	720
tttttcttcc tatacataca	aaggatattg tcaaaaatgg	cgttcttctc ttgtggcctg	780
ttattctgat tgctgctgta	tacagttttg tcaactctta	gtttttagtt aagcatactg	840
atagactttc ctctaaaagc	cattcactcc agattttacc	tggggaatat tctacatact	900
gcttactttc tctataaaac	tcatcaataa atcatgaaag	gcaactgagtt ttgtaaatca	960
ggaccctaaa tgtttaattg	taaataagtt tcagataatt	a	1001

<210> 453

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-365-374 : deletion A

<220>

<221> misc_binding

<222> 481..500

<223> 10-365-374.misl, potential

<220>

<221> primer_bind

<222> 128..145

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 530..548

<223> downstream amplification primer, complement

<400> 453

tcaaattctt cttttacacg	atgactctta ggtgaccaat	ttatgacgtt tggttgtctg	60
ttttagtacc ttaacaagaa	atatccgaca taggagagga	gaaaagggtg tcatcaatgt	120
accaagtaag tctactgaga	ggtgggtgggg tgggagagag	acatgttgta ttgttgttta	180
atcctggatt ctaaaccatt	tttatttttg tatttttata	atacagtatt taaggacaag	240
aatacaccat ctccatttat	agaaacattt actgaggatg	atgaagcttc aagggtcttc	300
aagccggatc atattttacat	ggatgccatg ggatttgga	tgggcaattg ctgtctccag	360

393

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gtatagtttc aaatatacag agaggcaaag tgttccatcc atttctgttt tttaacttct 420
ttatatatgc atgtttcctg ttccaaaaat cacattttta tgaggttgaa atggtagctg 480
gtatgccttt ctgaaaaaca atgaagtat attagtaa atcattggaag ctgtctatga 540
ctaatagttc tacagactct gttgttcacc acaaaggat atacggtata tataccttta 600
taactgtaat ttcagttaac ttaaaatgca atataattctg tcattgtttc ccttctcttt 660
ttatatgcct agtttttact gccatctcgt gacaggctag tgaggtggtt taaatattgt 720
tcaaaactct gaaaatgagc tctgatggaa gtattccaat gattttgtga tccaagggat 780
ttgtgcaaag ctgtctagcg gtacaaaaag aataaatatt tagcagcttg tgtttgctct 840
gccctgagt aaagtataca ggagcctgtc tctgtttacc catttaaaaa tttcctgga 900
tctgtttaa tgatgggtcc cctggcagtg agtgtgtcca agctcactta ggaccagagt 960
ggaagagcat ggaacccatc aggtggccac acacaagcct g 1001

```

<210> 454

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-367-58 : insertion GTGGAG

<220>

<221> misc_binding

<222> 481..500

<223> 10-367-58.misl, potential

<220>

<221> primer_bind

<222> 444..461

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 855..874

<223> downstream amplification primer, complement

<400> 454

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ttccttctct gacttcactg cttggggagc atgctaata ttccttggtg ttaataactt 60
tgcaattctt aaacaggtga cattccaagc ctgcagtata tctgaggcca gataccttta 120
tgatcagttg gctactatct gtccaattgt tgtaagtaga aattacctct tattttaaat 180
actacttcgt atgaaataag atagcatgtg cagaatttac tgacagtgtg ctatttaagt 240
ccagttaaga cctcagtcag agatggacta atataaatag tatgtaggtt taggtataat 300
gaactgagag tctacactgt agaagtttac tcttgctagt acaacattga tttgttaa at 360
gtgaagtttg aatgtggcca ttttccctcc cccatacttc atgtcctcac attagagaga 420
ggatgattta agtgaatcaa acccaaggaa ctggattctt cctggtatat ttcactgtaa 480
gataggcaca ggtacatgtg ctctgtatgg gttgcataaa catgcttttt gatcagaa at 540
ataactgcat ggagcttttt ttagcatgta agtgacactt tgaatttgca ggagctgact 600
tttgtttggt tttgatggc tttgagtgt gcatctccct tttaccgagg ctatgtgtca 660
gacattgatt gtcgctgggg agtgatttct gcatctgtag atgatagaac tcgggaggag 720
cgaggactgg aggtgggaat tgtttttcct taatagccct ttttaagtcaa gcaggtaaaa 780
tggatctttt gtaactactt gcaatttcag gatgtctccc tgcaattttt atctgaaatg 840
gggaaaaga tttggtctag gtggggaggt aatttttacc gtatgttgat gtctgtattt 900
gttttagctt catttaaaat tagtagtccg attttctcat attttggaag tgctgatggc 960
tgtttttacc aaaaggcttt ttggtgccac atgagtgttt t 1001

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<210> 455

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

394

<222> 501
 <223> 12-468-424 : insertion T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-468-424.misl, potential

<220>
 <221> primer_bind
 <222> 76..95
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 583..603
 <223> downstream amplification primer, complement

<220>
 <221> misc_feature
 <222> 13,23,255,639,967,971
 <223> n=a, g, c or t

<400> 455
 gtataagtgc tgnttaagag tanttgattg ccttttcttg gtttaaatatt aaaccagggg 60
 gttctgccaa agaccgcata gtttctctga tatgggtcca aagggatatt ctttccactg 120
 aaacactgta tgtataccag taaatgcttc ctaatggtag atgataaata tttttgttgc 180
 ttgtagatag aatTTTTTcca tctagtgtaa gcttaggatt gttttctttt tcccagtgac 240
 atgtacagtt tcacntactc cacttaaaaa aaatcggttag ctcagataaa gtgtgtggca 300
 catgaaatga attttgccaa ttcaccaccg aaatccctgc tttatatctc ttcagtggaa 360
 cactaaacca acttctttcc caagtacact gatttgatct ttacaaatta tatgaatgta 420
 ttaaattatc acatgtgccc tgaaactgtg tacatctatt atgtatcatt agagagatgg 480
 aaaaaaaaaa agaaaactgc ttagtaaaagt agaaaaata gttttaaagt aattttgtaa 540
 ggctaattga agacttactg tataaaaacaa aaaggatttt aaccacattc aaattattga 600
 ctgttttggg gcttttcagg aatcacttaa aaagcaccna agttcacagc caggcacggg 660
 ggctcatgcc tgtaatccca gcactttggg aggctgaggt gggcagatca cttgaggtca 720
 ggagtttgag acaagcctgg tcatcatggc aaaatctcat ctctactaaa aatacaaaaa 780
 ttagacctgg tggcatgtgc ctgtaatccc agctactgag gagtctgagg catgagaaac 840
 gcttgaacct gggaggcgga ggttgcaagt agccaagatc gtgccactgc attccagcct 900
 ggggaacaga gcaagtcttt gtctcaaaaa aaaaaaaaaa aaaagcacta agttcatgac 960
 aggttanggt nagccctcc ccccccccc caaagtcagt t 1001

<210> 456
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-481-293 : insertion T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-481-293.misl, potential

<220>
 <221> primer_bind
 <222> 774..793
 <223> upstream amplification primer, complement

<220>

395

<221> primer_bind
 <222> 333..353
 <223> downstream amplification primer

<400> 456
 taccattga actctgatgg ctgttatcaa aggaactttt ctttgtttaa atttgctgat 60
 gcaggaatta agtttaaaca caactctata gaaagaaagg agattattac ccagaattca 120
 catgtagtga ttattaagga caattttttt ttttaactaa aaaagttggc ggcaggggtg 180
 ggggggtggca atcatttttc ttcctataca tacaaaggat attgtcaaaa atggcggtct 240
 tctcttggtg cctgttattc tgattgctgc tgtatacagt tttgtcactc tttagttttt 300
 agttaagcat actgatagac tttcctctaa aagccattca ctccagattt tacctgggga 360
 atattctaca tactgcttac tttctctata aaactcatca ataaatcatg aaaggcactg 420
 agttttgtaa acaggaccc taaatgttta attgtaaata agtttcagat aattattata 480
 gctttgcgtt gaagtttggt gttttttttc tcaactagtt aagtcaactg cttctgaaat 540
 aactctgtat tgtagattat gcagatcttt acaggcataa atatttaaac tgtaatatgc 600
 taactgaag agattgcaat aaagctgctt cagctaaccg tgtttatggt taaatactag 660
 ggtttgttct atattttata catgcatttt ggtgatttaa agaatgcctg gttttcgttt 720
 gcaatttgct tgtgtaaata aggttgtaaa aaggcagata aattgaaatg tttgtggtat 780
 gaggaataaa aagaatggaa ttagctttca ttcagaaacc tttgagtgtg tgtgagtccc 840
 acagctaac aaatagtaga agagtttggg ttttgtaatt aaccctaaata ccatgaaatt 900
 attttttcat cattgcgacc tcagatgttt ctagaaagaa gcatagtgat gaagacaaac 960
 agatgccgta tctcccctag tagctatcaa ccccggtggg g 1001

<210> 457
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-499-86 : deletion GGG

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-499-86.mis1, potential

<220>
 <221> primer_bind
 <222> 567..586
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 136..156
 <223> downstream amplification primer

<220>
 <221> misc_feature
 <222> 77,302,451,665
 <223> n=a, g, c or t

<400> 457
 aaacttactg caacctttgc tttccagcct tccacacaca cacaagtctc catggaatca 60
 cagggcagtt gcaactnccc ctttcaacag gaaaactgca acagcctccc ttctacccaa 120
 aaggcatcac gtcatttaaa agaaggatga ggcagggcag tcagtaataa caatggcaac 180
 cacaataggt gtcactccat tttgatgtta ggaaactcaa cagagaaaaat cagagagggt 240
 gaatgagttg ctcaaggtca cagacctaa aaaaccatgc tcaggatttg aaccaaggac 300
 tngcctctct ccaaacacac ctatgccatc tcccataaaa ggactggatt ttttctgtc 360
 ccatggctgt ttttacctct tgctgagcct atcagctgag gtacgtaggg taagggtgtg 420
 ggaagcacia actcctccat gtgcaatggg nttgaaacac ctattccaca ttactgctgt 480
 tgttgcagca gggataaagg ggggggtcgt gacctaccaa aaggcccctg aatttatttt 540

396

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tcagcttttta gcttatatatt ttgtttctat tgtaccattt gatgcatgca cttaagtgcc 600
tttaaaaagg aaactccaaa cagctgagaa agaaacgtta taaaattgat gacatctttt 660
ttttnttttt tttttttttt tttttgagac agagtcttgc tctgtcgccc aggctggagt 720
gcagtggcat ggtcttgggc cactgcaatc tccctctcct ggcctcaagc aattctcctg 780
cctcagcctc ctgagtagct gggactacag ccacctgcca ccacaccag ctaagttttg 840
tatttttagt agagacgggg tttcaccatg ttggccaggc tggctctcaa ctctgaact 900
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<210> 458
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-500-217 : insertion CAATA

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-500-217.misl, potential

<220>
 <221> primer_bind
 <222> 286..306
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 714..734
 <223> downstream amplification primer, complement

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<400> 458
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gggctgaaat gatcgctcctc ctgctgcctc agccttccag gtagctggaa ttacagacac 180
aaaccaccat gctcagcttt ggaaagagtt cttaaaggaa ttctaattag tggcctcaga 240
caaattctag agaggttcag tcacatccat aaaacaagta ttatagattg tgcttattta 300
atgggtgagta ttctcaccag tagagcagat gttgaatatc caaggtagtg atttaaaaga 360
ccaaatgaag attaatccca gcaggatggt gaagaaatgg aaattatgga aatcctgaag 420
catggaaagc tctggaaaat tcaatgtttg tgtaataatt tagaagagga gaatagttta 480
tataggaaag atatacaata atcaaagaaa taatagaatt tttccttaat aagtcttcct 540
taaggatgag acaaatatatt aactcaaatg taggcattta ttaatctcaa agagaaaatt 600
aactgtccgg acaggagaaa aaattaggag acatgaaaag gggggaaaat caactgatat 660
tacttttcat ttgcaacatt aaatgctaga tggaaagaag ttttcagaat ctcgagagg 720
aaagaattaa caaccacaga attatcttct cagccaaatt attctttaa tttcaggtga 780
ttctaacaaa actgaatgga tcaagttagg gctaaaagta tgccagaagt cttatctagt 840
gtcttggttt gtttgggctg ctgtaacaaa aataccttac agtgggtggc ttataaacia 900
caggaatgta ttgctcacag ttctggaggc tgggaagttc acgatcaagt caccggcagt 960
ttcggtgtgt ggtgagagct tttgctctct ggttcataca t 1001

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<210> 459
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 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-511-101 : deletion A

397

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-511-101.misl, potential

<220>
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 <222> 585..602
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 152..172
 <223> downstream amplification primer

<220>
 <221> misc_feature
 <222> 129,588,664
 <223> n=a, g, c or t

<400> 459
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 aactcccact tagacttcta ggaactcatc tttgcagctc cctccttact ggtaccatgc 120
 cctgcaaaant tccaaacttt ttgcatccct gaacttcagt ctctgcctct tcagctcagg 180
 gagactgctg tgctctgttt gggctccact tcatggcctc tgttggttcaa aaagttgccc 240
 ccaaacctgg ggcaaatgtg ctgctcactt cataggcttc ctttctctga aggagcacag 300
 ttctatgctg ccttgcttcc aacgtccgaa aatagctgtc atttattttg tcatttaaaa 360
 accttgaatt acagtaaggg aaagcatatt cataaatgaa atgatgtaaa gactttaagt 420
 ctacctaaaca tctagttttt ttcttttttg ctaattggac tattcctctt ttcattcatg 480
 tcctttaagt ttgtttatgg aaaaaaatta tgacgaccac actcttctgt gggtatagga 540
 actttcacac ccattacaac attatgcatt tatattctga cgaccttnga tgggacacac 600
 aaaacctgat tcttgcaact ttgccatgaa ctttgtgatt tccagagact ggtaaccact 660
 tagnccccac aaacttctaa ttctctacac agattatctc tctttccttg actcttatgg 720
 tttgtaaaata aatgtctttt acacacaact ctgaagcgcg tcagatttta tggtaaccaca 780
 tagggctata atgcctatag aaatgggacc aaattgaaat tttggaaatc tctcttggt 840
 ttgtagacta gttggtcgta acttccaag tcacacttct gatacacctg tgagggatta 900
 ctgctttgtg ccacactaga tgacctgcaa ggttttctaa ccatagataa agccagtctg 960
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<210> 460
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-586-443 : deletion C

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-586-443.misl, potential

<220>
 <221> primer_bind
 <222> 59..78
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 523..543
 <223> downstream amplification primer, complement

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<400> 460
ttgacatttt atgttcagct tgcacttctc tttctcttct ttagtgctg caacttctca      60
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gcacattgac tgtaattttt agccagtatg ttgataactg atttctccac agcagcccag      180
attacctatt cctgggtttt gctgctttta agcaacttgt catgggcata gcattgtatt      240
tgaaaattta tgacatactg ctctggtatt cattctaatt tttcagagtc cgaacactga      300
cttctgaaga taaaagtact cctttgtgtc tcttagagtg attatcagat gggaaacatt      360
ttggcttttt catgactcct ttggaggaga atattctatg gggagggtgg atgttattct      420
ttgccagggt acaaggaaac cctgagggtc ctggtggcat aaagttttat tgacttcaac      480
aaagagtga gtaaacactt cagagaatct ctgtgttatt cactcaattc tagtcagctt      540
gaccttaaac cctcccggct cattcctgcc ttgggggtctt tgcacaccta ctatttcttt      600
gcctggaatt gcctttctcc aggtattgcc atggttggtc cccttacctc tttcattttt      660
ctactccatt atcacctcct gtgagtcgac tctgttaaca cctgataata aatctgacag      720
ctgtctgaaa ctttctacct acccctcttt cctgctttat tttttgctat agcactaatt      780
actacctgat gctttttaaa gtgtttgttg agtgggtttat tgtctgtctt aagctccagg      840
gaggcagatc ctctgccata ttattagaac aatgcctagt acatggaagg tgcaccactg      900
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<210> 461
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-593-287 : insertion TAAAT

<220>
<221> misc_binding
<222> 481..500
<223> 12-593-287.mis1, potential

<220>
<221> primer_bind
<222> 771..788
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 251..271
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 135,300,327,765,797
<223> n=a, g, c or t

<400> 461
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aacgtatcct ttccatattc ccctctctca tccctgttct ccttcagtct gctaggtcaa      120
agtataagga ttctncaaaa atgcagagta attatgaaaa ttctgtttta aaagcttcag      180
aatagaatgt ttatatagca ttgatttgga gctaagggtc atattctggg aacataacaa      240
ggtgctatct agtgaatgtg tgattgtgta gtcatggagc tgatgtccct gccatagaan      300
ttacagaatt atctaaaaag ggaaatncta taataatggc cttcaatgct cccacacttg      360
gactagccat tgccataggc agaaaggcaa tctcatcttt actgtgtgtg caaacagtac      420
tttaatgtaa tgtgtgctta atataagctt tctttaaaaa aaaaaagggt ggctcctgtt      480
tttgaatagc tatttttaag atagatatag ttagggaatct aaatgtgttc tatatagtta      540
atatccatta tgagggtggc ctgaaaaaat aacctagtat aagttggatg gctttgcttt      600
tctgcttctg ttataaccca tttttctaga aaagcttcca cttctactta aagataagag      660
gcaaatcatt ttctgttcc cttatgcaca tagatgttca cttaccaaat atttatagag      720

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399

tggcccagcc	ctctgcagac	agtgggtgagc	aaaaccagac	atggnttcct	gccctcatag	780
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ttatagcagt	gatgaaatag	ttgtgtgtgt	tgctggagat	cacataacgt	tgggggacct	900
gttatgagaa	agtgggtgtt	gaaataagac	ctgaagatgt	gaaatcaaag	gcgtgaggct	960
gggtgtggta	gctcacgcct	gtaatcccag	cactttggga	g		1001

<210> 462

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-795-383 : insertion CA

<220>

<221> misc_binding

<222> 481..500

<223> 12-795-383.misl, potential

<220>

<221> primer_bind

<222> 119..136

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 679..696

<223> downstream amplification primer, complement

<220>

<221> misc_feature

<222> 408,416..417

<223> n=a, g, c or t

<400> 462

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ctagggctgc	tcttttttagt	aaagctaaac	aaaacctggc	gtcctacagc	cttactaacc	120
tttggttaatc	cgctgctcg	tcacatcttt	gtatggcatc	tgtgctcact	catgggggaa	180
agagattctg	gaagaagcaa	cagcaataac	caaggcaaat	gtggggaagt	gtctgcatgg	240
gttggttagca	tgatgtgtgg	ggcctaggtt	ttacttcatt	ttcttcgaat	agtgaggtcg	300
ttaagtcacg	ccatttgaat	aattttgtat	gaccataggg	tgacatactc	atccctgttg	360
tcaattctcc	taagaaattt	ggtggcaaat	ttcatcactt	aagccagnaa	agtggnnaaa	420
tttggattag	ggatgccaaa	taagcaaate	tttatattga	tagaaatgta	cataggcgta	480
tgtcttaata	gacttccaca	ttattgaggg	gttttttttg	gttttgtttt	gttttttagt	540
ttttttggtc	ttatttttaa	atttggttaa	ggcttttttg	cttgcttttt	cttcgattta	600
attttccttt	tttacatttt	aattttggtt	attttggggc	cattttttga	ttttgttttt	660
ccaaaggacg	cggattctga	tagcggggac	gattctgaca	agaggctcgtg	tgaagagagc	720
tggaaactga	ttacttctct	gagagaaaag	ctacctccca	gcaagttgca	aaccattggt	780
aaaaaatgtg	gcctcccaag	cagtgggaag	aaacgtgaac	caattaaat	gtatcagata	840
ccccaaagaa	ggcgcttgag	ttaagattcc	aagtgggtca	caatctcaga	tcttaaaatt	900
caggctgtca	aagagatttg	ctatgaggtt	gctctcaatg	acttcaggca	cagtcggcag	960
gagattgaag	ccctggccat	tgtcaagatg	aaggagcttt	g		1001

<210> 463

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

400

<223> 10-494-332 : insertion ATAAAA

<220>

<221> misc_binding

<222> 481..500

<223> 10-494-332.misl, potential

<220>

<221> primer_bind

<222> 170..188

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 574..591

<223> downstream amplification primer, complement

<400> 463

tttttcatat	agtggtttgc	cacatatagt	tttcttttga	aaagtgtaac	aacttttttaa	60
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tttccttata	tacctaatta	tgaaattaag	gaaatgaaat	atgagtattc	tatttacatc	180
agtcgagta	gttcttgta	cttaacatcc	cttggtcttc	tcattgttaa	tctctttaga	240
tttctaacat	tctatgactt	ttgagttcca	ctcatggaat	aagatatttt	cttcaactga	300
acaggttctg	tggagatttg	atgggaataa	accagatact	ttaggactca	atactcggct	360
gtacaagtgg	ataccccaga	atgatcttct	tggttaagtct	ctgaagaaca	aatactgaat	420
atattagtaa	cagattatta	aagtgttaat	agttatcatg	aaacaagctt	actgaacatt	480
tgttatggaa	aaacttaaaa	tgaaacttct	ttatatttat	ttccagtc	cgggggaaaa	540
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agagtatctt	tatttcaggt	gttattacct	cccacagaat	tttctggca	cttctgggt	660
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tttcaaagt	cactaaaagt	aacagctctt	ctgctatcac	cagggatgct	gcattttctg	780
taggattaaa	tccctaattc	taatcaaaaa	gtgatgacac	atttcataat	gaaatgtgac	840
ctgtctttcc	tcaattctag	caccaccacc	acctcactgc	ctgctgcctt	gcacacccta	900
catatcacac	tccgtgactg	tacttaagag	aacacattct	ggctgggcac	ggtggctcac	960
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<210> 464

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-494-380 : deletion GATAAT

<220>

<221> misc_binding

<222> 481..500

<223> 10-494-380.misl, potential

<220>

<221> primer_bind

<222> 122..140

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 526..543

<223> downstream amplification primer, complement

<400> 464

acaacttttt	aaatacttga	acttttctatt	gattatctta	tttgtctaag	ctactatttt	60
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401

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gaaaaatcat gatttcctta tatacctaata tatgaaatta aggaaatgaa atatgagtat 120
tctatattaca tcagttctgag tagttcttgt tacttaacat cccttggtct tctcattggt 180
aatctcttta gatttctaac attctatgac ttttgagttc cactcatgga ataagatatt 240
ttcttcaactg taacagggttc tgtggagatt tgatgggaat aaaccagata ctttaggact 300
caatactcgg ctgtacaagt ggatacccca gaatgatctt cttggtaagt ctctgaagaa 360
caaatactga atatattagt aacagattat taaagtgtta atagttatca tgaaacaagc 420
ttactgaaca tttgttatgg aaaaacttaa aatgaaactt ctttatattt attttccagt 480
cccgggggaa aagaataaat gataattgtt ggcattttat gatatgcacc cacattcttt 540
acaatcagag tcagagtatc tttatttcag gtgttattac ctcccacaga atttttctgg 600
cacttctgg gttgtcttc tttctcatat ttctacaact ttacacctgt tctttctcc 660
tctgtagggt tatttcaaat gtcactaaaa gtaacagctc ttctgctatc accagggatg 720
ctgcattttc tgtaggatta aatccctaata cttaatcaaa aagtgatgac acatttcata 780
atgaaatgtg acctgtcttt cctcaattct agcaccacca ccacctact gcctgctgcc 840
ttgcacaccc tacatatcac actccgtgac tgtacttaag agaacacatt ctggctgggc 900
acggtggctc acgcctgcaa tcctagcact ttggggaggct gatgcagggt gattgactga 960
gctcaggagt tcaagaccat cctgggcaac atggtgaaac t 1001

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<210> 465

<211> 929

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 429

<223> 12-659-251 : deletion TT

<220>

<221> misc_binding

<222> 409..428

<223> 12-659-251.misl, potential

<220>

<221> primer_bind

<222> 179..198

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 611..631

<223> downstream amplification primer, complement

<220>

<221> misc_feature

<222> 80,605

<223> n=a, g, c or t

<400> 465

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tattgagata ataaatgaan cattcaaata tttaagtaat cattaggcag acataattcc 120
agtgtaaaga tgagtaaaaa attactaatg gtccccaccc tttttattaa tgtattttact 180
acattcactt tcaacttcca aataatgtta agcttttcat ttctaaagca atgaaaaggg 240
agtgagttta cttatatcca cttgtttcat aagttatatt cccatatctg atgattttaca 300
aagaaagcaa atctatcaat catctatgtc tgagaaatac attaactctg ttaaaaggca 360
catataattt gtttcgatt acaaattatt aagcactttt tccaagaaaa aaattcaagt 420
gacttttttt cccatatgtg cagaataata tcgcatgtgc tacaattgga aattatttaa 480
aggtggaaaa gactgatttg cagttcttta ataataggtc tgtttaaaat atcccaaatt 540
tgtggtgatg ctaaatttca ttctgctggc tcttaactct tcagtggcac aatccaaagc 600
gttgnacgca gtggtttata tggctgctga tagctaagcc atgtagtaca tgcctagtac 660
caacatgtgg tactgatttt ggaattacca agcaatcttc ataaactagt gtataatcta 720
caagttttta acgtgtactt gctatctgag ttttaaaagt aactacacat ttgcatcaaa 780
aaattagtat aggtgattac aagaatgtta tacaggatat aaaactaaaa actgctttat 840
aaatattcaa atatcaaagt tgcctgcatca gctcagagac gctgaagctg tgctggaggc 900

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402

agcagagtta atggcggcaa gtccctgtg

929

<210> 466

<211> 987

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-912-419 : deletion A

<220>

<221> misc_binding

<222> 481..500

<223> 12-912-419.mis1, potential

<220>

<221> primer_bind

<222> 83..103

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 554..574

<223> downstream amplification primer, complement

<220>

<221> misc_feature

<222> 86

<223> n=a, g, c or t

<400> 466

aagtttactt	attatcctgt	gaagtatatt	ttcatacctg	aattttacct	agcttcagcc	60
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gtgactatat	tctaaaatca	ttgtagtcac	gaaatcatat	gaataacctgc	ttggcctctc	180
cggatagggt	caagtttctc	acataagcaa	aatttactta	tttggcatat	acaatgtgaa	240
cataatctta	aaacctgact	ttggcttttg	gtgttattaa	taaggttctt	aatccaattt	300
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gtggctcacg	cctgtaatcc	cagcactttg	ggatgacaag	atgtttggat	cacctgaggt	780
caggagtgtg	agaccagact	ggacaatgcg	gtaaaactcc	gtccctgcta	aaaatacaaa	840
aattaaccag	gcatggtagc	acatgcctgc	aatcccagct	actcaggaga	ctaaggcaca	900
agaattgcat	gaaccaagaa	ggcagaagtt	gcagtgaagt	gagatcgag	cactgcactc	960
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<210> 467

<211> 806

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 306

<223> 12-914-28 : deletion T

<220>

<221> misc_binding

403

<222> 286..305
 <223> 12-914-28.misl, potential

<220>
 <221> primer_bind
 <222> 279..298
 <223> upstream amplification primer

<220>
 <221> primer_bind
 <222> 773..793
 <223> downstream amplification primer, complement

<220>
 <221> misc_feature
 <222> 536
 <223> n=a, g, c or t

<400> 467
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 atcttttagga ttgctgattc cttactctgt ttgaccaagt ctgctgttga agttttctac 180
 tgagtttttc aattcacttc acatatctttt tattaattgg atttcttttt attttttaaaa 240
 catttccact tctttgcaaa atttatcatc attttcctgg attattctct aaagtgtggt 300
 ttttttcaac tctctattca tatgtgctgt gatttctgaa cttttaaaat aggtgtgcac 360
 tgaatttctt gtcaaaaatt ttatggagca tctgaacctt aattctgcac tgtaacttaa 420
 aactagactt gcagtgattt ctaggctctgt gagatactta agcaataact ggagcttaat 480
 ctcaaatggt atacttggtt gcaggtcata gaaaagctcc gtatgagtaa ctgggnatta 540
 taaaaatacc tgccaaagat tcaggccttc ctttggtatt tggcccctgc agtggtatgg 600
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 aacccaaaag attcacagat ccatga 806

<210> 468
 <211> 1001
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 501
 <223> 12-624-307 : deletion T

<220>
 <221> misc_binding
 <222> 481..500
 <223> 12-624-307.misl, potential

<220>
 <221> primer_bind
 <222> 788..808
 <223> upstream amplification primer, complement

<220>
 <221> primer_bind
 <222> 340..360
 <223> downstream amplification primer

<220>
 <221> misc_feature
 <222> 132,690,865
 <223> n=a, g, c or t

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<400> 468
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aacttaaaatt gaccagcaat ccggtgctct ctatctgata aatttacagc ctgttttttg      120
acacctactt gnatatttta aatatttatt aataaatata ttagaatgtt aattaaaatt      180
tttaattatg gctaaaattt tagtaaacaa atttttaaaa ttttaatgtc ttatgtcaac      240
attttatgaa ttctacagta gtttagtgat ttcttcta attttaagggtt atatttgtag      300
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ctgtgaaatt tagcaaattt tgtggctgtc tcaaaaaaga gaatatagtg gaagttagga      420
gcttaacttc caaagctcaa aaaaattgtt aatacatttt ctctgtctgt ccttctgtcc      480
ttttctctgt gtttctgtca ttcttttttc ctttttctct gtctctccac tcgctttgga      540
gccctgtgct atatccacag tccccaggag aaatatacca tttggtgtag aaatacatat      600
gtatgcctaa taagtcacaa ttggccagc actgcagtag cttgagactt ttaatactaa      660
tcaccagata tgtgagtgat taaccttc an gatgattagc ccaagctacc ttaggacagt      720
aaccaactga gaaatgctgt gccataaaca cctaattgag cctggccaac aacctagaat      780
taaaacagat gatgataaaa tgttgctgtt ctaagcacct tcatttcaga gcagttgggt      840
aagcagtgat agacaaccag aaaaatatt ttacatatt tgagttatac tcctgtaata      900
atattaaaat taatatatac ctacaaaaaa agtgaatcta tattacattt tgtaactacc      960
tgtaacccag aaagagtagt cagcatagga tgggtgggtaa g                                1001

<210> 469
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-290-326 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-290-326.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-290-326.mis2, potential complement

<220>
<221> primer_bind
<222> 177..196
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 576..595
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-290-326 potential probe

<400> 469
atgctttgaa tgttcaaaga aaccaagtga tctctatggc taggcattcc cttaaactta      60
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aggacagcct acctcaggac tctcagcttc cttattacag tccagtttgt cactttttctc      180
cctcatgtcc actctgcagg atcaccggtt tccgactgag tctggggatt ttggccttgt      240
tgacctcctc aggtgccctg ggaattgcaa acagctttct ggatgaatat ctggacctca      300
atattgcaa gaaactgagg cggcaattct aactttttct cttcccttta atgcttgtag      360
aagctgttcc caccatgaag gtaatatggt atcatttgtt aaataaaaaa aaagctctta      420

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405

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ttctgttttt cttgaaatgg cttttagtaa acacacactt tagagaatac atttcctgtt 480
taagaactga aatttgcttg rggtaggtac atccatatca tcagtgggaag tgtgttggtgc 540
cctagtttta gaaatgcatg ctgaagtcac gaccggttgt gtagggacac agcagcctga 600
cccgtgtgct ggccgttccg aggactactg acatatcctg ccactctgac tgcttctctc 660
ttgatggaaa gtttcagaca gaagctgata aagcagctga gccctttcat tggttatagg 720
aaaacaacag ataggaaggc atgtggggga catcaggcaa acacatagag tagccagaga 780
agggagtcac caactgatag cacaaaaaca aacagggttat agaaggctgg gcgtgggtggc 840
tcattgcctgt aatcccagca ctttgagaag ccgaggcggg cagatcacia ggtcaggaga 900
tcgagaccat cctggctaac acagtgaac cctgtctcta ctaaagatac aaaaaattag 960
ccgggcatgg tggcgggtgc ctgtagtcc agctactcgg 1000

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<210> 470

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-290-37 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 10-290-37.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-290-37.mis2, potential complement

<220>

<221> primer_bind

<222> 465..484

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 864..883

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-290-37 potential probe

<400> 470

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aaaaaacggt aaggagaacc cagtaatttt gtattttatgc aaaaagtagc aggataaggt 60
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taatccatac tgtctgaggt caagtcttgc cagttcatac acaattagga atgagatggg 180
aaaatgcaag tataaaactg tgcaactgaat gtggactcta gttccttgca aaaattttgc 240
attgtctcca gaaagttacc gaggaaataa tcctgcctag ccttgataat gctttgaatg 300
ttcaaaagaaa ccaagtgatc tctatggcta ggcattccct ttaacttatg tgatgagcta 360
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ctcaggactc tcagcttcct tattacagtc cagtttgtca cttttctccc tcattgtccac 480
tctgcaggat caccggtttc ygactgagtc tggggatttt ggccttggtg accctcctag 540
gtgccctggg aattgcaaac agctttctgg atgaatatct ggacctcaat attgccaaga 600
aactgaggcg gcaattctaa cttttctctc tccctttaat gcttgacaga gctgttccca 660
ccatgaaggt aatatgggat cattttgttaa ataaaaataa agtctttatt ctgtttttct 720
tgaaatggct ttgtagaaac acacacttta gagaatacat ttctgttta agaactgaaa 780
tttgcctggg gtatgtacat ccatatcatc agtggaagtg tggttgcccc tagttttaga 840
aatgcatgct gaagtcatga ccggttggtg agggacacag cagcctgacc cgtgtgctgg 900
ccgttccgag gactactgac atatcctgcc actctgactg cttctctctt gatggaaagt 960

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406

ttcagacaga agctgataaa gcagctgagc ccttttcattg

1000

<210> 471

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-523-232 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 10-523-232.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-523-232.mis2, potential complement

<220>

<221> primer_bind

<222> 270..288

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 527..545

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-523-232 potential probe

<400> 471

acttcaggag	attttaaggg	aattatttaa	agaccatttt	gtaatgttct	gggtaactca	60
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agtaatctct	taagttcttt	agataagata	tggagtgatc	tttaggctca	ggaggcctgt	180
cttttgggaa	agtgtctataa	ctcacttcta	ctaccggcaa	cttaatacgt	aagagaatat	240
tcttggccct	gctctgaggt	ttaaacaatg	ttcaaccttg	aaagattgat	tttaaattga	300
aaggtcattt	aaactctttt	gtaagttctt	atattttgtt	aaaataggct	gaacattttac	360
ctctagatga	aaaatcaatg	cttcagtgtg	tacttttctc	ataaaataac	ctatgtcttt	420
atttttttct	gcagacaaaa	ctgtgtggag	ttttatccta	tattcataat	tacattgttg	480
atggctgggt	ggtatttcaa	ycaggtaat	gttaaaatac	agtcaactgt	gttctaattga	540
tgactatgat	gcttaaacga	ttaaggagta	gatatatggc	caggcacggt	ggctcacacc	600
tatattccca	gcactttggg	aggcccaggt	gggtggatca	cctgagggtca	ggagttcgag	660
accagcctgg	ccaaaatggg	gaaaccctgt	ctctactaaa	aatacaaaaa	ttagctaagt	720
gtggtggcgc	atgcctgtaa	tcccagctac	ttgggaggct	gagacaggag	aatcacttga	780
acccaggagg	tggaggctgc	agtgaactga	gatcgtgcca	ctacactcca	gtctgggtga	840
cagagactcc	atctcaaaaa	aacaacaaca	aaaaggagca	gatatgcaac	tatatagcta	900
ccaatcctgg	agactaaaca	aaataaacag	tgtgtgcatc	agagtgtctat	gttgcaggta	960
tatgaacttt	ggcttcattc	taatttaatt	caataatgaa			1000

<210> 472

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

407

<222> 501
<223> 12-449-300 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-449-300.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-449-300.mis2, potential complement

<220>
<221> primer_bind
<222> 783..800
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 325..345
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-449-300 potential probe

<400> 472
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actaactctt tctccaaaag aggatccaaa gtccctttat ccctctttgg gccatgatta 180
tttgtcttct aacagagtca cattgtctcc ttgagacgta aagatgcatt tagatgcagg 240
gggacggaag aaaggaaaag aaaaaatagt ttatatgtat atacatttgt atcaaaataa 300
gaaataaata ctcataatta ttacaatttt cctctgaaaag tagtcacatg gttatacctg 360
gtattttatt attttttatt attattatta ttatttgaga cagggtctca ccctgtcaca 420
caggctggag tgcagtgggt caattatggc tctctgctac ctctgccacc tgggctcaag 480
ccatcctctc accttagcct yctgaacagc tgggatacat gtgcactaat tttttttttt 540
ttgaaacaaa aatatattgtg tagaaggcac aaaagctaca atcacagact ccactgtgca 600
aaggcgcaac ctgcctcatt gatctctagt gtacaccaac ccagcttccc tttccattca 660
gcctgtgaaa ggagatagtg cttgggccat ttggtaaaag aaggggatgg gagatgatca 720
aaaccccaag taaggttcat ccaatatggt gtctaagcag caaatgacta attgctgaag 780
aaggagacta gacagaggat tagaggcagc catggggcca gtgcagctgt ggagagctct 840
gagcaaagaa acaagggttg caggtgagga ggcctaggat agaggccaga aggccaaagcc 900
tggggctgca tgtgcaactaa tttttgtatt tttttgcttt tttgatagag atgagatttc 960
atcatgttgc acagggtgggt cttgaagtcc tgggctcaag 1000

<210> 473
<211> 432
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 212
<223> 10-186-212 : polymorphic base G or C

<220>
<221> misc_binding
<222> 192..211
<223> 10-186-212.mis1, potential

<220>

408

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<221> misc_binding
<222> 213..232
<223> 10-186-212.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 413..432
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 200..224
<223> 10-186-212 potential probe

<400> 473
agtatgacga taggcagatg ttgtcttgca aaacgagcaa acagggcatat gaaatcagat      60
acctagctgc caaactatat gtgaggcatt tccgaagaat ttaacgacct cgatagagcg      120
cagtcaagtt tggatgaacag aatatgtctc tgaactagag gaggcctcac acaaggagta      180
gggtcagacc ccgcagtggg ggaggaggga gsagtagaaa cagtccagct cgccgcccga      240
gtaacctggg tcctgaatcg gcccgccctg gccagtgctc cagaagcgcg gagagggaacg      300
ggctggggcc caaaaaagag gggggagcct gaacgtccgg gggaaagttc ggaggcgcg      360
gaaccacgg atggaaccct gtctttgggg aaaaggacca cacctgtcag cagagtccgt      420
cagacgtgag aa                                     432

<210> 474
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-286-289 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 10-286-289.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-286-289.mis2, potential complement

<220>
<221> primer_bind
<222> 213..231
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 613..631
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-286-289 potential probe

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<400> 474
aaaaaaaaa gtatgattat tatcagagtc tctaggtgac agtgagagggc agcctgggtgc      60
aggggatagg gcacagtgtg aatctgctag actgggttca aatcctaaat cggccattca      120
gagcgtgaat acattagaac tggcttaaat tagcatttaa aatgtcaaca ggattaagta      180
agtagttcct tctcactttt tccacaggag gtgagaaaagg tctcagcaag gccctaggag      240
ggaagggcgt ggggatgaaa gggatccaga gagtctgtgc attggcagag aagatagtgt      300
aactggcact gcggctggag ggctggcccc acagtggagct acagccctgc ccgctggccg      360
tgggagagggc ttaaaacaaa cgccggaagc aactcccagc ccataaaaga tctgtgaccg      420
gcagccccag acctgcctgc ctctctgact tctgttccag agcaaaggtc attcagccgc      480
ttgaatcagc cttttccccc sacccgggtcc ccaactttgt ttaccgata aggaagggtca      540
gcattcaaag tcaagaagcg ccatttatct tcccgtgcgc tctacaaata gttccgtgag      600
aaagatggcc ggggaactcga tcctgctggc tgctgtctct attctctcgg cctgtcagca      660
aagtaagagg catgggaagt tcgtgtgtgt gcgctgtgtg gcgtgtgtgt gtgtgtgtga      720
caaggcttgc gggagagaga gggagggagg gagatgggtc cgggtgtttg ttctctactt      780
gcccttgtag gtagctctgg gtccctcagag cacagtcgcc tcagggtcac ccatgccgcc      840
tgctaccctc cttcccaggg gcaagcagag actgagaaca ttccagagat tagttctccc      900
aactggaacg ctgtggggcc tcagagctca gcgattctgc atcatctgtg attacgaccc      960
acagcccggt caaacgagcg ttagtagcct gtaacctgc                               1000

<210> 475
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-286-345 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-286-345.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-286-345.mis2, potential complement

<220>
<221> primer_bind
<222> 158..176
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 558..576
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-286-345 potential probe

<400> 475
ggtgcagggg atagggcaca gttgtaatct gctagactgg gttcaaatcc taaatcggcc      60
attcagagcg tgaatacatt agaactggct taaattagca tttaaaaatgt caacaggatt      120
aagtaagtag ttccttctca ctttttccac aggaggtgag aaaggctctca gcaaggccct      180
aggaggggaag ggcgtgggga tgaaagggat ccagagagtc tgtgcattgg cagagaagat      240
agtgtaactg gcactgcggc tggagggctg gtcccacagt gagctacagc cctgcccgtc      300
ggcgtggga gaggtttaa acaaacgccg gaagcaactc ccagcccat aaagatctgt      360
gaccggcagc cccagacctg cctgccttcc tgacttctgt tccagagcaa aggtcattca      420

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410

gccgcttgaa	tcagcctttt	ccccccaccc	ggtccccaac	tttgtttacc	cgataaggaa	480
ggtcagcatt	caaagtcaag	wagcgccatt	tatcttcccc	tgcgctctac	aaatagttcc	540
gtgagaaaga	tggccgggaa	ctcgatcctg	ctggctgctg	tctctattct	ctcggcctgt	600
cagcaaagta	agaggcatgg	gaagttcgtg	tgtgtgcgcg	tgtgtgcgtg	tgtgtgtgtg	660
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tacttgccct	tgcaggtagc	tctgggtcct	cagagcacag	tcgcctcagg	gtcaccatg	780
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ctcccaactg	gaacgctgtg	gggcctcaga	gctcagcgat	tctgcatcat	ctgtgattac	900
gacccacagc	ccgttcaaac	gagcgtagt	agcctgctaa	cctgcaggaa	gtgggtgtgaa	960
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<210> 476

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-286-375 : polymorphic base A or G

<220>

<221> misc_binding

<222> 481..500

<223> 10-286-375.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-286-375.mis2, potential complement

<220>

<221> primer_bind

<222> 128..146

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 528..546

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-286-375 potential probe

<400> 476

gctagactgg	gttcaaattcc	taaatcggcc	attcagagcg	tgaatacatt	agaactggct	60
taaattagca	tttaaaatgt	caacaggatt	aagtaagtag	ttccttctca	ctttttccac	120
aggaggtgag	aaaggtctca	gcaaggccct	aggaggggaag	ggcgtgggga	tgaagggat	180
ccagagagtc	tgtgcattgg	cagagaagat	agtgtaaactg	gcactgcggc	tggagggctg	240
gtcccacagt	gagctacagc	cctgcccgt	ggccgtggga	gaggcttaaa	acaaacgccg	300
gaagcaactc	ccagcccat	aaagatctgt	gaccggcagc	cccagacctg	cctgccttcc	360
tgacttctgt	tccagagcaa	aggtcattca	gccgcttgaa	tcagcctttt	ccccccaccc	420
ggtccccaac	tttgtttacc	cgataaggaa	ggtcagcatt	caaagtcaag	aagcgccatt	480
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tgtgtgcgcg	tgtgtgcgtg	tgtgtgtgtg	tgtgacaagg	cttgccggag	agagagggag	660
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agcctgctaa	cctgcaggaa	gtgggtgtgaa	tattaattac	aagtgttcca	aaggaaacgt	960

411

gcctgcttct aaacctgggt gtgatttctt gaacgttgat 1000

<210> 477

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 10-289-201 : polymorphic base C or T

<220>

<221> misc_binding

<222> 481..500

<223> 10-289-201.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 10-289-201.mis2, potential complement

<220>

<221> primer_bind

<222> 307..324

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 700..719

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 10-289-201 potential probe

<400> 477

tgcaacctcc	acctcctggg	ttcaaacgat	tctcctgcct	cagcttcctg	agtagctggg	60
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cacaatgttg	gccaggctgg	tcttgaactc	ctgacctcaa	gtgattcacc	ccccctcggc	180
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gtgggaattt	gttgatgttg	aatcatgttg	aaacattttt	cttgagatta	ttggcacatt	300
tgtttccttc	ctatgtggat	tctctctata	ttctgaatat	aagtatcttg	tccaatatat	360
gttttgtgaa	tattttctca	gtcgtcgtac	aacatcttaa	gagactgctg	ttgtattttg	420
tgctttttct	ttttttttcc	caccccccta	tagtttttgc	tacttgctcg	ggctctgggt	480
acatatatgg	ccgtcaccta	yacttctggg	gatattcaga	agctgctaaa	aaacggtaag	540
gagaacccag	taattttgta	tttatgcaaa	aagtagcagg	ataaggtctg	ggtcagtttc	600
cttctcctga	gagatattaa	cagcactgtg	agttgtgggtg	gcaaaaagtaa	tccatactgt	660
ctgagggtcaa	gtcttgccag	ttcatacaca	attaggcatg	agatgggaaa	atgcaagtat	720
aaaactgtgc	actgaatgtg	gactctagtt	ccttgcaaaa	atTTTgcatt	gtctccagaa	780
agttaccgag	gaaataatcc	tgcttagcct	tgataatgct	ttgaatgttc	aaagaaacca	840
agtgatctct	atggctaggc	attcccttta	acttatgtga	tgagctaaaa	ttttcaaatt	900
gcaaaaatat	agaagttctg	gacagtgtta	acgataggac	agctaccttc	aggactctca	960
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<210> 478

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

412

<222> 501
 <223> 10-321-28 : polymorphic base A or G

 <220>
 <221> misc_binding
 <222> 481..500
 <223> 10-321-28.mis1, potential

 <220>
 <221> misc_binding
 <222> 502..521
 <223> 10-321-28.mis2, potential complement

 <220>
 <221> primer_bind
 <222> 474..491
 <223> upstream amplification primer

 <220>
 <221> primer_bind
 <222> 890..909
 <223> downstream amplification primer, complement

 <220>
 <221> misc_binding
 <222> 489..513
 <223> 10-321-28 potential probe

<400> 478
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 gctgctgctg ggggtggcccc gacccaagat ttacctggga atgggtagcc tcactcagaa 180
 ggggtgcccctg atgtgggggc acaggtgggt ctttggggac ccctcctggg tgggtgccagg 240
 gagagaatag cggcttcagc atgcttcggg gcagctgtaa aacgaggggg tcctgcaaag 300
 cgtgcagggg aagtgggtgc tgggtgggagc cccgggtcct agccagggt cttctgcctc 360
 cacggctgca gctttggagc gatgggtgtat tcaccacgga caggcatcat cctcaacaac 420
 gagctcctgg acttatgcga gcgatgcccc cgggggttcg gcaccacccc ctcacctggt 480
 gagaacaaaag cttcccacccc rgggtccaca agggcccccc accaggggag aggagggagg 540
 gggctgggct ggggttgcat gctaaccctt ggatgggtca ctgcacttgc caagacgctg 600
 tttgctcagc agtgagtggg gacaggggtg gtggagctcc cggaagggtg tggccccag 660
 ttccaggcga gcgttcccca tctccatgg tgcctccat cttgatcaac aaagcccagg 720
 ggtcgaagct agtgattggc ggggctggcg gggagctcat catctctgct gtggcccagg 780
 tgagtctggg gctcctggct cgagtgtctc ctctctgggc agcatactgt ctgactgtct 840
 ctggagtggg gatgtgagg ctgatgtagg gtagcagggt gcccccttc tccctgaaac 900
 cctcatctct cccccaggcc atcatgagca agctgtggct tggctttgac ctgagagcgg 960
 ccattgcagc ccccatcctg catgtcaaca gcaagggctg 1000

<210> 479
 <211> 422
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> allele
 <222> 265
 <223> 10-98-265 : polymorphic base A or G

<220>
 <221> misc_binding
 <222> 245..264
 <223> 10-98-265.mis1, potential

<220>

413

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<221> misc_binding
<222> 266..285
<223> 10-98-265.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..422
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 253..277
<223> 10-98-265 potential probe

<400> 479
ctgtcttcag gaaactcaca ggctagggcc agagaaagct aatgctggat acatacatag      60
cagatacttg ggaaatgatg gtttccttgt ttctgtcttc cttctttcct caccttacac      120
tacacggttc aggatttgac acagtcacca cagccatctc ctggagcctc atgtaccttg      180
tgaccaagcc tgagatacag aggaagatcc agaaggwgct gggtagatgg gggcccccaa      240
ccctatagcc aggagaagcc ttgaraccca ggttggttgt tcagtctaca aacacctgtt      300
atgtgcctgc tgtgtgcaag ccctgggcac acagtagtgc ctgcccttgc ctagaagatg      360
tgggagggtta gtggggtcgc agacttgtga atagacagtc ttacatagag tgacatgggg      420
ta                                                                                   422

<210> 480
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-157-115 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-157-115.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-157-115.mis2, potential complement

<220>
<221> primer_bind
<222> 387..407
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 833..853
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-157-115 potential probe

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<400> 480
gggagtgtctg ccgccatcat ggtcaccaaa agccaccacc ccctgcttgt gttggacagg      60
cgggtcatcaa ggcagaaccg actgacaacc tggtttctcc agtgcgagcc ttggcgatgg      120
aggccctctc gcacctgagg tgagctgggt tccccacctc accccatccc aaggggtagg      180
gaaaagtcca agaccattcc tcggtgctcc ttcaggggtt gtgcctcctt tttcctctcc      240
tccctctgta gcagggggtct cacttgccgg ctccccaggg caatgggcca gcctagatga      300
tgggggtcgg cctcagccac tcttttctat aattctcagc cagatttcaa gttgggtgct      360
tctccttgga tttatggcac atgggtgggc tgcctttcca ttgattgggg atattttgag      420
caaaataaca gtgataacac tgaagagcat tgcaagcatc cttcaagatg agtcaggctc      480
agtgagttag ttgaagggtc yagtcaacta tttgttgata ccactggtac aaaatgatct      540
aaagcccaag acttaccttc ctggagatgc caatccattg gtggggaggg ggaaagggga      600
agaagttagt gatattataa attagtattt aaagagtttg ggtcatctct aagaatacct      660
cccttatagg ggaagattca ttacttaggc gcatagcaga actatctgtt actttaagct      720
gcatcaaaca ggcagatttt aaaataaatg tcatgaacat caactaagca caatgatag      780
ctgagtactg aagggacaca gagatacata agacctagtc ccagcctttt aaggacttag      840
agataagaca gacacataca aacaggatta taggtcaaag ctgactaaca ggactgtgtt      900
tacaggtaaa cccacacaca catcagcaaa aaaatatctg agaacaaaaa aaaaggggct      960
actaacaaaa gcaactcagt ttatacaaaa ggagctatca                                1000

<210> 481
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-472-48 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-472-48.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-472-48.mis2, potential complement

<220>
<221> primer_bind
<222> 454..472
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 919..939
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-472-48 potential probe

<400> 481
atgaagcggt gttaacttgc ccctctctgc ccagcacctt ccttctctga cttcactgct      60
tggggagcat gctaattgatt ccttgggtgt aataactttg caattcttaa acaggtgaca      120
ttccaagcct gcagtatata tgaggccaga tacctttatg atcagttggc tactatctgt      180
ccaattgttg taagtagaaa ttacctctta ttttaaatac tacttcgtat gaaataagat      240
agcatgtgca gaatttactg acagtgtgct atttaagtcc agttaagacc tcagtcagag      300
atggactaat ataaatagta tgtaggttta ggtataatga actgagagtc tacactgtag      360
aagtttactc ttgctagtac aacattgatt tgtaaagtgt gaagtttgaa tgtggccatt      420

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415

ttccctcccc	catacttcat	gtcctcacat	tagagagagg	atgatttaag	tgaatcaaac	480
ccaaggaact	ggattcttcc	kggtatat	cactgtaaga	taggcacagg	tacatgtgct	540
ctgtatgggt	tgataaaca	tgcttttga	tcagaaatat	aactgcatgg	agcttttttt	600
agcatgtaag	tgacactttg	aatttgcagg	agctgacttt	tgtttgtttt	tagatggctt	660
tgagtgtctg	atctcccttt	taccgaggct	atgtgtcaga	cattgattgt	cgctggggag	720
tgatttctgc	atctgtagat	gatagaactc	gggaggagcg	aggactggag	gtgggaattg	780
tttttcctta	atagcccttt	taagtcaagc	aggtaaaatg	gatcttttgt	aactacttgc	840
aatttcagga	tgtctccctg	caatttttat	ctgaaatggg	gaaaaagatt	tggtctaggt	900
ggggagttaa	tttttatcgt	atgttgatgt	ctgtatttgt	tttagcttca	tttaaaatta	960
gtagtccgat	ttttctatat	tttggaagtg	ctgatggctg			1000

<210> 482

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-477-151 : polymorphic base G or A

<220>

<221> misc_binding

<222> 481..500

<223> 12-477-151.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-477-151.mis2, potential complement

<220>

<221> primer_bind

<222> 631..651

<223> upstream amplification primer, complement

<220>

<221> primer_bind

<222> 113..133

<223> downstream amplification primer

<220>

<221> misc_binding

<222> 489..513

<223> 12-477-151 potential probe

<220>

<221> misc_feature

<222> 419

<223> n=a, g, c or t

<400> 482

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gtgttagcag	atgtactcat	tgattgggtac	tgtctgtagt	ttcattttga	agcataaacc	180
tgagttaacat	tcagtaagac	tctgtatgtt	cagaaaagat	gtcacaatat	taattgagcc	240
tctaacaatca	ctatttatgt	ttctgaacat	ttttacatac	tgtcaaggca	tctgaatata	300
ttcttaaagt	tagaaaactg	tatatgaagc	attactgata	ttgctgggtat	tactggaaag	360
accatatcct	aacgagcttg	ctaattagta	ctctgtttct	acatttcatg	atataatcna	420
gggtgttttta	aaaaaacatt	ttaacagctt	tattgagtta	taattaacat	aaagttaact	480
gcacatatatt	aaaatgtaca	rtttggtaag	ttttgatata	tgtatacatc	ataaaatcac	540
ctctgataat	aagtatatcc	attatctcca	aaaatgtcat	catgcccttc	tggttaatttc	600
ttcctctggc	catcccatgc	agctgatttg	ctttctgtag	tttgcatttt	ctagattttc	660

416

atattttaaga aatcatagtt tgcatttgat atctagtttc atatacctag gaaatcatcc	720
agcatatcct cttttgggtct gccttcttag agtctacata aatattttga gatccatcca	780
tgttggtaca tgtgtcagta gttcattcct tttcgtcgct gagtaatatt tcattccatg	840
gttataccag tttgtttata cattcaccat ttgtgttgca ttcagttttt cactattata	900
aaaaaattat atgaacatta acatacaagt ttgtatgtat ggactaatgc ttttcttcat	960
cttattaccc taggagtagc gtgttggttaa ctttttaagg	1000

<210> 483

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 501

<223> 12-479-214 : polymorphic base G or T

<220>

<221> misc_binding

<222> 481..500

<223> 12-479-214.mis1, potential

<220>

<221> misc_binding

<222> 502..521

<223> 12-479-214.mis2, potential complement

<220>

<221> primer_bind

<222> 288..305

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 753..773

<223> downstream amplification primer, complement

<220>

<221> misc_binding

<222> 489..513

<223> 12-479-214 potential probe

<220>

<221> misc_feature

<222> 519

<223> n=a, g, c or t

<400> 483

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tcttagatct gcctcctctc ctgttactcc cccttctctc actccactcc agccatacta	120
gcctccttac tgttctttga ccactctagc ttccctccct gcctgaggcc tttgtatcag	180
ctgttccttc tgccctggaat ggctgaattt ccttacctcc ttcaaatcct tgcttaatcc	240
ctccttctca aagagacctc aacacctggc ccaccttctt taatataata ttctgacct	300
gcacctaac tcaacctgc atccctgct ctaactctgc tttttcataa tgtttatcaa	360
cttctgactt tctatatagt tatttattgt gcatgtgtgt tgccctccct tgctaaaatg	420
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agaacagtac ttgctgatg ktgagtgtc aatgaacant ttgcagaaaa atgaatgaat	540
gaatgccagg cattcataag cccacaaaaa aaatctatgt gtcattctac accttactg	600
tagcctaatt cttcatgtc caaaaagaaa gaagaggcat cattttctct gtttcctgtg	660
ctccacctct cgcacattcc ccactctcct agctgtgtgc tttccctga cttttttgtc	720
tagtaacaag aactccctgc ctggtgaaa ctggcatttt cttctcaatt tacttctaaa	780
tattagtgtc tttgtttacc ctgtgaagca gatggtaaca gttaatgtaa taaccagact	840
gtctcctctc tcttggttga cacagtagat gtcatgagcc atattttccc ttgggttat	900

417

ttgttaaata gaagacagga gatctgctat atgggtcaaca ttaggtctgg tcaactgcttt 960
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<210> 484

<211> 1000

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 500

<223> 10-290-328 : deletion of G

<220>

<221> misc_binding

<222> 481..499

<223> 10-290-328.misl, potential

<220>

<221> primer_bind

<222> 174..193

<223> upstream amplification primer

<220>

<221> primer_bind

<222> 573..592

<223> downstream amplification primer, complement

<400> 484

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gatgagctaa aattttcaaa ttgcaaaaat atagaagttc tggacagtgt taacgatagg 120
acagcctacc tcaggactct cagcttcctt attacagtcc agtttgtcac ttttctccct 180
catgtccact ctgcaggatc accggtttcc gactgagtct ggggattttg gccttgttga 240
ccctcctagg tgccctggga attgcaaaca gctttctgga tgaatatctg gacctcaata 300
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tgtttttctt gaaatggctt tgtagaaaca cacactttag agaatacatt tcctgtttaa 480
gaactgaaat ttgcttgggg taggtacatc catatcatca gtggaagtgt gttgtgccct 540
agtttttagaa atgcatgctg aagtcatgac cggtttgtga gggacacagc agcctgaccc 600
gtgtgctggc cgttccgagg actactgaca tatcctgcca ctctgactgc ttctctcttg 660
atggaaagtt tcagacagaa gctgataaag cagctgagcc ctttcattgg ttataggaaa 720
acaacagata ggaaggcatg tgggggacat caggcaaaaca catagagtag ccagagaagg 780
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<210> 485

<211> 49312

<212> DNA

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<221> misc_feature

<222> 5466..7466

<223> 5'regulatory region

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<222> 7467..7725

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<222> 45966..49312
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<220>
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<222> 7564
<223> 10-286-289 : polymorphic base G or C

<220>
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<223> 10-286-345 : polymorphic base A or T

<220>
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<223> 10-286-375 : polymorphic base A or G

<220>
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<223> 12-425-57 : polymorphic base A or G

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<223> 12-421-135 : insertion of T

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<223> 12-421-140 : polymorphic base A or G

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<223> 10-523-232 : polymorphic base C or T

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<223> 10-289-201 : polymorphic base C or T

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<223> 10-290-37 : polymorphic base C or T

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<223> 10-290-326 : polymorphic base A or G

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<223> 10-290-328 : deletion of G

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<223> 10-286.rp complement

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<222> 16839..16856
<223> 12-425.rp

<220>
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<222> 17297..17314
<223> 12-425.pu complement

<220>
<221> primer_bind
<222> 21456..21474
<223> 12-421.pu

<220>
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<222> 21886..21906
<223> 12-421.rp complement

<220>
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<222> 36740..36758
<223> 10-523.pu

<220>
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<222> 36997..37015
<223> 10-523.rp complement

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<222> 45020..45037
<223> 10-289.pu

<220>
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<222> 45413..45432
<223> 10-289.rp complement

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<222> 45705..45724
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<220>
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<222> 46104..46123
<223> 10-290.rp complement

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<222> 7545..7563
<223> 10-286-289.mis

<220>
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<222> 7565..7583
<223> 10-286-289.mis complement

<220>
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<222> 7600..7618
<223> 10-286-345.mis

<220>
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<222> 7620..7638
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<220>
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<222> 7650..7668
<223> 10-286-375.mis complement

<220>
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<222> 17239..17257
<223> 12-425-57.mis

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<222> 17259..17277
<223> 12-425-57.mis complement

<220>
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<222> 21576..21594
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<222> 21596..21614
<223> 12-421-140.mis complement

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<222> 36972..36990
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<223> 10-289-201.mis

<220>
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<222> 45215..45233
<223> 10-289-201.mis complement

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<223> 10-290-37.mis

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<223> 10-290-37.mis complement

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<222> 46030..46048
<223> 10-290-326.mis complement

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<223> 10-286-289.probe

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<222> 7607..7631
<223> 10-286-345.probe

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<222> 7637..7661
<223> 10-286-375.probe

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<222> 17246..17270
<223> 12-425-57.probe

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<222> 21583..21607

<223> 12-421-140.probe

<220>

<221> misc_binding

<222> 36959..36983

<223> 10-523-232.probe

<220>

<221> misc_binding

<222> 45202..45226

<223> 10-289-201.probe

<220>

<221> misc_binding

<222> 45729..45753

<223> 10-290-37.probe

<220>

<221> misc_binding

<222> 46017..46041

<223> 10-290-326.probe

<400> 485

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ctgtcct	tct	ctctccacc	caggcatact	gtaaactcct	ccagtggaaa	ccagcatttc	180
tcttggg	ctg	caccctgag	gcctacaggt	cccattctatt	cccagcctca	cctcttccct	240
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agaatgggaa	taatatatgc	actttactgt	ttgactatgc	agattagttg	agataattct		900
gtccagtggt	tggcataggg	cctagtacag	tgccttctgt	tgactggatt	tgggagctgg		960
cagggtgggc	atgagaggcc	cccatcagag	tgaggccttc	tcagcagccc	tgggctcatc		1020
cagaacacct	caggctctg	ggctccaggc	tgtcccgtct	cttgctgctc	tatcccagca		1080
agttcaacag	tcgagctctg	agcatggcct	acaggagcca	gggcacgttc	acgccagtga		1140
ccctgtttta	aagtatctaa	tacaaagtac	tattcagttt	aaaaagtgtg	taatgattcc		1200
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cattttctta atccagtcta tcattgttgg acatttgggt tggttccaag tctttgctat 49200
tgtgaataat gccgcaataa acatacgtgt gcatgtgtct ttatagcaag cagcatgatt 49260
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<210> 486

<211> 750

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..201

<220>

<221> CDS

<222> 202..645

<220>

<221> 3'UTR

<222> 646..750

<220>

<221> polyA_signal

<222> 721..726

<220>

<221> allele

<222> 98

<223> 10-286-289 : polymorphic base G or C

<220>

<221> allele

<222> 153

<223> 10-286-345 : polymorphic base A or T

<220>

<221> allele

<222> 183

<223> 10-286-375 : polymorphic base A or G

436

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<220>
<221> allele
<222> 426
<223> 10-523-232 : polymorphic base C or T
```

```
<220>
<221> allele
<222> 478
<223> 10-289-201 : polymorphic base C or T
```

```
<220>
<221> allele
<222> 526
<223> 10-290-37 : polymorphic base C or T
```

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<220>  
<221> misc_feature  
<222> 57  
<223> n=a, g, c or t
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[illegible]

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<210> 487
<211> 650
<212> DNA
<213> Homo sapiens
```

<220>

437

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<221> 5'UTR
<222> 1..201

<220>
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<222> 202..294

<220>
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<222> 295..650

<220>
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<222> 621..626

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<223> 10-286-289 : polymorphic base G or C

<220>
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<223> 10-286-345 : polymorphic base A or T

<220>
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<223> 10-286-375 : polymorphic base A or G

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<223> 10-523-232 : polymorphic base C or T

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<223> 10-289-201 : polymorphic base C or T

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<223> 10-290-37 : polymorphic base C or T

<220>
<221> misc_feature
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<223> n=a, g, c or t

<400> 487
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aaaggtcatt cagccgcttg aatcagcctt ttcccccsac ccggtcccca actttgttta      120
cccgataagg aaggtcagca ttcaaagtca agwagcgcca tttatcttcc cgtgcgctct      180
acraatagtt ccgtgagaaa g atg gcc ggg aac tcg atc ctg ctg gct gct      231
                               Met Ala Gly Asn Ser Ile Leu Leu Ala Ala
                               1           5           10
gtc tct att ctc tcg gcc tgt cag caa aac aaa act gtg tgg agt ttt      279
Val Ser Ile Leu Ser Ala Cys Gln Gln Asn Lys Thr Val Trp Ser Phe
                               15           20           25
atc cta tat tca taa ttacattgtg gatggctggg tggattttca aycaagtttt      334
Ile Leu Tyr Ser *
                               30

```

438

```

tgctacttgt ctgggtctgg tgtacatata tggcgcgtcac ctayacttct ggggatattc 394
agaagctgct aaaaaacgga tcaccggttt cygactgagt ctggggattt tggccttggt 454
gaccctccta ggtgccctgg gaattgcaaa cagctttctg gatgaatattc tggacctcaa 514
tattgccaaag aaactgaggg ggcaattcta actttttctc ttccctttaa tgcttgacaga 574
agctgttccc accatgaagg taatatggta tcatttggtta aataaaaaata aagtctttat 634
tctgtttttc ttgaaa 650

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<210> 488
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> 93
 <223> Xaa=Tyr or His

<220>
 <221> VARIANT
 <222> 109
 <223> Xaa=Arg or Stop

<400> 488

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Met Ala Gly Asn Ser Ile Leu Leu Ala Ala Val Ser Ile Leu Ser Ala
1          5          10          15
Cys Gln Gln Ser Tyr Phe Ala Leu Gln Val Gly Lys Ala Arg Leu Lys
20          25          30
Tyr Lys Val Thr Pro Pro Ala Val Thr Gly Ser Pro Glu Phe Glu Arg
35          40          45
Val Phe Arg Ala Gln Gln Asn Cys Val Glu Phe Tyr Pro Ile Phe Ile
50          55          60
Ile Thr Leu Trp Met Ala Gly Trp Tyr Phe Asn Gln Val Phe Ala Thr
65          70          75          80
Cys Leu Gly Leu Val Tyr Ile Tyr Gly Arg His Leu Xaa Phe Trp Gly
85          90          95
Tyr Ser Glu Ala Ala Lys Lys Arg Ile Thr Gly Phe Xaa Leu Ser Leu
100         105         110
Gly Ile Leu Ala Leu Leu Thr Leu Leu Gly Ala Leu Gly Ile Ala Asn
115         120         125
Ser Phe Leu Asp Glu Tyr Leu Asp Leu Asn Ile Ala Lys Lys Leu Arg
130         135         140
Arg Gln Phe
145

```

<210> 489
 <211> 30
 <212> PRT
 <213> Homo sapiens

<400> 489

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Met Ala Gly Asn Ser Ile Leu Leu Ala Ala Val Ser Ile Leu Ser Ala
1          5          10          15
Cys Gln Gln Asn Lys Thr Val Trp Ser Phe Ile Leu Tyr Ser
20          25          30

```

<210> 490
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 490

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ataaagatct gtgaccggca gccccagacc tgccctgcctt cctgacttct gttccagagc 60
aaaggtcatt cagccgcttg aatcagcctt ttccccccac ccggtcccca actttgttta 120

```


439

cccgataagg	aaggtcagca	ttcaaagtca	agaagcgcca	tttatcttcc	cgtgcgctct	180
acaaatagtt	ccgtgagaaa	gatggccggg	aactcgatcc	tgctggctgc	tgtctctatt	240
ctctcggcct	gtcagcaaag	ttatcttgct	ttgcaagttg	gaaaggcaag	attaaratac	300
aaagttacgc	ccccagcagt	cactgggtca	ccagagtttg	agagagtatt	tcgggca	357

<210> 491

<211> 274

<212> DNA

<213> Homo sapiens

<400> 491

ccccaacttt	gtttaccgga	taaggaaggt	cagcattcaa	agtcaagaag	cgccatttat	60
cttcccgctg	gctctacaaa	tagttccgtg	agaaagatgg	ccgggaactc	gacctgctg	120
gctgctgtct	ctattctctc	ggcctgtcag	caaaacaaaa	ctgtgtggag	ttttatccta	180
tattcataat	tacattgtgg	atggctgggt	ggtatttcaa	ccaagttttt	gctacttgtc	240
tgggtctggt	gtacatatat	ggccgtcact	tggg			274

<210> 492

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> sequencing oligonucleotide PrimerPU

<400> 492

tgtaaaacga cggccagt

18

<210> 493

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> sequencing oligonucleotide PrimerRP

<400> 493

caggaaacag ctatgacc

18